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(54) Title: HIGHLY CONSERVED GENES AND THEIR USE TO GENERATE SPECIES-SPECIFIC, GENUS-SPECIFIC, FAMILY-SPECIFIC, GROUP-SPECIFIC AND UNIVERSAL NUCLEIC ACID PROBES AND AMPLIFICATION PRIMERS TO RAPIDLY DETECT AND IDENTIFY ALGAL, ARCHAEAL, BACTERIAL, FUNGAL AND PARASITICAL MICROORGANISMS FROM CLINICAL SPECIMENS FOR DIAGNOSIS

(57) Abstract: Four highly conserved genes, encoding translation elongation factor Tu, translation elongation factor G, the catalytic subunit of proton-translocating ATPase and the RecA recombinase, are used to generate a sequence repertoire or bank and species-specific, genus-specific, family-specific, group-specific and universal nucleic acid probes and amplification primers to rapidly detect and identify algal, archaeal, bacterial, fungal and parasitological microorganisms from specimens for diagnosis. The detection of associated antimicrobial agents resistance and toxin genes are also under the scope of the present invention.

TITLE OF THE INVENTION

HIGHLY CONSERVED GENES AND THEIR USE TO GENERATE SPECIES-SPECIFIC, GENUS-SPECIFIC, FAMILY-SPECIFIC, GROUP-SPECIFIC AND UNIVERSAL NUCLEIC ACID PROBES AND AMPLIFICATION PRIMERS TO RAPIDLY DETECT AND IDENTIFY ALGAL, ARCHAEAL, BACTERIAL, FUNGAL AND PARASITICAL MICROORGANISMS FROM CLINICAL SPECIMENS FOR DIAGNOSIS

BACKGROUND OF THE INVENTION***Classical methods for the identification of microorganisms***

Microorganisms are classically identified by their ability to utilize different substrates as a source of carbon and nitrogen through the use of biochemical tests such as the API20E™ system (bioMérieux). For susceptibility testing, clinical microbiology laboratories use methods including disk diffusion, agar dilution and broth microdilution. Although identifications based on biochemical tests and antibacterial susceptibility tests are cost-effective, generally two days are required to obtain preliminary results due to the necessity of two successive overnight incubations to identify the bacteria from clinical specimens as well as to determine their susceptibility to antimicrobial agents. There are some commercially available automated systems (i.e. the MicroScan™ system from Dade Behring and the Vitek™ system from bioMérieux) which use sophisticated and expensive apparatus for faster microbial identification and susceptibility testing (Stager and Davis, 1992, Clin. Microbiol. Rev. 5:302-327). These systems require shorter incubation periods, thereby allowing most bacterial identifications and susceptibility testing to be performed in less than 6 hours. Nevertheless, these

faster systems always require the primary isolation of the bacteria or fungi as a pure culture, a process which takes at least 18 hours for a pure culture or 2 days for a mixed culture. So, the shortest time from sample reception to identification of the pathogen is around 24 hours. Moreover, fungi other than yeasts are often difficult or very slow to grow from clinical specimens. Identification must rely on labor-intensive techniques such as direct microscopic examination of the specimens and by direct and/or indirect immunological assays. Cultivation of most parasites is impractical in the clinical laboratory. Hence, microscopic examination of the specimen, a few immunological tests and clinical symptoms are often the only methods used for an identification that frequently remains presumptive.

The fastest bacterial identification system, the autoSCAN-Walk-Away™ system (Dade Behring) identifies both gram-negative and gram-positive bacterial species from standardized inoculum in as little as 2 hours and gives susceptibility patterns to most antibiotics in 5 to 6 hours. However, this system has a particularly high percentage (i.e. 3.3 to 40.5%) of non-conclusive identifications with bacterial species other than *Enterobacteriaceae* (Croizé J., 1995, Lett. Infectiol. 10:109-113; York *et al.*, 1992, J. Clin. Microbiol. 30:2903-2910). For *Enterobacteriaceae*, the percentage of non-conclusive identifications was 2.7 to 11.4%. The list of microorganisms identified by commercial systems based on classical identification methods is given in Table 15.

A wide variety of bacteria and fungi are routinely isolated and identified from clinical specimens in microbiology laboratories. Tables 1 and 2 give the incidence for the most commonly isolated bacterial and fungal pathogens from various types of clinical specimens. These pathogens are the main organisms associated with nosocomial and community-acquired human infections and are therefore considered the most clinically important.

Clinical specimens tested in clinical microbiology laboratories

Most clinical specimens received in clinical microbiology laboratories are urine and blood samples. At the microbiology laboratory of the Centre Hospitalier de l'Université Laval (CHUL), urine and blood account for approximately 55% and 30% of the specimens received, respectively (Table 3). The remaining 15% of clinical specimens comprise various biological fluids including sputum, pus, cerebrospinal fluid, synovial fluid, and others (Table 3). Infections of the urinary tract, the respiratory tract and the bloodstream are usually of bacterial etiology and require antimicrobial therapy. In fact, all clinical samples received in the clinical microbiology laboratory are tested routinely for the identification of bacteria and antibiotic susceptibility.

Conventional pathogen identification from clinical specimens

Urine specimens

The search for pathogens in urine specimens is so preponderant in the routine microbiology laboratory that a myriad of tests have been developed. However, the gold standard remains the classical semi-quantitative plate culture method in which 1 μL of urine is streaked on agar plates and incubated for 18-24 hours. Colonies are then counted to determine the total number of colony forming units (CFU) per liter of urine. A bacterial urinary tract infection (UTI) is normally associated with a bacterial count of 10^7 CFU/L or more in urine. However, infections with less than 10^7 CFU/L in urine are possible, particularly in patients with a high incidence of diseases or those catheterized (Stark and Maki, 1984, N. Engl. J. Med. **311**:560-564). Importantly, approximately 80% of urine specimens tested in clinical microbiology laboratories are considered negative (i.e. bacterial count of less than 10^7 CFU/L; Table 3). Urine specimens found positive by culture are further characterized using standard biochemical tests to identify the bacterial pathogen and are also tested for susceptibility to antibiotics. The biochemical and susceptibility testing normally require 18-24 hours of incubation.

Accurate and rapid urine screening methods for bacterial pathogens would allow a faster identification of negative specimens and a more efficient treatment and care management of patients. Several rapid identification methods (Uriscreen™, UTIscreen™, Flash Track™ DNA probes and others) have been compared to slower standard biochemical methods, which are based on culture of the bacterial pathogens. Although much faster, these rapid tests showed low sensitivities and poor specificities as well as a high number of false negative and false positive results (Koenig *et al.*, 1992, J. Clin. Microbiol. 30:342-345; Pezzlo *et al.*, 1992, J. Clin. Microbiol. 30:640-684).

Blood specimens

The blood specimens received in the microbiology laboratory are always submitted for culture. Blood culture systems may be manual, semi-automated or completely automated. The BACTEC™ system (from Becton Dickinson) and the BacTAlert™ system (from Organon Teknika Corporation) are the two most widely used automated blood culture systems. These systems incubate blood culture bottles under optimal conditions for growth of most bacteria. Bacterial growth is monitored continuously to detect early positives by using highly sensitive bacterial growth detectors. Once growth is detected, a Gram stain is performed directly from the blood culture and then used to inoculate nutrient agar plates. Subsequently, bacterial identification and susceptibility testing are carried out from isolated bacterial colonies with automated systems as described previously. Blood culture bottles are normally reported as negative if no growth is detected after an incubation of 6 to 7 days. Normally, the vast majority of blood cultures are reported negative. For example, the percentage of negative blood cultures at the microbiology laboratory of the CHUL for the period February 1994-January 1995 was 93.1% (Table 3).

Other clinical samples

Upon receipt by the clinical microbiology laboratory, all body fluids other than blood and urine that are from normally sterile sites (i.e. cerebrospinal, synovial, pleural, pericardial and others) are processed for direct microscopic examination and subsequent culture. Again, most clinical samples are negative for culture (Table 3). In all these normally sterile sites, tests for the universal detection of algae, archaea, bacteria, fungi and parasites would be very useful.

Regarding clinical specimens which are not from sterile sites such as sputum or stool specimens, the laboratory diagnosis by culture is more problematic because of the contamination by the normal flora. The bacterial or fungal pathogens potentially associated with the infection are grown and separated from the colonizing microbes using selective methods and then identified as described previously. Of course, the DNA-based universal detection of bacteria would not be useful for the diagnosis of bacterial infections at these non-sterile sites. On the other hand, DNA-based assays for species or genus or family or group detection and identification as well as for the detection of antimicrobial agents resistance genes from these specimens would be very useful and would offer several advantages over classical identification and susceptibility testing methods.

DNA-based assays with any specimen

There is an obvious need for rapid and accurate diagnostic tests for the detection and identification of algae, archaea, bacteria, fungi and parasites directly from clinical specimens. DNA-based technologies are rapid and accurate and offer a great potential to improve the diagnosis of infectious diseases (Persing *et al.*, 1993, Diagnostic Molecular Microbiology: Principles and Applications, American Society for Microbiology, Washington, D.C.; Bergeron and Ouellette, 1995, Infection 23:69-72; Bergeron and Ouellette, 1998, J Clin Microbiol. 36:2169-72). The DNA probes and amplification primers which are objects of the present invention are applicable for the detection and identification of algae, archaea, bacteria, fungi, and parasites directly from any clinical specimen such as blood,

urine, sputum, cerebrospinal fluid, pus, genital and gastro-intestinal tracts, skin or any other type of specimens (Table 3). These assays are also applicable to detection from microbial cultures (e.g. blood cultures, bacterial or fungal colonies on nutrient agar, or liquid cell cultures in nutrient broth). The DNA-based tests proposed in this invention are superior in terms of both rapidity and accuracy to standard biochemical methods currently used for routine diagnosis from any clinical specimens in microbiology laboratories. Since these tests can be performed in one hour or less, they provide the clinician with new diagnostic tools which should contribute to a better management of patients with infectious diseases. Specimens from sources other than humans (e.g. other primates, birds, plants, mammals, farm animals, livestock, food products, environment such as water or soil, and others) may also be tested with these assays.

A high percentage of culture-negative specimens

Among all the clinical specimens received for routine diagnosis, approximately 80% of urine specimens and even more (around 95%) for other types of normally sterile clinical specimens are negative for the presence of bacterial pathogens (Table 3). It would also be desirable, in addition to identify bacteria at the species or genus or family or group level in a given specimen, to screen out the high proportion of negative clinical specimens with a DNA-based test detecting the presence of any bacterium (i.e. universal bacterial detection). As disclosed in the present invention, such a screening test may be based on DNA amplification by PCR of a highly conserved genetic target found in all bacteria. Specimens negative for bacteria would not be amplified by this assay. On the other hand, those that are positive for any bacterium would give a positive amplification signal. Similarly, highly conserved genes of fungi and parasites could serve not only to identify particular species or genus or family or group but also to detect the presence of any fungi or parasite in the specimen.

Towards the development of rapid DNA-based diagnostic tests

A rapid diagnostic test should have a significant impact on the management of infections. DNA probe and DNA amplification technologies offer several advantages over conventional methods for the identification of pathogens and antimicrobial agents resistance genes from clinical samples (Persing *et al.*, 1993, Diagnostic Molecular Microbiology: Principles and Applications, American Society for Microbiology, Washington, D.C.; Ehrlich and Greenberg, 1994, PCR-based Diagnostics in Infectious Disease, Blackwell Scientific Publications, Boston, MA). There is no need for culture of the pathogens, hence the organisms can be detected directly from clinical samples, thereby reducing the time associated with the isolation and identification of pathogens. Furthermore, DNA-based assays are more accurate for microbial identification than currently used phenotypic identification systems which are based on biochemical tests and/or microscopic examination. Commercially available DNA-based technologies are currently used in clinical microbiology laboratories, mainly for the detection and identification of fastidious bacterial pathogens such as *Mycobacterium tuberculosis*, *Chlamydia trachomatis*, *Neisseria gonorrhoeae* as well as for the detection of a variety of viruses (Tang Y. and Persing D. H., Molecular detection and identification of microorganisms, In: P. Murray *et al.*, 1999, Manual of Clinical Microbiology, ASM press, 7th edition, Washington D.C.). There are also other commercially available DNA-based assays which are used for culture confirmation assays.

Others have developed DNA-based tests for the detection and identification of bacterial pathogens which are objects of the present invention, for example: *Staphylococcus* sp. (US patent serial no. 5,437,978), *Neisseria* sp. (US patent serial no. 5,162,199 and European patent serial no. 0,337,896,131) and *Listeria monocytogenes* (US patent serial nos. 5,389,513 and 5,089,386). However, the diagnostic tests described in these patents are based either on rRNA genes or on genetic targets different from those described in the present invention. To our knowledge there are only four patents published by others mentioning the use of

any of the four highly conserved gene targets described in the present invention for diagnostic purposes (PCT international publication number WO92/03455 and WO00/14274, European patent publication number 0 133 671 B1, and European patent publication number 0 133 288 A2). WO92/03455 is focused on the inhibition of *Candida* species for therapeutic purposes. It describes antisense oligonucleotide probes hybridizing to *Candida* messenger RNA. Two of the numerous mRNA proposed as targets are coding for translation elongation factor 1 (tef1) and the beta subunit of ATPase. DNA amplification or hybridization are not under the scope of their invention and although diagnostic use is briefly mentioned in the body of the application, no specific claim is made regarding diagnostics. WO00/14274 describes the use of bacterial *recA* gene for identification and speciation of bacteria of the *Burkholderia cepacia* complex. Specific claims are made on a method for obtaining nucleotide sequence information for the *recA* gene from the target bacteria and a following comparison with a standard library of nucleotide sequence information (claim 1), and on the use of PCR for amplification of the *recA* gene in a sample of interest (claims 4 to 7, and 13). However, the use of a discriminatory restriction enzyme in a RFLP procedure is essential to fulfill the speciation and WO00/14274 did not mention that multiple *recA* probes could be used simultaneously. Patent EP 0 133 288 A2 describes and claims the use of bacterial *tuf* (and *fus*) sequence for diagnostics based on hybridization of a *tuf* (or *fus*) probe with bacterial DNA. DNA amplification is not under the scope of EP 0 133 288 A2. Nowhere it is mentioned that multiple *tuf* (or *fus*) probes could be used simultaneously. No mention is made regarding speciation using *tuf* (or *fus*) DNA nucleic acids and/or sequences. The sensitivities of the *tuf* hybridizations reported are 1×10^6 bacteria or 1-100 ng of DNA. This is much less sensitive than what is achieved by our assays using nucleic acid amplification technologies.

Although there are phenotypic identification methods which have been used for more than 125 years in clinical microbiology laboratories, these methods do not provide information fast enough to be useful in the initial management of patients.

There is a need to increase the speed of the diagnosis of commonly encountered bacterial, fungal and parasitical infections. Besides being much faster, DNA-based diagnostic tests are more accurate than standard biochemical tests presently used for diagnosis because the microbial genotype (e.g. DNA level) is more stable than the phenotype (e.g. physiologic level).

----- Bacteria, fungi and parasites encompass numerous well-known microbial pathogens. Other microorganisms could also be pathogens or associated with human diseases. For example, achlorophyllous algae of the *Prototheca* genus can infect humans. Archae, especially methanogens, are present in the gut flora of humans (Reeve, J.H., 1999, J. Bacteriol. **181**:3613-3617). However, methanogens have been associated to pathologic manifestations in the colon, vagina, and mouth (Belay *et al.*, 1988, Appl. Enviro. Microbiol. **54**:600-603; Belay *et al.*, 1990, J. Clin. Microbiol. **28**:1666-1668; Weaver *et al.*, 1986, Gut **27**:698-704).

In addition to the identification of the infectious agent, it is often desirable to identify harmful toxins and/or to monitor the sensitivity of the microorganism to antimicrobial agents. As revealed in this invention, genetic identification of the microorganism could be performed simultaneously with toxin and antimicrobial agents resistance genes.

Knowledge of the genomic sequences of algal, archaeal, bacterial, fungal and parasitical species continuously increases as testified by the number of sequences available from public databases such as GenBank. From the sequences readily available from those public databases, there is no indication therefrom as to their potential for diagnostic purposes. For determining good candidates for diagnostic purposes, one could select sequences for DNA-based assays for (i) the species-specific detection and identification of commonly encountered bacterial, fungal and parasitical pathogens, (ii) the genus-specific detection and identification of commonly encountered bacterial, fungal or parasitical pathogens, (iii) the family-specific detection and identification of commonly encountered bacterial, fungal or parasitical pathogens, (iv) the group-specific detection and identification of commonly encountered bacterial, fungal or parasitical pathogens, (v) the

universal detection of algal, archaeal, bacterial, fungal or parasitical pathogens, and/or (vi) the specific detection and identification of antimicrobial agents resistance genes, and/or (vii) the specific detection and identification of bacterial toxin genes. All of the above types of DNA-based assays may be performed directly from any type of clinical specimens or from a microbial culture.

~~In our assigned U.S. patent 6,001,564 and our WO98/20157 patent~~ publication, we described DNA sequences suitable for (i) the species-specific detection and identification of clinically important bacterial pathogens, (ii) the universal detection of bacteria, and (iii) the detection of antimicrobial agents resistance genes.

The WO98/20157 patent publication describes proprietary *tuf* DNA sequences as well as *tuf* sequences selected from public databases (in both cases, fragments of at least 100 base pairs), as well as oligonucleotide probes and amplification primers derived from these sequences. All the nucleic acid sequences described in that patent publication can enter in the composition of diagnostic kits or products and methods capable of a) detecting the presence of bacteria and fungi b) detecting specifically at the species, genus, family or group levels, the presence of bacteria and fungi and antimicrobial agents resistance genes associated with these pathogens. However, these methods and kits need to be improved, since the ideal kit and method should be capable of diagnosing close to 100% of microbial pathogens and associated antimicrobial agents resistance genes and toxins genes. For example, infections caused by *Enterococcus faecium* have become a clinical problem because of its resistance to many antibiotics. Both the detection of these bacteria and the evaluation of their resistance profiles are desirable. Besides that, novel DNA sequences (probes and primers) capable of recognizing the same and other microbial pathogens or the same and additional antimicrobial agents resistance genes are also desirable to aim at detecting more target genes and complement our earlier patent applications.

The present invention improves the assigned application by disclosing new proprietary *tuf* nucleic acids and/or sequences as well as describing new ways to

obtain *tuf* nucleic acids and/or sequences. In addition we disclose new proprietary *atpD* and *recA* nucleic acids and/or sequences. In addition, new uses of *tuf*, *atpD* and *recA* DNA nucleic acids and/or sequences selected from public databases (Table 11) are disclosed.

Highly conserved genes for identification and diagnostics

Highly conserved genes are useful for identification of microorganisms. For bacteria, the most studied genes for identification of microorganisms are the universally conserved ribosomal RNA genes (rRNA). Among those, the principal targets used for identification purposes are the small subunit (SSU) ribosomal 16S rRNA genes (in prokaryotes) and 18S rRNA genes (in eukaryotes) (Relman and Persing, Genotyping Methods for Microbial Identification, *In*: D.H. Persing, 1996, PCR Protocols for Emerging Infectious Diseases, ASM Press, Washington D.C.). The rRNA genes are also the most commonly used targets for universal detection of bacteria (Chen *et al.*, 1988, FEMS Microbiol. Lett. **57**:19-24; McCabe *et al.*, 1999, Mol. Genet. Metabol. **66**:205-211) and fungi (Van Burik *et al.*, 1998, J. Clin. Microbiol. **36**:1169-1175).

However, it may be difficult to discriminate between closely related species when using primers derived from the 16S rRNA. In some instances, 16S rRNA sequence identity may not be sufficient to guarantee species identity (Fox *et al.*, 1992, Int. J. Syst. Bacteriol. **42**:166-170) and it has been shown that inter-operon sequence variation as well as strain to strain variation could undermine the application of 16S rRNA for identification purposes (Clayton *et al.*, 1995, Int. J. Syst. Bacteriol. **45**:595-599). The heat shock proteins (HSP) are another family of very conserved proteins. These ubiquitous proteins in bacteria and eukaryotes are expressed in answer to external stress agents. One of the most described of these HSP is HSP 60. This protein is very conserved at the amino acid level, hence it has been useful for phylogenetic studies. Similar to 16S rRNA, it would be difficult to

discriminate between species using the HSP 60 nucleotide sequences as a diagnostic tool. However, Goh *et al.* identified a highly conserved region flanking a variable region in HSP 60, which led to the design of universal primers amplifying this variable region (Goh *et al.*, US patent serial no. 5,708,160). The sequence variations in the resulting amplicons were found useful for the design of species-specific assays.

SUMMARY OF THE INVENTION

It is an object of the present invention to provide a specific, ubiquitous and sensitive method using probes and/or amplification primers for determining the presence and/or amount of nucleic acids:

- from any algal, archaeal, bacterial, fungal or parasitical species in any sample suspected of containing said nucleic acids, and optionally,
- from specific microbial species or genera selected from the group consisting of the species or genera listed in Table 4, and optionally,
- from an antimicrobial agents resistance gene selected from the group consisting of the genes listed in Table 5, and optionally,
- from a toxin gene selected from the group consisting of the genes listed in Table 6,

wherein each of said nucleic acids or a variant or part thereof comprises a selected target region hybridizable with said probes or primers;

said method comprising the steps of contacting said sample with said probes or primers and detecting the presence and/or amount of hybridized probes or amplified products as an indication of the presence and/or amount of said any

microbial species, specific microbial species or genus or family or group and antimicrobial agents resistance gene and/or toxin gene.

In a specific embodiment, a similar method directed to each specific microbial species or genus or family or group detection and identification, antimicrobial agents resistance genes detection, toxin genes detection, and universal bacterial detection, separately, is provided.

In a more specific embodiment, the method makes use of DNA fragments from conserved genes (proprietary sequences and sequences obtained from public databases), selected for their capacity to sensitively, specifically and ubiquitously detect the targeted algal, archaeal, bacterial, fungal or parasitical nucleic acids.

In a particularly preferred embodiment, oligonucleotides of at least 12 nucleotides in length have been derived from the longer DNA fragments, and are used in the present method as probes or amplification primers. To be a good diagnostic candidate, an oligonucleotide of at least 12 nucleotides should be capable of hybridizing with nucleic acids from given microorganism(s), and with substantially all strains and representatives of said microorganism(s); said oligonucleotide being species-, or genus-, or family-, or group-specific or universal.

In another particularly preferred embodiment, oligonucleotides primers and probes of at least 12 nucleotides in length are designed for their specificity and ubiquity based upon analysis of our databases of *tuf*, *atpD* and *recA* sequences. These databases are generated using both proprietary and public sequence information. Altogether, these databases form a sequence repertory useful for the design of primers and probes for the detection and identification of algal, archaeal, bacterial, fungal and parasitical microorganisms. The repertory can also be subdivided into subrepertories for sequence analysis leading to the design of various primers and probes.

The *tuf*, *atpD* and *recA* sequences databases as a product to assist the design of oligonucleotides primers and probes for the detection and identification of algal, archaeal, bacterial, fungal and parasitical microorganisms are also covered.

The proprietary oligonucleotides (probes and primers) are also another object of this invention.

Diagnostic kits comprising probes or amplification primers such as those for the detection of a microbial species or genus or family or phylum or group selected from the following list consisting of *Abiotrophia adiacens*, *Acinetobacter baumannii*, *Actinomycetae*, *Bacteroides*, *Cytophaga* and *Flexibacter* phylum, *Bacteroides fragilis*, *Bordetella pertussis*, *Bordetella* sp., *Campylobacter jejuni* and *C. coli*, *Candida albicans*, *Candida dubliniensis*, *Candida glabrata*, *Candida guilliermondii*, *Candida krusei*, *Candida lusitaniae*, *Candida parapsilosis*, *Candida tropicalis*, *Candida zeylanoides*, *Candida* sp., *Chlamydia pneumoniae*, *Chlamydia trachomatis*, *Clostridium* sp., *Corynebacterium* sp., *Cryptococcus neoformans*, *Cryptococcus* sp., *Cryptosporidium parvum*, *Entamoeba* sp., *Enterobacteriaceae* group, *Enterococcus casseliflavus-flavescens-gallinarum* group, *Enterococcus faecalis*, *Enterococcus faecium*, *Enterococcus gallinarum*, *Enterococcus* sp., *Escherichia coli* and *Shigella* sp. group, *Gemella* sp., *Giardia* sp., *Haemophilus influenzae*, *Klebsiella pneumoniae*, *Legionella pneumophila*, *Legionella* sp., *Leishmania* sp., *Mycobacteriaceae* family, *Mycoplasma pneumoniae*, *Neisseria gonorrhoeae*, platelets contaminants group (see Table 14), *Pseudomonas aeruginosa*, *Pseudomonads* group, *Staphylococcus aureus*, *Staphylococcus epidermidis*, *Staphylococcus haemolyticus*, *Staphylococcus hominis*, *Staphylococcus saprophyticus*, *Staphylococcus* sp., *Streptococcus agalactiae*, *Streptococcus pneumoniae*, *Streptococcus pyogenes*, *Streptococcus* sp., *Trypanosoma brucei*, *Trypanosoma cruzi*, *Trypanosoma* sp., *Trypanosomatidae* family, are also objects of the present invention.

Diagnostic kits further comprising probes or amplification primers for the detection of an antimicrobial agents resistance gene selected from the group listed in Table 5 are also objects of this invention.

Diagnostic kits further comprising probes or amplification primers for the detection of a toxin gene selected from the group listed in Table 6 are also objects of this invention.

Diagnostic kits further comprising probes or amplification primers for the detection of any other algal, archaeal, bacterial, fungal or parasitical species than those specifically listed herein, comprising or not comprising those for the detection of the specific microbial species or genus or family or group listed above, and further comprising or not comprising probes and primers for the antimicrobial agents resistance genes listed in Table 5, and further comprising or not comprising probes and primers for the toxin genes listed in Table 6 are also objects of this invention.

In a preferred embodiment, such a kit allows for the separate or the simultaneous detection and identification of the above-listed microbial species or genus or family or group; or universal detection of algae, archaea, bacteria, fungi or parasites; or antimicrobial agents resistance genes; or toxin genes; or for the detection of any microorganism (algae, archaea, bacteria, fungi or parasites).

In the above methods and kits, probes and primers are not limited to nucleic acids and may include, but are not restricted to analogs of nucleotides such as: inosine, 3-nitropyrrole nucleosides (Nichols *et al.*, 1994, Nature **369**:492-493), Linked Nucleic Acids (LNA) (Koskin *et al.*, 1998, Tetrahedron **54**:3607-3630), and Peptide Nucleic Acids (PNA) (Egholm *et al.*, 1993, Nature **365**:566-568).

In the above methods and kits, amplification reactions may include but are not restricted to: a) polymerase chain reaction (PCR), b) ligase chain reaction (LCR), c) nucleic acid sequence-based amplification (NASBA), d) self-sustained sequence replication (3SR), e) strand displacement amplification (SDA), f) branched DNA signal amplification (bDNA), g) transcription-mediated amplification (TMA), h) cycling probe technology (CPT), i) nested PCR, j) multiplex PCR, k) solid phase amplification (SPA), l) nuclease dependent signal amplification (NDSA), m) rolling circle amplification technology (RCA), n) Anchored strand displacement amplification, o) Solid-phase (immobilized) rolling circle amplification.

In the above methods and kits, detection of the nucleic acids of target genes may include real-time or post-amplification technologies. These detection

technologies can include, but are not limited to, fluorescence resonance energy transfer (FRET)-based methods such as adjacent hybridization to FRET probes (including probe-probe and probe-primer methods), TaqMan, Molecular Beacons, scorpions, nanoparticle probes and Sunrise (Amplifluor). Other detection methods include target genes nucleic acids detection via immunological methods, solid phase hybridization methods on filters, chips or any other solid support, whether the hybridization is monitored by fluorescence, chemiluminescence, potentiometry, mass spectrometry, plasmon resonance, polarimetry, colorimetry, or scanometry. Sequencing, including sequencing by dideoxy termination or sequencing by hybridization, e.g. sequencing using a DNA chip, is another possible method to detect and identify the nucleic acids of target genes.

In a preferred embodiment, a PCR protocol is used for nucleic acid amplification, in diagnostic method as well as in method of construction of a repertory of nucleic acids and deduced sequences.

In a particularly preferred embodiment, a PCR protocol is provided, comprising, an initial denaturation step of 1-3 minutes at 95 °C, followed by an amplification cycle including a denaturation step of one second at 95 °C and an annealing step of 30 seconds at 45-65°C, without any time allowed specifically for the elongation step. This PCR protocol has been standardized to be suitable for PCR reactions with most selected primer pairs, which greatly facilitates the testing because each clinical sample can be tested with universal, species-specific, genus-specific, antimicrobial agents resistance gene and toxin gene PCR primers under uniform cycling conditions. Furthermore, various combinations of primer pairs may be used in multiplex PCR assays.

It is also an object of the present invention that *tuf*, *atpD* and *recA* sequences could serve as drug targets and these sequences and means to obtain them revealed in the present invention can assist the screening, design and modeling of these drugs.

It is also an object of the present invention that *tuf*, *atpD* and *recA* sequences could serve for vaccine purposes and these sequences and means to obtain them

revealed in the present invention can assist the screening, design and modeling of these vaccines.

We aim at developing a universal DNA-based test or kit to screen out rapidly samples which are free of algal, archaeal, bacterial, fungal or parasitical cells. This test could be used alone or combined with more specific identification tests to detect and identify the above algal and/or archaeal and/or bacterial and/or fungal and/or parasitical species and/or genera and/or family and/or group and to determine rapidly the bacterial resistance to antibiotics and/or presence of bacterial toxins. Although the sequences from the selected antimicrobial agents resistance genes are available from public databases and have been used to develop DNA-based tests for their detection, our approach is unique because it represents a major improvement over current diagnostic methods based on bacterial cultures. Using an amplification method for the simultaneous or independent or sequential microbial detection-identification and antimicrobial resistance genes detection, there is no need for culturing the clinical sample prior to testing. Moreover, a modified PCR protocol has been developed to detect all target DNA sequences in approximately one hour under uniform amplification conditions. This procedure should save lives by optimizing treatment, should diminish antimicrobial agents resistance because less antibiotics will be prescribed, should reduce the use of broad spectrum antibiotics which are expensive, decrease overall health care costs by preventing or shortening hospitalizations, and side effects of drugs, and decrease the time and costs associated with clinical laboratory testing.

In another embodiment, sequence repertories and ways to obtain them for other gene targets are also an object of this invention, such is the case for the *hexA* nucleic acids and/or sequences of *Streptococci*.

In yet another embodiment, for the detection of mutations associated with antibiotic resistance genes, we built repertories to distinguish between point mutations reflecting only gene diversity and point mutations involved in resistance. Such repertories and ways to obtain them for *pbp1a*, *pbp2b* and *pbp2x* genes of sensitive and penicillin-resistant *Streptococcus pneumoniae* and also for *gyrA* and

parC gene fragments from various bacterial species are also an object of the present invention.

The diagnostic kits, primers and probes mentioned above can be used to identify algae, archaea, bacteria, fungi, parasites, antimicrobial agents resistance genes and toxin genes on any type of sample, whether said diagnostic kits, primers and probes are used for *in vitro* or *in situ* applications. The said samples may include but are not limited to: any clinical sample, any environment sample, any microbial culture, any microbial colony, any tissue, and any cell line.

It is also an object of the present invention that said diagnostic kits, primers and probes can be used alone or in conjunction with any other assay suitable to identify microorganisms, including but not limited to: any immunoassay, any enzymatic assay, any biochemical assay, any lysotypic assay, any serological assay, any differential culture medium, any enrichment culture medium, any selective culture medium, any specific assay medium, any identification culture medium, any enumeration culture medium, any cellular stain, any culture on specific cell lines, and any infectivity assay on animals.

In the methods and kits described herein below, the oligonucleotide probes and amplification primers have been derived from larger sequences (i.e. DNA fragments of at least 100 base pairs). All DNA fragments have been obtained either from proprietary fragments or from public databases. DNA fragments selected from public databases are newly used in a method of detection according to the present invention, since they have been selected for their diagnostic potential.

In another embodiment, the amino acid sequences translated from the repertory of *tuf*, *atpD* and *recA* nucleic acids and/or sequences are also an object of the present invention.

It is clear to the individual skilled in the art that other oligonucleotide sequences appropriate for (i) the universal detection of algae, archaea, bacteria, fungi or parasites, (ii) the detection and identification of the above microbial species or genus or family or group, and (iii) the detection of antimicrobial agents resistance genes, and (iv) the detection of toxin genes, other than those listed in

Annexes I to III, XXI to XXII, XXXII to XXXVII, XXXIX to XLI, and XLIII to LIV may also be derived from the proprietary fragments or selected public database sequences. For example, the oligonucleotide primers or probes may be shorter or longer than the ones chosen; they may also be selected anywhere else in the proprietary DNA fragments or in the sequences selected from public databases; they may be also variants of the same oligonucleotide. If the target DNA or a variant thereof hybridizes to a given oligonucleotide, or if the target DNA or a variant thereof can be amplified by a given oligonucleotide PCR primer pair, the converse is also true; a given target DNA may hybridize to a variant oligonucleotide probe or be amplified by a variant oligonucleotide PCR primer. Alternatively, the oligonucleotides may be designed from any DNA fragment sequences for use in amplification methods other than PCR. Consequently, the core of this invention is the identification of universal, species-specific, genus-specific, family-specific, group-specific, resistance gene-specific, toxin gene-specific genomic or non-genomic DNA fragments which are used as a source of specific and ubiquitous oligonucleotide probes and/or amplification primers. Although the selection and evaluation of oligonucleotides suitable for diagnostic purposes requires much effort, it is quite possible for the individual skilled in the art to derive, from the selected DNA fragments, oligonucleotides other than the ones listed in Annexes I to III, XXI to XXII, XXXII to XXXVII, XXXIX to XLI, and XLIII to LIV which are suitable for diagnostic purposes. When a proprietary fragment or a public databases sequence is selected for its specificity and ubiquity, it increases the probability that subsets thereof will also be specific and ubiquitous.

Since a high percentage of clinical specimens are negative for bacteria (Table 3), DNA fragments having a high potential for the selection of universal oligonucleotide probes or primers were selected from proprietary and public database sequences. The amplification primers were selected from genes highly conserved in algae, archaea, bacteria, fungi and parasites, and are used to detect the presence of any algal, archaeal, bacterial, fungal or parasitical pathogen in clinical specimens in order to determine rapidly whether it is positive or negative for algae,

archaea, bacteria, fungi or parasites. The selected genes, designated *tuf*, *fus*, *atpD* and *recA*, encode respectively 2 proteins (elongation factors Tu and G) involved in the translational process during protein synthesis, a protein (beta subunit) responsible for the catalytic activity of proton pump ATPase and a protein responsible for the homologous recombination of genetic material. The alignments of *tuf*, *atpD* and *recA* sequences used to derive the universal primers include both proprietary and public database sequences. The universal primer strategy allows the rapid screening of the numerous negative clinical specimens (around 80% of the specimens received, see Table 3) submitted for microbiological testing.

Table 4 provides a list of the archaeal, bacterial, fungal and parasitical species for which *tuf* and/or *atpD* and/or *recA* nucleic acids and/or sequences are revealed in the present invention. Tables 5 and 6 provide a list of antimicrobial agents resistance genes and toxin genes selected for diagnostic purposes. Table 7 provides the origin of *tuf*, *atpD* and *recA* nucleic acids and/or sequences listed in the sequence listing. Tables 8-10 and 12-14 provide lists of species used to test the specificity, ubiquity and sensitivity of some assays described in the examples. Table 11 provides a list of microbial species for which *tuf* and/or *atpD* and/or *recA* sequences are available in public databases. Table 15 lists the microorganisms identified by commercial systems. Tables 16-18 are part of Example 42, whereas Tables 19-20 are part of Example 43. Tables 21-22 illustrate Example 44, whereas Tables 23-25 illustrate Example 45.

In accordance with the present invention is provided a method for generating a repertory of nucleic acids of *tuf*, *fus*, *atpD* and/or *recA* genes from which are derived probes or primers, or both, useful for the detection of one, more than one related microorganisms, or substantially all microorganisms of a group selected from algae, archaea, bacteria, fungi and parasites, which comprises the step of:

- amplifying the nucleic acids of a plurality of determined algal, archaeal, bacterial, fungal and parasitical species with any combination of the primer pairs defined in SEQ ID NOs.: 558-561, 562-574, 636-655, 664, 681-683, 696-697, 699-700, 708, 812-815, 911-917, 919-922, 935-938, 1203-1207, 1212-1213, 1221-1229, 1605-1606, 1974-1984, 1999- 2003, 2282-2285.

The terms "related microorganisms" are intended to cover microorganisms that share a common evolutive profile up to the speciation e.g. those that belong to a species, a genus, a family or a phylum. The same terms are also intended to cover a group of different species that are grouped for a specific reason, for example, because they all have a common host tissue or cell. In one specific example, a group of microorganisms potentially found in platelet preparations are grouped together and are considered "related" organisms for the purpose of their simultaneous detection in that particular type of sample.

The repertories *per se* of nucleic acids and of sequences derived therefrom are also provided, as well as "gene banks" comprising these repertories.

For generating sequences of probes or primers, the above method is reproduced or one may start from the sequence repertory or gene bank itself, and the following steps are added:

- aligning a subset of nucleic acid sequences of said repertory,
- locating nucleic acid stretches that are present in the nucleic acids of strains or representatives of said one, more than one related microorganisms, or substantially all microorganisms of said group, and not present in the nucleic acid sequences of other microorganisms, and

deriving consensus nucleic acid sequences useful as probes or primers from said stretches.

Once the sequences of probes or primers are designed, they are converted into real molecules by nucleic acid synthesis.

From the above methods and resulting repertoires, probes and primers for the universal detection of any one of alga, archaeon, bacterium, fungus and parasite are obtainable.

More specifically, the following probes or primers having the sequence defined in SEQ ID NOs.: 543, 556-574, 636-655, 658-661, 664, 681-683, 694, 696, 697, 699, 700, 708, 812-815, 911-917, 919-922, 935-938, 1203-1207, 1212-1213, 1221-1229, 1605-1606, 1974-1984, 1999-2000, 2282-2285 or any variant of at least 12 nucleotides capable of hybridizing with the targeted microorganism(s) and these sequences and a diagnostic method using the same are provided.

Further, probes or primers having specific and ubiquitous properties for the detection and identification of any one of an algal, archaeal, bacterial, fungal and parasitital species, genus, family and group are also designed and derived from the same methods and repertoires.

More specifically, are provided definite probes or primers having specific and ubiquitous properties for the detection and identification of microorganisms.

Indeed, a general method is provided for detecting the presence in a test sample of any microorganism that is an alga, archaeum, bacterium, fungus or parasite, which comprises:

a) putting in contact any test sample *tuf* or *atpD* or *recA* sequences and nucleic acid primers and/or probes, said primers and/or probes having been selected to be sufficiently complementary to hybridize to

one or more *tuf* or *atpD* or *recA* sequences that are specific to said microorganism:

b) allowing the primers and/or probes and any test sample *tuf* or *atpD* or *recA* sequences to hybridize under specified conditions such as said primers and/or probes hybridize to the *tuf* or *atpD* or *recA* sequences of said microorganism and does not delectably hybridize to *tuf* or *atpD* or *recA* sequences from other microorganisms; and,

c) testing for hybridization of said primers and/or probes to any test sample *tuf* or *atpD* or *recA* sequences.

In the latter, step c) is based on a nucleic acid target amplification method, or on a signal amplification method.

The terms "sufficiently complementary" cover perfect and imperfect complementarity.

In addition to the universal or the specific detection and/or identification of microorganisms, the simultaneous detection of antimicrobial agent resistance gene or of a toxin gene is provided in compositions of matter as well as in diagnostic methods. Such detection is brought by using probes or primers having at least 12 nucleotides in length capable of hybridizing with an antimicrobial agent resistance gene and/or toxin gene, a definite set thereof being particularly provided.

Of course, any propriatory nucleic acid and nucleotide sequence derived therefrom, and any variant of at least 12 nucleotides capable of a selective hybridization with the following nucleic acids are within the scope of this invention as well as derived recombinant vectors and hosts:

SEQ ID NOs.: 1-73, 75-241, 399-457, 498-529, 612-618, 621-624, 675, 677, 717-736, 779-792, 840-855, 865, 868-888, 897-910, 932, 967-989, 992, 1266-1297, 1518-1526, 1561-1575, 1578-1580, 1662-1664, 1666-1667, 1669-1670, 1673-1683, 1685-1689, 1786-1843, 1874-1881, 1956-1960, 2183-2185, 2187-2188, 2193-2201, 2214-2249, 2255-2272, which are all *tuf* sequences;

SEO ID NOs.: 242-270, 272-398, 458-497, 530-538, 663, 667, 673-676, 678-680, 737-778, 827-832, 834-839, 856-862, 866-867, 889-896, 929-931, 941-966, 1245-1254, 1256-1265, 1527, 1576-1577, 1600-1604, 1638-1647, 1649-1660, 1671, 1684, 1844-1848, 1849-1865, 2189-2192, which are all *atpD* sequences;

SEQ ID NOs.: 990-991, 1003, 1288-1289, 1714, 1756-1763, 1866-1873 and 2202-2212, which are all *recA* sequences; and

SEQ ID NOs.: 1004-1075, 1255, 1607-1608, 1648, 1764-1785, 2013-2014, 2056-2064, 2273-2280, which are antimicrobial agent resistance or toxin gene sequences found to be suitable for the detection and identification of microbial species.

To complement the following repertories, another one comprising *hexA* nucleic acids and derived sequences have been construed through amplification of nucleic acids of any streptococcal species with any combination of primers SEO ID NOs.: 1179, 1181, 1182 and 1184 to 1191. From this particular repertory, primers and/or probes for detecting *Streptococcus pneumoniae* have been designed and obtained. Particularly, a nucleic acid sequence of at least 12 nucleotides capable of hybridizing with *Streptococcus pneumoniae* and with any one of SEQ ID NOs.: 1184 to 1187 or with SEQ ID NOs.: 1179, 1180, 1181 or 1182 are provided.

The remarkable sequence diversity of nucleic acids that encode proteins also provides diversity of peptide sequences which constitute another repertory that is also within the scope of this invention. From the protein and nucleic acid sequence repertories is derived a use therefrom for the design of a therapeutic agent effective against a target microorganism, for example, an antibiotic, a vaccine or a genic therapeutic agent.

Due to the constant evolution in the diagnostic methods, here is finally provided a method for the identification of a microorganism in a test sample, comprising the steps of:

a) obtaining a nucleic acid sequence from a *tuf*, *fus*, *atpD*, and/or *recA* genes of said microorganisms, and

b) comparing said nucleic acid sequence with the nucleic acid sequences of a bank as defined in claim 5, said repertory comprising a nucleic acid sequence obtained from the nucleic acids of said microorganism, whereby said microorganism is identify when there is a match between the sequences.

In this method, any way by which the specified given sequence is obtained is contemplated, and this sequence is simply compared to the sequences of a bank or a repertory. If the comparison results in a match, e.g. if bank comprises the nucleic acid sequence of interest, the identification of the microorganism is provided.

DETAILED DESCRIPTION OF THE INVENTION**HIGHLY CONSERVED GENES AND THEIR USE TO GENERATE SPECIES-SPECIFIC, GENUS-SPECIFIC, FAMILY-SPECIFIC, GROUP-SPECIFIC AND UNIVERSAL NUCLEIC ACID PROBES AND AMPLIFICATION PRIMERS TO RAPIDLY DETECT AND IDENTIFY ALGAL, ARCHAEAL, BACTERIAL, FUNGAL AND PARASITICAL MICROORGANISMS FROM CLINICAL SPECIMENS FOR DIAGNOSIS**

The present inventors reasoned that comparing the published *Haemophilus influenzae* and *Mycoplasma genitalium* genomes and searching for conserved genes could provide targets to develop useful diagnostic primers and probes. This sequence comparison is highly informative as these two bacteria are distantly related and most genes present in the minimal genome of *M. genitalium* are likely to be present in every bacterium. Therefore genes conserved between these two bacteria are likely to be conserved in all other bacteria.

Following the genomic comparison, it was found that several protein-coding genes were conserved in evolution. Highly conserved proteins included the translation elongation factors G (EF-G) and Tu (EF-Tu) and the β subunit of F₀F₁ type ATP-synthase, and to a lesser extent, the RecA recombinase. These four proteins coding genes were selected amongst the 20 most conserved genes on the basis that they all possess at least two highly conserved regions suitable for the design of universal amplification and sequencing primers. Moreover, within the fragment amplified by these primers, highly conserved and more variable regions are also present hence suggesting it might be possible to rapidly obtain sequence information from various microbial species to design universal as well as species-, genus-, family-, or group-specific primers and probes of potential use for the detection and identification and/or quantification of microorganisms.

Translation elongation factors are members of a family of GTP-binding proteins which intervene in the interactions of tRNA molecules with the ribosome machinery during essential steps of protein synthesis. The role of elongation factor Tu is to facilitate the binding of aminoacylated tRNA molecules to the A site of the ribosome. The eukaryotic, archaeal (archaebacterial) and algal homolog of EF-Tu is called elongation-factor-1 alpha (EF-1 α). All protein synthesis factors originated from a common ancestor via gene duplications and fusions (Cousineau *et al.*, 1997, J. Mol. Evol. **45**:661-670). In particular, elongation factor G (EF-G), although having a functional role in promoting the translocation of aminoacyl-tRNA molecules from the A site to the P site of the ribosome, shares sequence homologies with EF-Tu and is thought to have arisen from the duplication and fusion of an ancestor of the EF-Tu gene.

In addition, EF-Tu is known to be the target for antibiotics belonging to the elfamycin's group as well as to other structural classes (Anborgh and Parmeggiani, 1991, EMBO J. **10**:779-784; Luiten *et al.*, 1992, European patent application serial No. EP 0 466 251 A1). EF-G for its part, is the target of the antibiotic fusidic acid. In addition to its crucial activities in translation, EF-Tu has chaperone-like functions in protein folding, protection against heat denaturation of proteins and interactions with unfolded proteins (Caldas *et al.*, 1998, J. Biol. Chem **273**:11478-11482). Interestingly, a form of the EF-Tu protein has been identified as a dominant component of the periplasm of *Neisseria gonorrhoeae* (Porcella *et al.*, 1996, Microbiology **142**:2481-2489), hence suggesting that at least in some bacterial species, EF-Tu might be an antigen with vaccine potential.

F₀F₁ type ATP-synthase belongs to a superfamily of proton-translocating ATPases divided in three major families: P, V and F (Nelson and Taiz, 1989, TIBS **14**:113-116). P-ATPases (or E₁-E₂ type) operate via a phosphorylated intermediate and are not evolutionarily related to the other two families. V-ATPases (or V₀V₁ type) are present on the vacuolar and other endomembranes of eukaryotes, on the plasma membrane of archaea (archaebacteria) and algae, and also on the plasma membrane of some eubacteria especially species belonging to the order

Spirochaetales as well as to the *Chlamydiaceae* and *Deinococcaceae* families. F-ATPases (or F₀F₁ type) are found on the plasma membrane of most eubacteria, on the inner membrane of mitochondria and on the thylakoid membrane of chloroplasts. They function mainly in ATP synthesis. They are large multimeric enzymes sharing numerous structural and functional features with the V-ATPases.

F and V-type ATPases have diverged from a common ancestor in an event preceding the appearance of eukaryotes. The β subunit of the F-ATPases is the catalytic subunit and it possesses low but significant sequence homologies with the catalytic A subunit of V-ATPases.

The translation elongation factors EF-Tu, EF-G and EF-1 α , and the catalytic subunit of F or V-types ATP-synthase, are highly conserved proteins sometimes used for phylogenetic analysis and their genes are also known to be highly conserved (Iwabe *et al.*, 1989, Proc. Natl. Acad. Sci. USA **86**:9355-9359, Gogarten *et al.*, 1989, Proc. Natl. Acad. Sci. USA **86**:6661-6665, Ludwig *et al.*, 1993, Antonie van Leeuwenhoek **64**:285-305). A recent BLAST (Altschul *et al.*, 1997, J. Mol. Biol. **215**:403-410) search performed by the present inventors on the GenBank, European Molecular Biology Laboratory (EMBL), DNA Database of Japan (DDBJ) and specific genome project databases indicated that throughout bacteria, the EF-Tu and the β subunit of F₀F₁ type ATP-synthase genes may be more conserved than other genes that are well conserved between *H. influenzae* and *M. genitalium*.

The RecA recombinase is a multifunctional protein encoded by the *recA* gene. It plays a central role in homologous recombination, it is critical for the repair of DNA damage and it is involved in the regulation of the SOS system by promoting the proteolytic digestion of the LexA repressor. It is highly conserved in bacteria and could serve as a useful genetic marker to reconstruct bacterial phylogeny (Miller and Kokjohn, 1990, Annu. Rev. Microbiol. **44**:365-394). Although RecA possesses some highly conserved sequence segments that we used to design universal primers aimed at sequencing the *recA* fragments, it is clearly not as well conserved EF-G, EF-Tu and β subunit of F₀F₁ type ATP-synthase.

Hence, RecA may not be optimal for universal detection of bacteria with high sensitivity but it was chosen because preliminary data indicated that EF-G, EF-Tu and β subunit of F₀F₁ type ATP-synthase may sometimes be too closely related to find specific primer pairs that could discriminate between certain very closely related species and genera. While RecA, EF-G, EF-Tu and β subunit of F₀F₁ type ATP-synthase genes, possesses highly conserved regions suitable for the design of universal sequencing primers, the less conserved region between primers should be divergent enough to allow species-specific and genus-specific primers in those cases.

Thus, as targets to design primers and probes for the genetic detection of microorganisms, the present inventors have focused on the genes encoding these four proteins: *tuf*, the gene for elongation factor Tu (EF-Tu); *fus*, the gene for the elongation factor G (EF-G); *atpD*, the gene for β subunit of F₀F₁ type ATP-synthase; and *recA*, the gene encoding the RecA recombinase. In several bacterial genomes *tuf* is often found in two highly similar duplicated copies named *tufA* and *tufB* (Filer and Furano, 1981, J. Bacteriol. 148:1006-1011, Sela *et al.*, 1989, J. Bacteriol. 171:581-584). In some particular cases, more divergent copies of the *tuf* genes can exist in some bacterial species such as some actinomycetes (Luiten *et al.*, European patent application publication No. EP 0 446 251 A1; Vijgenboom *et al.*, 1994, Microbiology 140:983-998) and, as revealed as part of this invention, in several enterococcal species. In several bacterial species, *tuf* is organized in an operon with its homolog gene for the elongation factor G (EF-G) encoded by the *fusA* gene (Figure 3). This operon is often named the *str* operon. The *tuf*, *fus*, *atpD* and *recA* genes were chosen as they are well conserved in evolution and have highly conserved stretches as well as more variable segments. Moreover, these four genes have eukaryotic orthologs which are described in the present invention as targets to identify fungi and parasites. The eukaryotic homolog of elongation factor Tu is called elongation factor 1-alpha (EF-1 α) (gene name: *tef*, *tefl*, *efl*, *ef-1* or *EF-1*). In fungi, the gene for EF-1 α occurs sometimes in two or more highly

similar duplicated copies (often named *tef1*, *tef2*, *tef3*...). In addition, eukaryotes have a copy of elongation factor Tu which is originating from their organelle genome ancestry (gene name: *tuf1*, *tufM* or *tufA*). For the purpose of the current invention, the genes for these four functionally and evolutionarily linked elongation factors (bacterial EF-Tu and EF-G, eukaryotic EF-1 α , and organellar EF-Tu) will hereafter be designated as «*tuf* nucleic acids and/or sequences». The eukaryotic (mitochondrial) F₀F₁ type ATP-synthase beta subunit gene is named *atp2* in yeast. For the purpose of the current invention, the genes of catalytic subunit of either F or V-type ATP-synthase will hereafter be designated as «*atpD* nucleic acids and/or sequences». The eukaryotic homologs of RecA are distributed in two families, typified by the Rad51 and Dmcl proteins. Archaeal homologs of RecA are called RadA. For the purpose of the current invention, the genes corresponding to the latter proteins will hereafter be designated as «*recA* nucleic acids and/or sequences».

In the description of this invention, the terms «nucleic acids» and «sequences» might be used interchangeably. However, «nucleic acids» are chemical entities while «sequences» are the pieces of information derived from (inherent to) these «nucleic acids». Both nucleic acids and sequences are equivalently valuable sources of information for the matter pertaining to this invention.

Analysis of multiple sequence alignments of *tuf* and *atpD* sequences permitted the design of oligonucleotide primers (and probes) capable of amplifying (or hybridizing to) segments of *tuf* (and/or *fus*) and *atpD* genes from a wide variety of bacterial species (see Examples 1 to 4, 24 and 26, and Table 7). Sequencing and amplification primer pairs for *tuf* nucleic acids and/or sequences are listed in Annex I and hybridization probes are listed in Annexes III and XLVII. Sequencing and amplification primer pairs for *atpD* nucleic acids and/or sequences are listed in Annex II. Analysis of the main subdivisions of *tuf* and *atpD* sequences (see Figures 1 and 2) permitted to design sequencing primers amplifying specifically each of these subdivisions. It should be noted that these sequencing primers could also be used as universal primers. However, since some of these sequencing primers

include several variable sequence (degenerated) positions, their sensitivity could be lower than that of universal primers developed for diagnostic purposes. Further subdivisions could be done on the basis of the various phyla where these genes are encountered.

Similarly, analysis of multiple sequence alignments of *recA* sequences present in the public databases permitted the design of oligonucleotide primers capable of amplifying segments of *recA* genes from a wide variety of bacterial species. Sequencing and amplification primer pairs for *recA* sequences are listed in Annex XXI. The main subdivisions of *recA* nucleic acids and/or sequences comprise *recA*, *radA*, *rad51* and *dmc1*. Further subdivisions could be done on the basis of the various phyla where these genes are encountered.

The present inventor's strategy is to get as much sequence data information from the four conserved genes (*tuf*, *fus*, *atpD* and *recA*). This ensemble of sequence data forming a repertory (with subrepertories corresponding to each target gene and their main sequence subdivisions) and then using the sequence information of the sequence repertory (or subrepertories) to design primer pairs that could permit either universal detection of algae or archaea or bacteria or fungi or parasites, detection of a family or group of microorganism (e.g. *Enterobacteriaceae*), detection of a genus (e.g. *Streptococcus*) or finally a specific species (e.g. *Staphylococcus aureus*). It should be noted that for the purpose of the present invention a group of microorganisms is defined depending on the needs of the particular diagnostic test. It does not need to respect a particular taxonomical grouping or phylum. See Example 12 where primers were designed to amplify a group a bacteria consisting of the 17 major bacterial species encountered as contaminants of platelet concentrates. Also remark that in that Example, the primers are not only able to sensitively and rapidly detect at least the 17 important bacterial species, but could also detect other species as well, as shown in Table 14. In these circumstances the primers shown in Example 12 are considered universal for platelet-contaminating bacteria. To develop an assay specific for the latter, one or more primers or probes specific to each species could be designed. Another

example of primers and/or probes for group detection is given by the *Pseudomonas* group primers. These primers were designed based upon alignment of *tuf* sequences from real *Pseudomonas* species as well as from former *Pseudomonas* species such as *Stenotrophomonas maltophilia*. The resulting primers are able to amplify all *Pseudomonas* species tested as well as several species belonging to different genera, hence as being specific for a group including *Pseudomonas* and other species, we defined that group as Pseudomonads, as several members were former *Pseudomonas*.

For certain applications, it may be possible to develop a universal, group, family or genus-specific reaction and to proceed to species identification using sequence information within the amplicon to design species-specific internal probes or primers, or alternatively, to proceed directly by sequencing the amplicon. The various strategies will be discussed further below.

The ensembles formed by public and proprietary *tuf*, *atpD* and *recA* nucleic acids and/or sequences are used in a novel fashion so they constitute three databases containing useful information for the identification of microorganisms.

Sequence repertories of other gene targets were also built to solve some specific identification problems especially for microbial species genetically very similar to each other such as *E. coli* and *Shigella* (see Example 23). Based on *tuf*, *atpD* and *recA* sequences, *Streptococcus pneumoniae* is very difficult to differentiate from the closely related species *S. oralis* and *S. mitis*. Therefore, we elected to built a sequence repertory from *hexA* sequences (Example 19), a gene much more variable than our highly conserved *tuf*, *atpD* and *recA* nucleic acids and/or sequences.

For the detection of mutations associated with antibiotic resistance genes, we also built repertories to distinguish between point mutations reflecting only gene diversity and point mutations involved in resistance. This was done for *pbp1a*, *pbp2b* and *pbp2x* genes of penicillin-resistant and sensitive *Streptococcus pneumoniae* (Example 18) and also for *gyrA* and *parC* gene fragments of various bacterial species for which quinolone resistance is important to monitor.

Oligonucleotide primers and probes design and synthesis

The *tuf*, *fus*, *atpD* and *recA* DNA fragments sequenced by us and/or selected from public databases (GenBank and EMBL) were used to design oligonucleotides primers and probes for diagnostic purposes. Multiple sequence alignments were made using subsets of the *tuf* or *atpD* or *recA* sequences repertory. Subsets were chosen to encompass as much as possible of the targetted microorganism(s) DNA sequence data and also include sequence data from phylogenetically related microorganisms from which the targetted microorganism(s) should be distinguished. Regions suitable for primers and probes should be conserved for the targetted microorganism(s) and divergent for the microorganisms from which the targetted microorganism(s) should be distinguished. The large amount of *tuf* or *atpD* or *recA* sequences data in our repertory permits to reduce trial and errors in obtaining specific and ubiquitous primers and probes. We also relied on the corresponding peptide sequences of *tuf*, *fus*, *atpD* and *recA* nucleic acids and/or sequences to facilitate the identification of regions suitable for primers and probes design. As part of the design rules, all oligonucleotides (probes for hybridization and primers for DNA amplification by PCR) were evaluated for their suitability for hybridization or PCR amplification by computer analysis using standard programs (i.e. the Genetics Computer Group (GCG) programs and the primer analysis software Oligo™ 5.0). The potential suitability of the PCR primer pairs was also evaluated prior to the synthesis by verifying the absence of unwanted features such as long stretches of one nucleotide and a high proportion of G or C residues at the 3' end (Persing *et al.*, 1993, Diagnostic Molecular Microbiology: Principles and Applications, American Society for Microbiology, Washington, D.C.). Oligonucleotide probes and amplification primers were synthesized using an automated DNA synthesizer (Perkin-Elmer Corp., Applied Biosystems Division).

The oligonucleotide sequence of primers or probes may be derived from either strand of the duplex DNA. The primers or probes may consist of the bases

A, G, C, or T or analogs and they may be degenerated at one or more chosen nucleotide position(s). The primers or probes may be of any suitable length and may be selected anywhere within the DNA sequences from proprietary fragments or from selected database sequences which are suitable for (i) the universal detection of algae or archaea or bacteria or fungi or parasites, (ii) the species-specific detection and identification of any microorganism, including but not limited to: *Abiotrophia adiacens*, *Bacteroides fragilis*, *Bordetella pertussis*, *Candida albicans*, *Candida dubliniensis*, *Candida glabrata*, *Candida guilliermondii*, *Candida krusei*, *Candida lusitaniae*, *Candida parapsilosis*, *Candida tropicalis*, *Candida zeylanoides*, *Campylobacter jejuni* and *C. coli*, *Chlamydia pneumoniae*, *Chlamydia trachomatis*, *Cryptococcus neoformans*, *Cryptosporidium parvum*, *Enterococcus faecalis*, *Enterococcus faecium*, *Enterococcus gallinarum*, *Escherichia coli*, *Haemophilus influenzae*, *Legionella pneumophila*, *Mycoplasma pneumoniae*, *Neisseria gonorrhoeae*, *Pseudomonas aeruginosa*, *Staphylococcus aureus*, *Staphylococcus epidermidis*, *Staphylococcus haemolyticus*, *Staphylococcus hominis*, *Staphylococcus saprophyticus*, *Streptococcus agalactiae*, *Streptococcus pneumoniae*, *Trypanosoma brucei*, *Trypanosoma cruzi*, (iii) the genus-specific detection of *Bordetella* species, *Candida* species, *Clostridium* species, *Corynebacterium* species, *Cryptococcus* species, *Entamoeba* species, *Enterococcus* species, *Gemella* species, *Giardia* species, *Legionella* species, *Leishmania* species, *Staphylococcus* species, *Streptococcus* species, *Trypanosoma* species, (iv) the family-specific detection of *Enterobacteriaceae* family members, *Mycobacteriaceae* family members, *Trypanosomatidae* family members, (v) the detection of *Enterococcus casseliflavus-flavescens-gallinarum* group, *Enterococcus*, *Gemella* and *Abiotrophia adiacens* group, *Pseudomonads* extended group, *Platelet-contaminating bacteria* group, (vi) the detection of clinically important antimicrobial agents resistance genes listed in Table 5, (vii) the detection of clinically important toxin genes listed in Table 6.

Variants for a given target microbial gene are naturally occurring and are attributable to sequence variation within that gene during evolution (Watson *et al.*, 1987, Molecular Biology of the Gene, 4th ed., The Benjamin/Cummings Publishing Company, Menlo Park, CA; Lewin, 1989, Genes IV, John Wiley & Sons, New York, NY). For example, different strains of the same microbial species may have a single or more nucleotide variation(s) at the oligonucleotide hybridization site.

The person skilled in the art is well aware of the existence of variant algal, archaeal, bacterial, fungal or parasitical DNA nucleic acids and/or sequences for a specific gene and that the frequency of sequence variations depends on the selective pressure during evolution on a given gene product. The detection of a variant sequence for a region between two PCR primers may be demonstrated by sequencing the amplification product. In order to show the presence of sequence variants at the primer hybridization site, one has to amplify a larger DNA target with PCR primers outside that hybridization site. Sequencing of this larger fragment will allow the detection of sequence variation at this site. A similar strategy may be applied to show variants at the hybridization site of a probe. Insofar as the divergence of the target nucleic acids and/or sequences or a part thereof does not affect the specificity and ubiquity of the amplification primers or probes, variant microbial DNA is under the scope of this invention. Variants of the selected primers or probes may also be used to amplify or hybridize to a variant DNA.

Sequencing of *tuf* nucleic acids and/or sequences from a variety of archaeal, bacterial, fungal and parasitical species

The nucleotide sequence of a portion of *tuf* nucleic acids and/or sequences was determined for a variety of archaeal, bacterial, fungal and parasitical species. The amplification primers (SEQ ID NOs. 664 and 697), which amplify a *tuf* gene portion of approximately 890 bp, were used along with newly designed sequencing primer pairs (See Annex I for the sequencing primers for *tuf* nucleic acids and/or

sequences). Most primer pairs can amplify different copies of *tuf* genes (*tufA* and *tufB*). This is not surprising since it is known that for several bacterial species these two genes are nearly identical. For example, the entire *tufA* and *tufB* genes from *E. coli* differ at only 13 nucleotide positions (Neidhardt *et al.*, 1996, *Escherichia coli* and *Salmonella*: Cellular and Molecular Biology, 2nd ed., American Society for Microbiology Press, Washington, D.C.). Similarly, some fungi are known to have two nearly identical copies of *tuf* nucleic acids and/or sequences (EF-1 α). These amplification primers are degenerated at several nucleotide positions and contain inosines in order to allow the amplification of a wide range of *tuf* nucleic acids and/or sequences. The strategy used to select these amplification primers is similar to that illustrated in Annex I for the selection of universal primers. The *tuf* sequencing primers even sometimes amplified highly divergent copies of *tuf* genes (*tufC*) as illustrated in the case of some enterococcal species (SEQ ID NOs.: 73, 75, 76, 614 to 618, 621 and 987 to 989). To prove this, we have determined the enterococcal *tuf* nucleic acids and/or sequences from PCR amplicons cloned into a plasmid vector. Using the sequence data from the cloned amplicons, we designed new sequencing primers specific to the divergent (*tufC*) copy of enterococci (SEQ ID NOs.: 658-659 and 661) and then sequenced directly the *tufC* amplicons. The amplification primers (SEQ ID NOs.: 543, 556, 557, 643-645, 660, 664, 694, 696 and 697) could be used to amplify the *tuf* nucleic acids and/or sequences from any bacterial species. The amplification primers (SEQ ID NOs.: 558, 559, 560, 653, 654, 655, 813, 815, 1974-1984, 1999-2003) could be used to amplify the *tuf* (EF-1 α) genes from any fungal and/or parasitical species. The amplification primers SEQ ID NOs. 1221-1228 could be used to amplify bacterial *tuf* nucleic acids and/or sequences of the EF-G subdivision (*fusA*) (Figure 3). The amplification primers SEQ ID NOs. 1224, and 1227-1229 could be used to amplify bacterial *tuf* nucleic acids and/or sequences comprising the end of EF-G (*fusA*) and the beginning of EF-Tu (*tuf*), including the intergenic region, as shown in Figure 3. Most *tuf* fragments to be sequenced were amplified using the following amplification protocol: One μ l of cell suspension (or of purified genomic DNA

0.1-100 ng/ μ l) was transferred directly to 19 μ l of a PCR reaction mixture. Each PCR reaction contained 50 mM KCl, 10 mM Tris-HCl (pH 9.0), 0.1% Triton X-100, 2.5 mM MgCl₂, 1 μ M of each of the 2 primers, 200 μ M of each of the four dNTPs, 0.5 unit of *Taq* DNA polymerase (Promega Corp., Madison, WI). PCR reactions were subjected to cycling using a PTC-200 thermal cycler (MJ Research Inc., Watertown, Mass.) as follows: 3 min at 94-96 °C followed by 30-45 cycles of 1 min at 95 °C for the denaturation step, 1 min at 50-55 °C for the annealing step and 1 min at 72 °C for the extension step. Subsequently, twenty microliters of the PCR-amplified mixture were resolved by electrophoresis in a 1.5% agarose gel. The amplicons were then visualized by staining with methylene blue (Flores *et al.*, 1992, Biotechniques, 13:203-205). The size of the amplification products was estimated by comparison with a 100-bp molecular weight ladder. The band corresponding to the specific amplification product was excised from the agarose gel and purified using the QIAquick™ gel extraction kit (QIAGEN Inc., Chatsworth, CA). The gel-purified DNA fragment was then used directly in the sequencing protocol. Both strands of the *tuf* genes amplification product were sequenced by the dideoxynucleotide chain termination sequencing method by using an Applied Biosystems automated DNA sequencer (model 377) with their Big Dye™ Terminator Cycle Sequencing Ready Reaction Kit (Applied Biosystems, Foster City, CA). The sequencing reactions were performed by using the same amplification primers and 10 ng/100 bp of the gel-purified amplicon per reaction. For the sequencing of long amplicons such as those of eukaryotic *tuf* (EF-1 α) nucleic acids and/or sequences, we designed internal sequencing primers (SEQ ID NOs.: 654, 655 and 813) to be able to obtain sequence data on both strands for most of the fragment length. In order to ensure that the determined sequence did not contain errors attributable to the sequencing of PCR artefacts, we have sequenced two preparations of the gel-purified *tuf* amplification product originating from two independent PCR amplifications. For most target microbial species, the sequences determined for both amplicon preparations were identical. In case of discrepancies, amplicons from a third independent PCR amplification

were sequenced. Furthermore, the sequences of both strands were 100% complementary thereby confirming the high accuracy of the determined sequence. The *tuf* nucleic acids and/or sequences determined using the above strategy are described in the Sequence Listing. Table 7 gives the originating microbial species and the source for each *tuf* sequence in the Sequence Listing.

~~The alignment of the *tuf* sequences determined by us or selected from~~ databases revealed clearly that the length of the sequenced portion of the *tuf* genes is variable. There may be insertions or deletions of several amino acids. In addition, in several fungi introns were observed. Intron nucleic acids and/or sequences are part of *tuf* nucleic acids and/or sequences and could be useful in the design of species-specific primers and probes. This explains why the size of the sequenced *tuf* amplification products was variable from one fungal species to another. Consequently, the nucleotide positions indicated on top of each of Annexes IV to XX, XXIII to XXXI, XXXVIII and XLII do not correspond for sequences having insertions or deletions.

It should also be noted that the various *tuf* nucleic acids and/or sequences determined by us occasionally contain base ambiguities. These degenerated nucleotides correspond to sequence variations between *tufA* and *tufB* genes (or copies of the EF-G subdivision of *tuf* nucleic acids and/or sequences, or copies of EF-1 α subdivision of *tuf* nucleic acids and/or sequences for fungi and parasites) because the amplification primers amplify both *tuf* genes. These nucleotide variations were not attributable to nucleotide misincorporations by the *Taq* DNA polymerase because the sequence of both strands was identical and also because the sequences determined with both preparations of the gel-purified *tuf* amplicons obtained from two independent PCR amplifications were identical.

The selection of amplification primers from *tuf* nucleic acids and/or sequences

The *tuf* sequences determined by us or selected from public databases were used to select PCR primers for universal detection of bacteria, as well as for genus-

specific, species-specific family-specific or group-specific detection and identification. The strategy used to select these PCR primers was based on the analysis of multiple sequence alignments of various *tuf* sequences. For more details about the selection of PCR primers from *tuf* sequences please refer to Examples 5, 7-14, 17, 22, 24, 28, 30-31, 33, 36, and 38-40, and to Annexes VI-IX, XI-XIX and XXV.

Sequencing of *atpD* and *recA* nucleic acids and/or sequences from a variety of archaeal, bacterial, fungal and parasitical species

The method used to obtain *atpD* and *recA* nucleic acids and/or sequences is similar to that described above for *tuf* nucleic acids and/or sequences.

The selection of amplification primers from *atpD* or *recA* nucleic acids and/or sequences

The comparison of the nucleotide sequence for the *atpD* or *recA* genes from various archaeal, bacterial, fungal and parasitical species allowed the selection of PCR primers (refer to Examples 6, 13, 29, 34 and 37, and to Annexes IV, V, X, and XX).

DNA amplification

For DNA amplification by the widely used PCR (polymerase chain reaction) method, primer pairs were derived from proprietary DNA fragments or from database sequences. Prior to synthesis, the potential primer pairs were analyzed by using the Oligo™ 5.0 software to verify that they were good candidates for PCR amplification.

During DNA amplification by PCR, two oligonucleotide primers binding respectively to each strand of the heat-denatured target DNA from the microbial

genome are used to amplify exponentially *in vitro* the target DNA by successive thermal cycles allowing denaturation of the DNA, annealing of the primers and synthesis of new targets at each cycle (Persing *et al.*, 1993, Diagnostic Molecular Microbiology: Principles and Applications, American Society for Microbiology, Washington, D.C.).

----- Briefly, the PCR protocols were as follows: Treated clinical specimens or -----
standardized bacterial or fungal or parasitical suspensions (see below) or purified genomic DNA from bacteria, fungi or parasites were amplified in a 20 μ l PCR reaction mixture. Each PCR reaction contained 50 mM KCl, 10 mM Tris-HCl (pH 9.0), 2.5 mM $MgCl_2$, 0.4 μ M of each primer, 200 μ M of each of the four dNTPs and 0.5 unit of *Taq* DNA polymerase (Promega) combined with the TaqStartTM antibody (Clontech Laboratories Inc., Palo Alto, CA). The TaqStartTM antibody, which is a neutralizing monoclonal antibody to *Taq* DNA polymerase, was added to all PCR reactions to enhance the specificity and the sensitivity of the amplifications (Kellogg *et al.*, 1994, Biotechniques **16**:1134-1137). The treatment of the clinical specimens varies with the type of specimen tested, since the composition and the sensitivity level required are different for each specimen type. It consists in a rapid protocol to lyse the microbial cells and eliminate or neutralize PCR inhibitors. For amplification from bacterial or fungal or parasitical cultures or from purified genomic DNA, the samples were added directly to the PCR amplification mixture without any pre-treatment step. An internal control was derived from sequences not found in the target microorganisms or in the human genome. The internal control was integrated into all amplification reactions to verify the efficiency of the PCR assays and to ensure that significant PCR inhibition was absent. Alternatively, an internal control derived from rRNA was also useful to monitor the efficiency of microbial lysis protocols.

PCR reactions were then subjected to thermal cycling (3 min at 94-96°C followed by 30 cycles of 1 second at 95°C for the denaturation step and 30 seconds at 50-65°C for the annealing-extension step) using a PTC-200 thermal cycler (MJ Research Inc.). The number of cycles performed for the PCR assays varies

according to the sensitivity level required. For example, the sensitivity level required for microbial detection directly from clinical specimens is higher for blood specimens than for urine specimens because the concentration of microorganisms associated with a septicemia can be much lower than that associated with a urinary tract infection. Consequently, more sensitive PCR assays having more thermal cycles are probably required for direct detection from blood specimens. Similarly, PCR assays performed directly from bacterial or fungal or parasitical cultures may be less sensitive than PCR assays performed directly from clinical specimens because the number of target organisms is normally much lower in clinical specimens than in microbial cultures.

The person skilled in the art of DNA amplification knows the existence of other rapid amplification procedures such as ligase chain reaction (LCR), transcription-mediated amplification (TMA), self-sustained sequence replication (3SR), nucleic acid sequence-based amplification (NASBA), strand displacement amplification (SDA), branched DNA (bDNA), cycling probe technology (CPT), solid phase amplification (SPA), rolling circle amplification technology (RCA), solid phase RCA, anchored SDA and nuclease dependent signal amplification (NDSA) (Lee *et al.*, 1997, Nucleic Acid Amplification Technologies: Application to Disease Diagnosis, Eaton Publishing, Boston, MA; Persing *et al.*, 1993, Diagnostic Molecular Microbiology: Principles and Applications, American Society for Microbiology, Washington, D.C.; Westin *et al.*, 2000, Nat. Biotechnol. 18:199-204). The scope of this invention is not limited to the use of amplification by PCR, but rather includes the use of any rapid nucleic acid amplification method or any other procedure which may be used to increase the sensitivity and/or the rapidity of nucleic acid-based diagnostic tests. The scope of the present invention also covers the use of any nucleic acids amplification and detection technology including real-time or post-amplification detection technologies, any amplification technology combined with detection, any hybridization nucleic acid chips or arrays technologies, any amplification chips or combination of amplification and

hybridization chips technologies. Detection and identification by any sequencing method is also under the scope of the present invention.

Any oligonucleotide suitable for the amplification of nucleic acids by approaches other than PCR or for DNA hybridization which are derived from the species-specific, genus-specific and universal DNA fragments as well as from selected antimicrobial agents resistance or toxin gene sequences included in this document are also under the scope of this invention.

Detection of amplification products

Classically, detection of amplification is performed by standard ethidium bromide-stained agarose gel electrophoresis. It is clear that other methods for the detection of specific amplification products, which may be faster and more practical for routine diagnosis, may be used. Such methods may be based on the detection of fluorescence after or during amplification. One simple method for monitoring amplified DNA is to measure its rate of formation by measuring the increase in fluorescence of intercalating agents such as ethidium bromide or SYBR[®] Green I (Molecular Probes). If more specific detection is required, fluorescence-based technologies can monitor the appearance of a specific product during the reaction. The use of dual-labeled fluorogenic probes such as in the TaqMan[™] system (Applied Biosystems) which utilizes the 5'-3' exonuclease activity of the *Taq* polymerase is a good example (Livak K.J. *et al.* 1995, PCR Methods Appl. 4:357-362). TaqMan[™] can be performed during amplification and this "real-time" detection can be done in a single closed tube hence eliminating post-PCR sample handling and consequently preventing the risk of amplicon carryover. Several other fluorescence-based detection methods can be performed in real-time. Fluorescence resonance energy transfer (FRET) is the principle behind the use of adjacent hybridization probes (Wittwer, C.T. *et al.* 1997. BioTechniques 22:130-138), molecular beacons (Tyagi S. and Kramer F.R. 1996. Nature Biotechnology 14:303-308) and scorpions (Whitcomb *et al.* 1999. Nature

Biotechnology 17:804-807). Adjacent hybridization probes are designed to be internal to the amplification primers. The 3' end of one probe is labelled with a donor fluorophore while the 5' end of an adjacent probe is labelled with an acceptor fluorophore. When the two probes are specifically hybridized in closed proximity (spaced by 1 to 5 nucleotides) the donor fluorophore which has been excited by an external light source emits light that is absorbed by a second acceptor that emit more fluorescence and yields a FRET signal. Molecular beacons possess a stem-and-loop structure where the loop is the probe and at the bottom of the stem a fluorescent moiety is at one end while a quenching moiety is at the other end. The beacons undergo a fluorogenic conformational change when they hybridize to their targets hence separating the fluorochrome from its quencher. The FRET principle is also used in an air thermal cycler with a built-in fluorometer (Wittwer, C.T. *et al.* 1997. *BioTechniques* 22:130-138). The amplification and detection are extremely rapid as reactions are performed in capillaries: it takes only 18 min to complete 45 cycles. Those techniques are suitable especially in the case where few pathogens are searched for. Boehringer-Roche Inc. sells the LightCycler™, and Cepheid makes the SmartCycler. These two apparatus are capable of rapid cycle PCR combined with fluorescent SYBR® Green I or FRET detection. We recently demonstrated in our laboratory, real-time detection of 10 CFU in less than 40 minutes using adjacent hybridization probes on the LightCycler™. Methods based on the detection of fluorescence are particularly promising for utilization in routine diagnosis as they are very rapid, quantitative and can be automated.

Microbial pathogens detection and identification may also be performed by solid support or liquid hybridization using species-specific internal DNA probes hybridizing to an amplification product. Such probes may be generated from any sequence from our repertory and designed to specifically hybridize to DNA amplification products which are objects of the present invention. Alternatively, the internal probes for species or genus or family or group detection and identification may be derived from the amplicons produced by a universal, family-, group-, genus- or species-specific amplification assay(s). The oligonucleotide

probes may be labeled with biotin or with digoxigenin or with any other reporter molecule (for more details see below the section on hybrid capture). Hybridization on a solid support is amendable to miniaturization.

At present the oligonucleotide nucleic acid microarray technology is appealing. Currently, available low to medium density arrays (Heller *et al.*, An integrated microelectronics hybridization system for genomic research and diagnostic applications. *In*: Harrison, D.J., and van den Berg, A., 1998, Micro total analysis systems '98, Kluwer Academic Publisher, Dordrecht.) could specifically capture fluorescent-labelled amplicons. Detection methods for hybridization are not limited to fluorescence; potentiometry, colorimetry and plasmon resonance are some examples of alternative detection methods. In addition to detection by hybridization, nucleic acid microarrays could be used to perform rapid sequencing by hybridization. Mass spectrometry could also be applicable for rapid identification of the amplicon or even for sequencing of the amplification products (Chiu and Cantor, 1999, Clinical Chemistry **45**:1578; Berkenkamp *et al.*, 1998, Science **281**:260).

For the future of our assay format, we also consider the major challenge of molecular diagnostics tools, *i.e.*: integration of the major steps including sample preparation, genetic amplification, detection, data analysis and presentation (Anderson *et al.*, Advances in integrated genetic analysis. *In*: Harrison, D.J., and van den Berg, A., 1998, Micro total analysis systems '98, Kluwer Academic Publisher, Dordrecht.).

To ensure PCR efficiency, glycerol, dimethyl sulfoxide (DMSO) or other related solvents can be used to increase the sensitivity of the PCR and to overcome problems associated with the amplification of a target DNA having a high GC content or forming strong secondary structures (Dieffenbach and Dveksler, 1995, PCR Primer: A Laboratory Manual, Cold Spring Harbor Laboratory Press, Plainview, New York). The concentration ranges for glycerol and DMSO are 5-15% (v/v) and 3-10% (v/v), respectively. For the PCR reaction mixture, the concentration ranges for the amplification primers and MgCl₂ are 0.1-1.5 μ M and

1.0-10.0 mM, respectively. Modifications of the standard PCR protocol using external and nested primers (i.e. nested PCR) or using more than one primer pair (i.e. multiplex PCR) may also be used (Persing *et al.*, 1993, Diagnostic Molecular Microbiology: Principles and Applications, American Society for Microbiology, Washington, D.C.). For more details about the PCR protocols and amplicon detection methods, see Examples.

Hybrid capture and chemiluminescence detection of amplification products

Hybridization and detection of amplicons by chemiluminescence were adapted from Nikiforov *et al.* (1994, PCR Methods and Applications 3:285-291 and 1995, Anal. Biochem. 227:201-209) and from the DIG™ system protocol of Boehringer Mannheim. Briefly, 50 µl of a 25 picomoles solution of capture probe diluted in EDC {1-ethyl-3-(3-dimethylaminopropyl) carbodiimide hydrochloride} are immobilized in each well of 96-wells plates (Microlite™ 2, Dynex) by incubation overnight at room temperature. The next day, the plates are incubated with a solution of 1% BSA diluted into TNTw (10 mM Tris-HCl, pH 7.5; 150 mM NaCl; 0.05% Tween™ 20) for 1 hour at 37 °C. The plates are then washed on a Wellwash Ascent™ (Labsystems) with TNTw followed by Washing Buffer (100 mM maleic acid pH7.5; 150 mM NaCl; 0.3% Tween™ 20).

The amplicons were labelled with DIG-11-dUTP during PCR using the PCR DIG Labelling Mix from Boehringer Mannheim according to the manufacturer's instructions. Hybridization of the amplicons to the capture probes is performed in triplicate at stringent temperature (generally, probes are designed to allow hybridization at 55 °C, the stringent temperature) for 30 minutes in 1.5 M NaCl; 10 mM EDTA. It is followed by two washes in 2 X SSC; 0.1% SDS, then by four washes in 0.1X SSC; 0.1% SDS at the stringent temperature (55 °C). Detection with 1,2 dioxetane chemiluminescent alkaline phosphatase substrates like CSPD® (Tropix Inc.) is performed according to the manufacturer's instructions but with shorter incubations times and a different antibody concentration. The plates are

agitated at each step, the blocking incubation is performed for only 5 minutes, the anti-DIG-AP1 is used at a 1:1000 dilution, the incubation with antibody lasts 15 minutes, the plates are washed twice for only 5 minutes. Finally, after a 2 minutes incubation into the detection buffer, the plates are incubated 5 minutes with CSPD® at room temperature followed by a 10 minutes incubation at 37 °C without agitation. Luminous signal detection is performed on a Dynex Microtiter Plate Luminometer using RLU (Relative Light Units).

Specificity, ubiquity and sensitivity tests for oligonucleotide primers and probes

The specificity of oligonucleotide primers and probes was tested by amplification of DNA or by hybridization with bacterial or fungal or parasitical species selected from a panel comprising closely related species and species sharing the same anatomo-pathological site (see Annexes and Examples). All of the bacterial, fungal and parasitical species tested were likely to be pathogens associated with infections or potential contaminants which can be isolated from clinical specimens. Each target DNA could be released from microbial cells using standard chemical and/or physical treatments to lyse the cells (Sambrook *et al.*, 1989, Molecular Cloning: A Laboratory Manual, 2nd ed., Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY) or alternatively, genomic DNA purified with the GNOME™ DNA kit (Bio101, Vista, CA) was used. Subsequently, the DNA was subjected to amplification with the primer pairs. Specific primers or probes amplified only the target microbial species, genus, family or group.

Oligonucleotides primers found to amplify specifically the target species, genus, family or group were subsequently tested for their ubiquity by amplification (i.e. ubiquitous primers amplified efficiently most or all isolates of the target species or genus or family or group). Finally, the sensitivity of the primers or probes was determined by using 10-fold or 2-fold dilutions of purified genomic DNA from the targeted microorganism. For most assays, sensitivity levels in the

range of 1-100 copies were obtained. The specificity, ubiquity and sensitivity of the PCR assays using the selected amplification primer pairs were tested either directly from cultures of microbial species or from purified microbial genomic DNA.

Probes were tested in hybrid capture assays as described above. An oligonucleotide probe was considered specific only when it hybridized solely to DNA from the species or genus or family or group from which it was selected. Oligonucleotide probes found to be specific were subsequently tested for their ubiquity (i.e. ubiquitous probes detected efficiently most or all isolates of the target species or genus or family or group) by hybridization to microbial DNAs from different clinical isolates of the species or genus or family or group of interest including ATCC reference strains. Similarly, oligonucleotide primers and probes could be derived from antimicrobial agents resistance or toxin genes which are objects of the present invention.

Reference strains

The reference strains used to build proprietary *tuf*, *atpD* and *recA* sequence data subrepertories, as well as to test the amplification and hybridization assays were obtained from (i) the American Type Culture Collection (ATCC), (ii) the Laboratoire de santé publique du Québec (LSPQ), (iii) the Centers for Disease Control and Prevention (CDC), (iv) the National Culture Type Collection (NCTC) and (v) several other reference laboratories throughout the world. The identity of our reference strains was confirmed by phenotypic testing and reconfirmed by analysis of *tuf*, *atpD* and *recA* sequences (see Example 13).

Antimicrobial agents resistance genes

Antimicrobial resistance complicates treatment and often leads to therapeutic failures. Furthermore, overuse of antibiotics inevitably leads to the emergence of

microbial resistance. Our goal is to provide clinicians, in approximately one hour, the needed information to prescribe optimal treatments. Besides the rapid identification of negative clinical specimens with DNA-based tests for universal algal, archaeal, bacterial, fungal or parasitical detection and the identification of the presence of a specific pathogen in the positive specimens with species- and/or genus- and/or family- and/or group-specific DNA-based tests, clinicians also need timely information about the ability of the microbial pathogen to resist antibiotic treatments. We feel that the most efficient strategy to evaluate rapidly microbial resistance to antimicrobials is to detect directly from the clinical specimens the most common and clinically important antimicrobial agents resistance genes (i.e. DNA-based tests for the specific detection of antimicrobial agents resistance genes). Since the sequence from the most important and common antimicrobial agents resistance genes are available from public databases, our strategy is to use the sequence from a portion or from the entire resistance gene to design specific oligonucleotide primers or probes which will be used as a basis for the development of sensitive and rapid DNA-based tests. The list of each of the antimicrobial agents resistance genes selected on the basis of their clinical relevance (i.e. high incidence and importance) is given in Table 5; descriptions of the designed amplification primers and internal probes are given in Annexes XXXIV-XXXVII, XXXIX, XLV, and L-LI. Our approach is unique because the antimicrobial agents resistance genes detection and the microbial detection and identification can be performed simultaneously, or independently, or sequentially in multiplex or parallel or sequential assays under uniform PCR amplification conditions. These amplifications can also be done separately.

Toxin genes

Toxin identification is often very important to prescribe optimal treatments. Besides the rapid identification of negative clinical specimens with DNA-based tests for universal bacterial detection and the identification of the presence of a

specific pathogen in the positive specimens with species- and/or genus- and/or family- and/or group-specific DNA-based tests, clinicians sometimes need timely information about the ability of certain bacterial pathogens to produce toxins. Since the sequence from the most important and common bacterial toxin genes are available from public databases, our strategy is to use the sequence from a portion or from the entire toxin gene to design specific oligonucleotide primers or probes which will be used as a basis for the development of sensitive and rapid DNA-based tests. The list of each of the bacterial toxin genes selected on the basis of their clinical relevance (i.e. high incidence and importance) is given in Table 6; descriptions of the designed amplification primers and internal probes are given in Annexes XXII, XXXII and XXXIII. Our approach is unique because the toxin genes detection and the bacterial detection and identification can be performed simultaneously, or independently, or sequentially, in multiplex or parallel or sequential assays under uniform PCR amplification conditions. These amplifications can also be done separately.

Universal bacterial detection

In the routine microbiology laboratory, a high percentage of clinical specimens sent for bacterial identification are negative by culture. Testing clinical samples with universal amplification primers or universal probes to detect the presence of bacteria prior to specific identification and screening out the numerous negative specimens is thus useful as it reduces costs and may rapidly orient the clinical management of the patients. Several amplification primers and probes were therefore synthesized from highly conserved portions of bacterial sequences from the *tuf*, *atpD* and *recA* nucleic acids and/or sequences. The universal primers selection was based on a multiple sequence alignment constructed with sequences from our repertory.

All computer analysis of amino acid and nucleotide sequences were performed by using the GCG programs. Subsequently, optimal PCR primers for

the universal amplification of bacteria were selected with the help of the Oligo™ program. The selected primers are degenerated at several nucleotide positions and contain several inosines in order to allow the amplification of all clinically relevant bacterial species. Inosine is a nucleotide analog able to specifically bind to any of the four nucleotides A, C, G or T. Degenerated oligonucleotides consist of an oligonucleotide mix having two or more of the four nucleotides A, C, G or T at the site of mismatches. The inclusion of inosine and/or of base ambiguities in the amplification primers allow mismatch tolerance thereby permitting the amplification of a wider array of target nucleotide sequences (Dieffenbach and Dveksler, 1995 PCR Primer: A Laboratory Manual, Cold Spring Harbor Laboratory Press, Plainview, NY).

The amplification conditions with the universal primers are very similar to those used for the species- and genus-specific amplification assays except that the annealing temperature is slightly lower. The original universal PCR assay described in our assigned WO98/20157 (SEQ ID NOs. 23-24 of the latter application) was specific and nearly ubiquitous for the detection of bacteria. The specificity for bacteria was verified by amplifying genomic DNA isolated from the 12 fungal species as well as genomic DNA from *Leishmania donovani*, *Saccharomyces cerevisiae* and human lymphocytes. None of the above eukaryotic DNA preparations could be amplified by the universal assay, thereby suggesting that this test is specific for bacteria. The ubiquity of the universal assay was verified by amplifying genomic DNAs from 116 reference strains which represent 95 of the most clinically relevant bacterial species. These species have been selected from the bacterial species listed in Table 4. We found that at least 104 of these strains could be amplified. However, the assay could be improved since bacterial species which could not be amplified with the original *tuf* nucleic acids and/or sequences-based assay included species belonging to the following genera: *Corynebacterium* (11 species) and *Stenotrophomonas* (1 species). Sequencing of the *tuf* genes from these bacterial species and others has been performed in the scope of the present invention in order to improve the universal assay. This

sequencing data has been used to select new universal primers which may be more ubiquitous and more sensitive. Also, we improved our primer and probes design strategy by taking into consideration the phylogeny observed in analysing our repertory of *tuf*, *atpD* and *recA* sequences. Data from each of the 3 main subrepertories (*tuf*, *atpD* and *recA*) was subjected to a basic phylogenetic analysis using the Pileup command from version 10 of the GCG package (Genetics Computer Group, inc.). This analysis indicated the main branches or phyla reflecting the relationships between sequences. Instead of trying to design primers or probes able to hybridize to all phyla, we designed primers or probes able to hybridize to the main phyla while trying to use the largest phylum possible. This strategy should allow less degenerated primers hence improving sensitivity and by combining primers in a multiplex assay, improve ubiquity. Universal primers SEQ ID NOs. 643-645 based on *tuf* sequences have been designed to amplify most pathogenic bacteria except *Actinomycetaceae*, *Clostridiaceae* and the *Cytophaga*, *Flexibacter* and *Bacteroides* phylum (pathogenic bacteria of this phylum include mostly *Bacteroides*, *Porphyromonas* and *Prevotella* species). Primers to fill these gaps have been designed for *Actinomycetaceae* (SEQ ID NOs. 646-648), *Clostridiaceae* (SEQ ID NOs. 796-797, 808-811), and the *Cytophaga*, *Flexibacter* and *Bacteroides* phylum (SEQ ID NOs. 649-651), also derived from *tuf* nucleic acids and/or sequences. These primers sets could be used alone or in conjunction to render the universal assay more ubiquitous.

Universal primers derived from *atpD* sequences include SEQ ID NOs. 562-565. Combination of these primers does not amplify human DNA but should amplify almost all pathogenic bacterial species except proteobacteria belonging to the epsilon subdivision (*Campylobacter* and *Helicobacter*), the bacteria from the *Cytophaga*, *Flexibacter* and *Bacteroides* group and some actinomycetes and corynebacteria. By analysing *atpD* sequences from the latter species, primers and probes to specifically fill these gaps could be designed and used in conjunction with primers SEQ ID NOs. 562-565, also derived from *atpD* nucleic acids and/or sequences.

In addition, universality of the assay could be expanded by mixing *atpD* sequences-derived primers with *tuf* sequences-derived primers. Ultimately, even *recA* sequences-derived primers could be added to fill some gaps in the universal assay.

It is important to note that the 95 bacterial species selected to test the ubiquity of the universal assay include all of the most clinically relevant bacterial species associated with a variety of human infections acquired in the community or in hospitals (nosocomial infections). The most clinically important bacterial and fungal pathogens are listed in Tables 1 and 2.

Amino acid sequences derived from *tuf*, *atpD* and *recA* nucleic acids and/or sequences

The amino acid sequences translated from the repertory of *tuf*, *atpD* and *recA* nucleic acids and/or sequences are also an object of the present invention. The amino acid sequence data will be particularly useful for homology modeling of three-dimensional (3D) structure of the elongation factor Tu, elongation factor G, elongation factor 1 α , ATPase subunit beta and RecA recombinase. For all these proteins, at least one structure model has been published using X-ray diffraction data from crystals. Based on those structural informations it is possible to use computer software to build 3D model structures for any other protein having peptide sequence homologies with the known structure (Greer, 1991, Methods in Enzymology, 202:239-252; Taylor, 1994, Trends Biotechnol., 12(5):154-158; Sali, 1995, Curr. Opin. Biotechnol. 6:437-451; Sanchez and Sali, 1997, Curr. Opin. Struct. Biol. 7:206-214; Fischer and Eisenberg, 1999, Curr. Opin. Struct. Biol. 9:208-211; Guex *et al.*, 1999, Trends Biochem. Sci. 24: 364-367). Model structures of target proteins are used for the design or to predict the behavior of ligands and inhibitors such as antibiotics. Since EF-Tu and EF-G are already known as antibiotic targets (see above) and since the beta subunit of ATPase and RecA recombinase are essential to the survival of the microbial cells in natural

conditions of infection, all four proteins could be considered antibiotic targets. Sequence data, especially the new data generated by us could be very useful to assist the creation of new antibiotic molecules with desired spectrum of activity. In addition, model structures could be used to improve protein function for commercial purposes such as improving antibiotic production by microbial strains or increasing biomass.

The following detailed embodiments and appended drawings are provided as illustrative examples of his invention, with no intention to limit the scope thereof.

DESCRIPTION OF THE DRAWINGS

Figures 1 and 2 illustrate the principal subdivisions of the *tuf* and *atpD* sequences repertoires, respectively. For the design of primers and probes, depending on the needs, one may want to use the complete data set illustrated on the top of the pyramid or use only a subset illustrated by the different branching points. Smaller subdivisions, representing groups, families, genus and species, could even be made to extend to the bottom of the pyramid. Because the *tuf* and *atpD* sequences are highly conserved and evolved with each species, the design of primers and probes does not need to include all the sequences within the database or its subdivisions. As illustrated in Annexes IV to XX, XXIII to XXXI, XXXVIII and XLII, depending on the use, sequences from a limited number of species can be carefully selected to represent: i) only the main phylogenetic branches from which the intended probes and primers need to be differentiating, and ii) only the species for which they need to be matching. However, for ubiquity purposes, and especially for primers and probes identifying large groups of species (genus, family, group or universal, or sequencing primers), the more data is included into the sequence analysis, the better the probes and primers will be suitable for each particular intended use. Similarly, for specificity purposes, a larger data set (or repertoire) ensures optimal primers and probes design by reducing the chance of employing nonspecific oligonucleotides.

Figure 3 illustrates the approach used to design specific amplification primers from *fusA* as well as from the region between the end of *fusA* and the beginning of *tuf* in the streptomycin (*str*) operon (referred to as the *fusA-tuf* intergenic spacer in Table 7).

Figures 4 to 6 are illustrations to Example 42, whereas Figures 7 to 10 illustrate Example 43. Figures 11 and 12 illustrate Example 44.

FIGURE LEGENDS

Figure 3. Schematic organization of universal amplification primers (SEQ ID NOs. 1221-1229) in the *str* operon. Amplicon sizes are given in bases pairs. Drawing not to scale, as the *fusA-tuf* intergenic spacer size varies depending on the bacterial species. Indicated amplicon lengths are for *E. coli*.

Figure 4. Abridged multiple amino acid sequence alignment of the partial *tuf* gene products from selected species illustrated using the program Alscript. Residues highly conserved in bacteria are boxed in grey and gaps are represented with dots. Residues in reverse print are unique to the enterococcal *tufB* as well as to streptococcal and lactococcal *tuf* gene products. Numbering is based on *E. coli* EF-Tu and secondary structure elements of *E. coli* EF-Tu are represented by cylinders (α -helices) and arrows (β -strands).

Figure 5. Distance matrix tree of bacterial EF-Tu based on amino acid sequence homology. The tree was constructed by the neighbor-joining method. The tree was rooted using archeal and eukaryotic EF-1 α genes as the outgroup. The scale bar represents 5% changes in amino acid sequence, as determined by taking the sum of all of the horizontal lines connecting two species.

Figure 6. Southern hybridization of *Bgl*III/*Xba*I digested genomic DNAs of some enterococci (except for *E. casseliflavus* and *E. gallinarum* whose genomic DNA was digested with *Bam*HI/*Pvu*II) using the *tufA* gene fragment of *E. faecium* as probes. The sizes of hybridizing fragments are shown in kilobases. Strains tested are listed in Table 16.

Figure 7. *Pantoea* and *Tatumella* species specific signature indel in *atpD* genes. The nucleotide positions given are for *E. coli atpD* sequence (GenBank accession no. V00267). Numbering starts from the first base of the initiation codon.

Figure 8: Trees based on sequence data from *tuf* (left side) and *atpD* (right side). The phylogenetic analysis was performed using the Neighbor-Joining method calculated using the Kimura two-parameter method. The value on each branch indicates the occurrence (%) of the branching order in 750 bootstrapped trees.

Figure 9: Phylogenetic tree of members of the family *Enterobacteriaceae* based on *tuf* (a), *atpD* (b), and 16S rDNA (c) genes. Trees were generated by neighbor-joining method calculated using the Kimura two-parameter method. The value on each branch is the percentage of bootstrap replications supporting the branch. 750 bootstrap replications were calculated.

Figure 10: Plot of *tuf* distances versus 16S rDNA distances (a), *atpD* distances versus 16S rDNA distances (b), and *atpD* distances versus *tuf* distances (c). Symbols: ○, distances between pairs of strains belonging to the same species; ●, distances between *E. coli* strains and *Shigella* strains; □, distances between pairs belonging to the same genus; ■, distances between pairs belonging to different genera; Δ, distances between pairs belonging to different families.

EXAMPLES AND ANNEXES

For sake of clarity, here is a list of Examples and Annexes:

- Example 1: Sequencing of bacterial *atpD* (F-type and V-type) gene fragments.
- Example 2: Sequencing of eukaryotic *atpD* (F-type and V-type) gene fragments.
- Example 3: Sequencing of eukaryotic *tuf* (EF-1) gene fragments.

- Example 4: Sequencing of eukaryotic *tuf* (organelle origin, M) gene fragments.
- Example 5: Specific detection and identification of *Streptococcus agalactiae* using *tuf* sequences.
- Example 6: Specific detection and identification of *Streptococcus agalactiae* using *atpD* sequences.
-
- Example 7: Development of a PCR assay for detection and identification of staphylococci at genus and species levels.
- Example 8: Differentiating between the two closely related yeast species *Candida albicans* and *Candida dubliniensis*.
- Example 9: Specific detection and identification of *Entamoeba histolytica*.
- Example 10: Sensitive detection and identification of *Chlamydia trachomatis*.
- Example 11: Genus-specific detection and identification of enterococci.
- Example 12: Detection and identification of the major bacterial platelets contaminants using *tuf* sequences with a multiplex PCR test.
- Example 13: The resolving power of the *tuf* and *atpD* sequences databases is comparable to the biochemical methods for bacterial identification.
- Example 14: Detection of group B streptococci from clinical specimens.
- Example 15: Simultaneous detection and identification of *Streptococcus pyogenes* and its pyrogenic exotoxin A.
- Example 16: Real-time detection and identification of Shiga toxin-producing bacteria.
- Example 17: Development of a PCR assay for the detection and identification of staphylococci at genus and species levels and its associated *mecA* gene.
- Example 18: Sequencing of *pbp1a*, *pbp2b* and *pbp2x* genes of *Streptococcus pneumoniae*.
- Example 19: Sequencing of *hexA* genes of *Streptococcus* species.
- Example 20: Development of a multiplex PCR assay for the detection of *Streptococcus pneumoniae* and its penicillin resistance genes.

- Example 21: Sequencing of the vancomycin resistance *vanA*, *vanC1*, *vanC2* and *vanC3* genes.
- Example 22: Development of a PCR assay for the detection and identification of enterococci at genus and species levels and its associated resistance genes *vanA* and *vanB*.
- Example 23: Development of a multiplex PCR assay for detection and identification of vancomycin-resistant *Enterococcus faecalis*, *Enterococcus faecium*, *Enterococcus gallinarum*, *Enterococcus casseliflavus*, and *Enterococcus flavescens*.
- Example 24: Universal amplification involving the EF-G (*fusA*) subdivision of *tuf* sequences.
- Example 25: DNA fragment isolation from *Staphylococcus saprophyticus* by arbitrarily primed PCR.
- Example 26: Sequencing of prokaryotic *tuf* gene fragments.
- Example 27: Sequencing of prokaryotic *recA* gene fragments.
- Example 28: Specific detection and identification of *Escherichia coli/Shigella* sp. using *tuf* sequences.
- Example 29: Specific detection and identification of *Klebsiella pneumoniae* using *atpD* sequences.
- Example 30: Specific detection and identification of *Acinetobacter baumannii* using *tuf* sequences.
- Example 31: Specific detection and identification of *Neisseria gonorrhoeae* using *tuf* sequences.
- Example 32: Sequencing of bacterial *gyrA* and *parC* gene fragments.
- Example 33: Development of a PCR assay for the specific detection and identification of *Staphylococcus aureus* and its quinolone resistance genes *gyrA* and *parC*.
- Example 34: Development of a PCR assay for the detection and identification of *Klebsiella pneumoniae* and its quinolone resistance genes *gyrA* and *parC*.

- Example 35: Development of a PCR assay for the detection and identification of *Streptococcus pneumoniae* and its quinolone resistance genes *gyrA* and *parC*.
- Example 36: Detection of extended-spectrum TEM-type β -lactamases in *Escherichia coli*.
- ~~Example 37: Detection of extended-spectrum SHV-type β -lactamases in~~
Klebsiella pneumoniae.
- Example 38: Development of a PCR assay for the detection and identification of *Neisseria gonorrhoeae* and its associated tetracycline resistance gene *tetM*.
- Example 39: Development of a PCR assay for the detection and identification of *Shigella* sp. and their associated trimethoprim resistance gene *dhfr1a*.
- Example 40: Development of a PCR assay for the detection and identification of *Acinetobacter baumannii* and its associated aminoglycoside resistance gene *aph(3')-VIa*.
- Example 41: Specific detection and identification of *Bacteroides fragilis* using *atpD* (V-type) sequences.
- Example 42: Evidence for horizontal gene transfer in the evolution of the elongation factor Tu in Enterococci.
- Example 43: Elongation factor Tu (*tuf*) and the F-ATPase beta-subunit (*atpD*) as phylogenetic tools for species of the family *Enterobacteriaceae*.
- Example 44: Testing new pairs of PCR primers selected from two species-specific genomic DNA fragments which are objects of US patent 6,001,564.
- Example 45: Testing modified versions of PCR primers derived from the sequence of several primers which are objects of US patent 6,001,564.

The various Annexes show the strategies used for the selection of a variety of DNA amplification primers, nucleic acid hybridization probes and molecular beacon internal probes:

- (i) Annex I shows the amplification primers used for nucleic acid amplification from *tuf* sequences.
- (ii) Annex II shows the amplification primers used for nucleic acid amplification from *atpD* sequences.
- (iii) Annex III shows the internal hybridization probes for detection of *tuf* sequences.
- (iv) Annex IV illustrates the strategy used for the selection of the amplification primers specific for *atpD* sequences of the F-type.
- (v) Annex V illustrates the strategy used for the selection of the amplification primers specific for *atpD* sequences of the V-type.
- (vi) Annex VI illustrates the strategy used for the selection of the amplification primers specific for the *tuf* sequences of organelle lineage (M, the letter M is used to indicate that in most cases, the organelle is the mitochondria).
- (vii) Annex VII illustrates the strategy used for the selection of the amplification primers specific for the *tuf* sequences of eukaryotes (EF-1).
- (viii) Annex VIII illustrates the strategy for the selection of *Streptococcus agalactiae*-specific amplification primers from *tuf* sequences.
- (ix) Annex IX illustrates the strategy for the selection of *Streptococcus agalactiae*-specific hybridization probes from *tuf* sequences.
- (x) Annex X illustrates the strategy for the selection of *Streptococcus agalactiae*-specific amplification primers from *atpD* sequences.
- (xi) Annex XI illustrates the strategy for the selection from *tuf* sequences of *Candida albicans/dubliniensis*-specific amplification primers, *Candida albicans*-specific hybridization probe and *Candida dubliniensis*-specific hybridization probe.

- (xii) Annex XII illustrates the strategy for the selection of *Staphylococcus*-specific amplification primers from *tuf* sequences.
- (xiii) Annex XIII illustrates the strategy for the selection of the *Staphylococcus*-specific hybridization probe from *tuf* sequences.
- (xiv) Annex XIV illustrates the strategy for the selection of *Staphylococcus saprophyticus*-specific and *Staphylococcus haemolyticus*-specific hybridization probes from *tuf* sequences.
- (xv) Annex XV illustrates the strategy for the selection of *Staphylococcus aureus*-specific and *Staphylococcus epidermidis*-specific hybridization probes from *tuf* sequences.
- (xvi) Annex XVI illustrates the strategy for the selection of the *Staphylococcus hominis*-specific hybridization probe from *tuf* sequences.
- (xvii) Annex XVII illustrates the strategy for the selection of the *Enterococcus*-specific amplification primers from *tuf* sequences.
- (xviii) Annex XVIII illustrates the strategy for the selection of the *Enterococcus faecalis*-specific hybridization probe, of the *Enterococcus faecium*-specific hybridization probe and of the *Enterococcus casseliflavus-flavescens-gallinarum* group-specific hybridization probe from *tuf* sequences.
- (xix) Annex XIX illustrates the strategy for the selection of primers from *tuf* sequences for the identification of platelets contaminants.
- (xx) Annex XX illustrates the strategy for the selection of the universal amplification primers from *atpD* sequences.
- (xxi) Annex XXI shows the amplification primers used for nucleic acid amplification from *recA* sequences.
- (xxii) Annex XXII shows the specific and ubiquitous primers for nucleic acid amplification from *speA* sequences.
- (xxiii) Annex XXIII illustrates the first strategy for the selection of *Streptococcus pyogenes*-specific amplification primers from *speA* sequences.

- (xxiv) Annex XXIV illustrates the second strategy for the selection of *Streptococcus pyogenes*-specific amplification primers from *speA* sequences.
- (xxv) Annex XXV illustrates the strategy for the selection of *Streptococcus pyogenes*-specific amplification primers from *tuf* sequences.
- ~~(xxvi) Annex XXVI illustrates the strategy for the selection of *stx*₁-specific amplification primers and hybridization probe.~~
- (xxvii) Annex XXVII illustrates the strategy for the selection of *stx*₂-specific amplification primers and hybridization probe.
- (xxviii) Annex XXVIII illustrates the strategy for the selection of *vanA*-specific amplification primers from *van* sequences.
- (xxix) Annex XXIX illustrates the strategy for the selection of *vanB*-specific amplification primers from *van* sequences.
- (xxx) Annex XXX illustrates the strategy for the selection of *vanC*-specific amplification primers from *vanC* sequences.
- (xxxi) Annex XXXI illustrates the strategy for the selection of *Streptococcus pneumoniae*-specific amplification primers and hybridization probes from *pbpla* sequences.
- (xxxii) Annex XXXII shows the specific and ubiquitous primers for nucleic acid amplification from toxin gene sequences.
- (xxxiii) Annex XXXIII shows the molecular beacon internal hybridization probes for specific detection of toxin sequences.
- (xxxiv) Annex XXXIV shows the specific and ubiquitous primers for nucleic acid amplification from *van* sequences.
- (xxxv) Annex XXXV shows the internal hybridization probes for specific detection of *van* sequences.
- (xxxvi) Annex XXXVI shows the specific and ubiquitous primers for nucleic acid amplification from *pbp* sequences.
- (xxxvii) Annex XXXVII shows the internal hybridization probes for specific detection of *pbp* sequences.

(xxxviii) Annex XXXVIII illustrates the strategy for the selection of *vanAB*-specific amplification primers and *vanA*- and *vanB*- specific hybridization probes from *van* sequences.

(xxxix) Annex XXXIX shows the internal hybridization probe for specific detection of *mecA*.

(xl) Annex XL shows the specific and ubiquitous primers for nucleic acid amplification from *hexA* sequences.

(xli) Annex XLI shows the internal hybridization probe for specific detection of *hexA*.

(xlii) Annex XLII illustrates the strategy for the selection of *Streptococcus pneumoniae* species-specific amplification primers and hybridization probe from *hexA* sequences.

(xlili) Annex XLIII shows the specific and ubiquitous primers for nucleic acid amplification from *pcp* sequences.

(xliv) Annex XLIV shows specific and ubiquitous primers for nucleic acid amplification of *S. saprophyticus* sequences of unknown coding potential.

(xlv) Annex XLV shows the molecular beacon internal hybridization probes for specific detection of antimicrobial agents resistance gene sequences.

(xlvi) Annex XLVI shows the molecular beacon internal hybridization probe for specific detection of *S. aureus* gene sequences of unknown coding potential.

(xlvii) Annex XLVII shows the molecular beacon hybridization internal probe for specific detection of *tuf* sequences.

(xlviii) Annex XLVIII shows the molecular beacon internal hybridization probes for specific detection of *ddl* and *mtl* sequences.

(xlix) Annex XLIX shows the internal hybridization probe for specific detection of *S. aureus* sequences of unknown coding potential.

(l) Annex L shows the amplification primers used for nucleic acid amplification from antimicrobial agents resistance genes sequences.

- (li) Annex LI shows the internal hybridization probes for specific detection of antimicrobial agents resistance genes sequences.
- (lii) Annex LII shows the molecular beacon internal hybridization probes for specific detection of *atpD* sequences.
- (liii) Annex LIII shows the internal hybridization probes for specific detection of *atpD* sequences.
- (liv) Annex LIVI shows the internal hybridization probes for specific detection of *ddl* and *mtl* sequences.

As shown in these Annexes, the selected amplification primers may contain inosines and/or base ambiguities. Inosine is a nucleotide analog able to specifically bind to any of the four nucleotides A, C, G or T. Alternatively, degenerated oligonucleotides which consist of an oligonucleotide mix having two or more of the four nucleotides A, C, G or T at the site of mismatches were used. The inclusion of inosine and/or of degeneracies in the amplification primers allows mismatch tolerance thereby permitting the amplification of a wider array of target nucleotide sequences (Dieffenbach and Dveksler, 1995 PCR Primer: A Laboratory Manual, Cold Spring Harbor Laboratory Press, Plainview, New York).

EXAMPLES

EXAMPLE 1:

Sequencing of bacterial *atpD* (F-type and V-type) gene fragments. As shown in Annex IV, the comparison of publicly available *atpD* (F-type) sequences from a variety of bacterial species revealed conserved regions allowing the design of PCR primers able to amplify *atpD* sequences (F-type) from a wide range of bacterial species. Using primers pairs SEQ ID NOs. 566 and 567, 566 and 814, 568 and 567, 570 and 567, 572 and 567, 569 and 567, 571 and 567, 700 and 567, it was possible to amplify and sequence *atpD* sequences SEQ ID NOs. 242-270, 272-398, 673-

674, 737-767, 866-867, 942-955, 1245-1254, 1256-1265, 1527, 1576, 1577, 1600-1604, 1640-1646, 1649, 1652, 1655, 1657, 1659-1660, 1671, 1844-1845, and 1849-1865.

Similarly, Annex V shows the strategy to design the PCR primers able to amplify *atpD* sequences of the V-type from a wide range of archaeal and bacterial species.

Using primers SEQ ID NOs. 681-683, it was possible to amplify and sequence *atpD* sequences SEQ ID NOs. 827-832, 929-931, 958 and 966. As the gene was difficult to amplify for several species, additional amplification primers were designed inside the original amplicon (SEQ ID NOs. 1203-1207) in order to obtain sequence information for these species. Other primers (SEQ ID NO. 1212, 1213, 2282-2285) were also designed to amplify regions of the *atpD* gene (V-type) in archaeobacteria.

EXAMPLE 2:

Sequencing of eukaryotic *atpD* (F-type and V-type) gene fragments. The comparison of publicly available *atpD* (F-type) sequences from a variety of fungal and parasitical species revealed conserved regions allowing the design of PCR primers able to amplify *atpD* sequences from a wide range of fungal and parasitical species. Using primers pairs SEQ ID NOs. 568 and 573, 574 and 573, 574 and 708, and 566 and 567, it was possible to amplify and sequence *atpD* sequences SEQ ID NOs. 458-497, 530-538, 663, 667, 676, 678-680, 768-778, 856-862, 889-896, 941, 1638-1639, 1647, 1650-1651, 1653-1654, 1656, 1658, 1684, 1846-1848, and 2189-2192.

In the same manner, the primers described in Annex V (SEQ ID NOs. 681-683) could amplify the *atpD* (V-type) gene from various fungal and parasitical species. This strategy allowed to obtain SEQ ID NOs. 834-839, 956-957, and 959-965.

EXAMPLE 3:

Sequencing of eukaryotic *tuf* (EF-1) gene fragments. As shown in Annex VII, the comparison of publicly available *tuf* (EF-1) sequences from a variety of fungal and parasitical species revealed conserved regions allowing the design of PCR primers able to amplify *tuf* sequences from a wide range of fungal and parasitical species.

Using primers pairs SEQ ID NOs. 558 and 559, 813 and 559, 558 and 815, 560 and 559, 653 and 559, 558 and 655, and 654 and 559, 1999 and 2000, 2001 and 2003, 2002 and 2003, it was possible to amplify and sequence *tuf* sequences SEQ ID NOs. 399-457, 509-529, 622-624, 677, 779-790, 840-842, 865, 897-903, 1266-1287, 1561-1571 and 1685.

EXAMPLE 4:

Sequencing of eukaryotic *tuf* (organelle origin, M) gene fragments. As shown in Annex VI, the comparison of publicly available *tuf* (organelle origin, M) sequences from a variety of fungal and parasitical organelles revealed conserved regions allowing the design of PCR primers able to amplify *tuf* sequences of several organelles belonging to a wide range fungal and parasitical species. Using primers pairs SEQ ID NOs. 664 and 652, 664 and 561, 911 and 914, 912 and 914, 913 and 915, 916 and 561, 664 and 917, it was possible to amplify and sequence *tuf* sequences SEQ ID NOs. 498-508, 791-792, 843-855, 904-910, 1664, 1666-1667, 1669-1670, 1673-1683, 1686-1689, 1874-1876, 1879, 1956-1960, and 2193-2199.

EXAMPLE 5:

Specific detection and identification of *Streptococcus agalactiae* using *tuf* sequences. As shown in Annex VIII, the comparison of *tuf* sequences from a variety of bacterial species allowed the selection of PCR primers specific for *S. agalactiae*. The strategy used to design the PCR primers was based on the analysis

of a multiple sequence alignment of various *tuf* sequences. The multiple sequence alignment includes the *tuf* sequences of four bacterial strains from the target species as well as *tuf* sequences from other species and bacterial genera, especially representatives of closely related species. A careful analysis of this alignment allowed the selection of oligonucleotide sequences which are conserved within the target species but which discriminate sequences from other species and genera, especially from the closely related species, thereby permitting the species-specific, ubiquitous and sensitive detection and identification of the target bacterial species.

The chosen primer pair, oligos SEQ ID NO. 549 and SEQ ID NO. 550, gives an amplification product of 252 bp. Standard PCR was carried out using 0.4 μ M of each primer, 2.5 mM $MgCl_2$, BSA 0.05 mM, 1X Taq Buffer (Promega), dNTP 0.2 mM (Pharmacia), 0.5 U *Taq* DNA polymerase (Promega) coupled with TaqStartTM antibody (Clontech Laboratories Inc., Palo Alto), 1 μ l of genomic DNA sample in a final volume of 20 μ l using a PTC-200 thermocycler (MJ Research Inc.). The optimal cycling conditions for maximum sensitivity and specificity were 3 minutes at 95 °C for initial denaturation, then forty cycles of two steps consisting of 1 second at 95 °C and 30 seconds at 62 °C, followed by terminal extension at 72 °C for 2 minutes. Detection of the PCR products was made by electrophoresis in agarose gels (2 %) containing 0.25 μ g/ml of ethidium bromide.

Specificity of the assay was tested by adding into the PCR reactions, 0.1 ng of genomic DNA from each of the bacterial species listed in Table 8. Efficient amplification was observed only for the 5 *S. agalactiae* strains listed. Of the other bacterial species, including 32 species representative of the vaginal flora and 27 other streptococcal species, only *S. acidominimus* yielded amplification. The signal with 0.1 ng of *S. acidominimus* genomic DNA was weak and the detection limit for this species was 10 pg (corresponding to more than 4000 genome copies) while the detection limit for *S. agalactiae* was 2.5 fg (corresponding to one genome copy) of genomic DNA.

To increase the specificity of the assay, internal probes were designed for FRET (Fluorescence Resonance Energy Transfer) detection using the LightCycler™ (Idaho Technology). As illustrated in Annex IX, a multiple sequence alignment of streptococcal *tuf* sequence fragments corresponding to the 252 bp region amplified by primers SEQ ID NO. 549 and SEQ ID NO. 550, was used for the design of internal probes TSagHF436 (SEQ ID NO. 582) and TSagHF465 (SEQ ID NO. 583). The region of the amplicon selected for internal probes contained sequences unique and specific to *S. agalactiae*. SEQ ID NO. 583, the more specific probe, is labelled with fluorescein in 3', while SEQ ID NO. 582, the less discriminant probe, is labelled with CY5 in 5' and blocked in 3' with a phosphate group. However, since the FRET signal is only emitted if both probes are adjacently hybridized on the same target amplicon, detection is highly specific.

Real-time detection of PCR products using the LightCycler™ was carried out using 0.4 μ M of each primer (SEQ ID NO. 549-550), 0.2 μ M of each probe (SEQ ID NO. 582-583), 2.5 mM MgCl₂, BSA 450 μ g/ml, 1X PC2 Buffer (AB Peptides, St-Louis, MO), dNTP 0.2 mM (Pharmacia), 0.5 U KlenTaq1™ DNA polymerase (AB Peptides) coupled with TaqStart™ antibody (Clontech Laboratories Inc., Palo Alto), 0.7 μ l of genomic DNA sample in a final volume of 7 μ l using a LightCycler thermocycler (Idaho Technology). The optimal cycling conditions for maximum sensitivity and specificity were 3 minutes at 94 °C for initial denaturation, then forty cycles of three steps consisting of 0 second (this setting meaning the LightCycler will reach the target temperature and stay at it for its minimal amount of time) at 94 °C, 10 seconds at 64 °C, 20 seconds at 72 °C. Amplification was monitored during each annealing steps using the fluorescence ratio. The streptococcal species having close sequence homologies with the *tuf* sequence of *S. agalactiae* (*S. acidominimus*, *S. anginosus*, *S. bovis*, *S. dysgalactiae*, *S. equi*, *S. ferus*, *S. gordonii*, *S. intermedius*, *S. parasanguis*, *S. parauberis*, *S. salivarius*, *S. sanguis*, *S. suis*) as well as *S. agalactiae* were tested in the

LightCycler with 0.07 ng of genomic DNA per reaction. Only *S. agalactiae* yielded an amplification signal, hence demonstrating that the assay is species-specific. With the LightCycler™ assay using the internal FRET probes, the detection limit for *S. agalactiae* was 1-2 genome copies of genomic DNA.

EXAMPLE 6:

Specific detection and identification of *Streptococcus agalactiae* using *atpD* sequences. As shown in Annex X, the comparison of *atpD* sequences from a variety of bacterial species allowed the selection of PCR primers specific for *S. agalactiae*. The primer design strategy is similar to the strategy described in the preceding Example except that *atpD* sequences were used in the alignment.

Four primers were selected, ASag42 (SEQ ID NO. 627), ASag52 (SEQ ID NO. 628), ASag206 (SEQ ID NO. 625) and ASag371 (SEQ ID NO. 626). The following combinations of these four primers give four amplicons; SEQ ID NO. 627 + SEQ ID NO. 625 = 190 bp, SEQ ID NO. 628 + SEQ ID NO. 625 = 180 bp, SEQ ID NO. 627 + SEQ ID NO. 626 = 355 bp, and SEQ ID NO. 628 + SEQ ID NO. 626 = 345 bp.

Standard PCR was carried out on PTC-200 thermocyclers (MJ Research Inc) using 0.4 μ M of each primers pair, 2.5 mM MgCl₂, BSA 0.05 mM, 1X *taq* Buffer (Promega), dNTP 0.2 mM (Pharmacia), 0.5 U *Taq* DNA polymerase (Promega) coupled with TaqStart™ antibody (Clontech Laboratories Inc., Palo Alto), 1 μ l of genomic DNA sample in a final volume of 20 μ L. The optimal cycling conditions for maximum sensitivity and specificity were adjusted for each primer pair. Three minutes at 95 °C for initial denaturation, then forty cycles of two steps consisting of 1 second at 95 °C and 30 seconds at the optimal annealing temperature specified below were followed by terminal extension at 72 °C for 2 minutes. Detection of the PCR products was made by electrophoresis in agarose gels (2 %) containing

0.25 $\mu\text{g/ml}$ of ethidium bromide. Since *atpD* sequences are relatively more specific than *tuf* sequences, only the most closely related species namely, the streptococcal species listed in Table 9, were tested.

All four primer pairs only amplified the six *S. agalactiae* strains. With an annealing temperature of 63 °C, the primer pair SEQ ID NO. 627 + SEQ ID NO. 625 had a sensitivity of 1-5 fg (equivalent to 1-2 genome copies). At 55 °C, the primer pair SEQ ID NO. 628 + SEQ ID NO. 625 had a sensitivity of 2.5 fg (equivalent to 1 genome copy). At 60 °C, the primer pair SEQ ID NO. 627 + SEQ ID NO. 626 had a sensitivity of 10 fg (equivalent to 4 genome copies). At 58 °C, the primer pair SEQ ID NO. 628 + SEQ ID NO. 626 had a sensitivity of 2.5-5 fg (equivalent to 1-2 genome copies). This proves that all four primer pairs can detect *S. agalactiae* with high specificity and sensitivity. Together with Example 5, this example demonstrates that both *tuf* and *atpD* sequences are suitable and flexible targets for the identification of microorganisms at the species level. The fact that 4 different primer pairs based on *atpD* sequences led to efficient and specific amplification of *S. agalactiae* demonstrates that the challenge is to find target genes suitable for diagnostic purposes, rather than finding primer pairs from these target sequences.

EXAMPLE 7:

Development of a PCR assay for detection and identification of staphylococci at genus and species levels.

Materials and Methods

Bacterial strains. The specificity of the PCR assay was verified by using a panel of ATCC (America Type Culture Collection) and DSMZ (Deutsche Sammlung von Mikroorganismen und Zellkulturen GmbH; German Collection of

Microorganisms and Cell Cultures) reference strains consisting of 33 gram-negative and 47 gram-positive bacterial species (Table 12). In addition, 295 clinical isolates representing 11 different species of staphylococci from the microbiology laboratory of the Centre Hospitalier Universitaire de Québec, Pavillon Centre Hospitalier de l'Université Laval (CHUL) (Ste-Foy, Québec, Canada) were also tested to further validate the *Staphylococcus*-specific PCR assay. These strains were all identified by using (i) conventional methods or (ii) the automated MicroScan Autoscan-4 system equipped with the Positive BP Combo Panel Type 6 (Dade Diagnostics, Mississauga, Ontario, Canada). Bacterial strains from frozen stocks kept at -80 °C in brain heart infusion (BHI) broth containing 10% glycerol were cultured on sheep blood agar or in BHI broth (Quelab Laboratories Inc, Montréal, Québec, Canada).

PCR primers and internal probes. Based on multiple sequence alignments, regions of the *tuf* gene unique to staphylococci were identified. *Staphylococcus*-specific PCR primers TStaG422 (SEQ ID NO. 553) and TStaG765 (SEQ ID NO. 575) were derived from these regions (Annex XII). These PCR primers are displaced by two nucleotide positions compared to original *Staphylococcus*-specific PCR primers described in our patent publication WO98/20157 (SEQ ID NOs. 17 and 20 in the said patent publication). These modifications were done to ensure specificity and ubiquity of the primer pair, in the light of new *tuf* sequence data revealed in the present patent application for several additional staphylococcal species and strains.

Similarly, sequence alignment analysis were performed to design genus and species-specific internal probes (see Annexes XIII to XVI). Two internal probes specific for *Staphylococcus* (SEQ ID NOs. 605-606), five specific for *S. aureus* (SEQ ID NOs. 584-588), five specific for *S. epidermidis* (SEQ ID NO. 589-593), two specific for *S. haemolyticus* (SEQ ID NOs. 594-595), three specific for *S. hominis* (SEQ ID NOs. 596-598), four specific for *S. saprophyticus* (SEQ ID NOs. 599-601 and 695), and two specific for coagulase-negative *Staphylococcus* species including

S. epidermidis, *S. hominis*, *S. saprophyticus*, *S. auricularis*, *S. capitis*, *S. haemolyticus*, *S. lugdunensis*, *S. simulans*, *S. cohnii* and *S. warneri* (SEQ ID NOs. 1175-1176) were designed. The range of mismatches between the *Staphylococcus*-specific 371-bp amplicon and each of the 20-mer species-specific internal probes was from 1 to 5, in the middle of the probe when possible. No mismatches were present in the two *Staphylococcus*-specific probes for the 11 species analyzed: *S. aureus*, *S. auricularis*, *S. capitis*, *S. cohnii*, *S. epidermidis*, *S. haemolyticus*, *S. hominis*, *S. lugdunensis*, *S. saprophyticus*, *S. simulans* and *S. warneri*. In order to verify the intra-specific sequence conservation of the nucleotide sequence, sequences were obtained for the 371-bp amplicon from five unrelated ATCC and clinical strains for each of the species *S. aureus*, *S. epidermidis*, *S. haemolyticus*, *S. hominis* and *S. saprophyticus*. The Oligo™ (version 5.0) primer analysis software (National Biosciences, Plymouth, Minn.) was used to confirm the absence of self-complementary regions within and between the primers or probes. When required, the primers contained inosines or degenerated nucleotides at one or more variable positions. Oligonucleotide primers and probes were synthesized on a model 394 DNA synthesizer (Applied Biosystems, Mississauga, Ontario, Canada). Detection of the hybridization was performed with the DIG-labeled dUTP incorporated during amplification with the *Staphylococcus*-specific PCR assay, and the hybridization signal was detected with a luminometer (Dynex Technologies) as described above in the section on luminescent detection of amplification products. Annexes XIII to XVI illustrate the strategy for the selection of several internal probes.

PCR amplification. For all bacterial species, amplification was performed from purified genomic DNA or from a bacterial suspension whose turbidity was adjusted to that of a 0.5 McFarland standard, which corresponds to approximately 1.5×10^8 bacteria per ml. One nanogram of genomic DNA or 1 μ l of the standardized bacterial suspension was transferred directly to a 19 μ l PCR mixture. Each PCR reaction contained 50 mM KCl, 10 mM Tris-HCl (pH 9.0), 0.1% Triton X-100, 2.5 mM

MgCl₂, 0.2 µM (each) of the two *Staphylococcus* genus-specific primers (SEQ ID NOs. 553 and 575), 200 µM (each) of the four deoxynucleoside triphosphates (Pharmacia Biotech), 3.3 µg/µl bovine serum albumin (BSA) (Sigma-Aldrich Canada Ltd, Oakville, Ontario, Canada), and 0.5 U *Taq* polymerase (Promega) coupled with *TaqStart*TM Antibody (Clontech). The PCR amplification was performed as follows: 3 min. at 94 °C for initial denaturation, then forty cycles of two steps consisting of 1 second at 95 °C and 30 seconds at 55 °C, plus a terminal extension at 72 °C for 2 minutes. Detection of the PCR products was made by electrophoresis in agarose gels (2 %) containing 0.25 µg/ml of ethidium bromide. Visualization of the PCR products was made under UV at 254 nm.

For determination of the sensitivities of the PCR assays, two-fold dilutions of purified genomic DNA were used to determine the minimal number of genome copies which can be detected.

Results

Amplifications with the *Staphylococcus* genus-specific PCR assay. The specificity of the assay was assessed by performing 30-cycle and 40-cycle PCR amplifications with the panel of gram-positive (47 species from 8 genera) and gram-negative (33 species from 22 genera) bacterial species listed in Table 12. The PCR assay was able to detect efficiently 27 of 27 staphylococcal species tested in both 30-cycle and 40-cycle regimens. For 30-cycle PCR, all bacterial species tested other than staphylococci were negative. For 40-cycle PCR, *Enterococcus faecalis* and *Macrococcus caseolyticus* were slightly positive for the *Staphylococcus*-specific PCR assay. The other species tested remained negative. Ubiquity tests performed on a collection of 295 clinical isolates provided by the microbiology laboratory of the Centre Hospitalier Universitaire de Québec, Pavillon Centre Hospitalier de l'Université Laval (CHUL), including *Staphylococcus aureus* (n=34), *S. auricularis* (n=2), *S. capitis* (n=19), *S. cohnii* (n=5), *S. epidermidis* (n=18), *S. haemolyticus*

(n=21), *S. hominis* (n=73), *S. lugdunensis* (n=17), *S. saprophyticus* (n=6), *S. simulans* (n=3), *S. warneri* (n=32) and *Staphylococcus* sp. (n=65), showed a uniform amplification signal with the 30-cycle PCR assays and a perfect relation between the genotype and classical identification schemes.

The sensitivity of the *Staphylococcus*-specific assay with 30-cycle and 40-cycle PCR protocols was determined by using purified genomic DNA from the 11 staphylococcal species previously mentioned. For PCR with 30 cycles, a detection limit of 50 copies of genomic DNA was consistently obtained. In order to enhance the sensitivity of the assay, the number of cycles was increased. For 40-cycle PCR assays, the detection limit was lowered to a range of 5-10 genome copies, depending on the staphylococcal species tested.

Hybridization between the *Staphylococcus*-specific 371-bp amplicon and species-specific or genus-specific internal probes. Inter-species polymorphism was sufficient to generate species-specific internal probes for each of the principal species involved in human diseases (*S. aureus*, *S. epidermidis*, *S. haemolyticus*, *S. hominis* and *S. saprophyticus*). In order to verify the intra-species sequence conservation of the nucleotide sequence, sequence comparisons were performed on the 371-bp amplicon from five unrelated ATCC and clinical strains for each of the 5 principal staphylococcal species: *S. aureus*, *S. epidermidis*, *S. haemolyticus*, *S. hominis* and *S. saprophyticus*. Results showed a high level of conservation of nucleotide sequence between different unrelated strains from the same species. This sequence information allowed the development of staphylococcal species identification assays using species-specific internal probes hybridizing to the 371-bp amplicon. These assays are specific and ubiquitous for those five staphylococcal species. In addition to the species-specific internal probes, the genus-specific internal probes were able to recognize all or most *Staphylococcus* species tested.

EXAMPLE 8:

Differentiating between the two closely related yeast species *Candida albicans* and *Candida dubliniensis*. It is often useful for the clinician to be able to differentiate between two very closely related species of microorganisms. *Candida albicans* is the most important cause of invasive human mycose. In recent years, a very closely related species, *Candida dubliniensis*, was isolated in immunosuppressed patients. These two species are difficult to distinguish by classic biochemical methods. This example demonstrates the use of *tuf* sequences to differentiate *Candida albicans* and *Candida dubliniensis*. PCR primers SEQ ID NOs. 11-12, from previous patent publication WO98/20157, were selected for their ability to specifically amplify a *tuf* (elongation factor 1 alpha type) fragment from both species (see Annex XI for primer positions). Within this *tuf* fragment, a region differentiating *C. albicans* and *C. dubliniensis* by two nucleotides was selected and used to design two internal probes (see Annex XI for probe design, SEQ ID NOs. 577 and 578) specific for each species. Amplification of genomic DNA from *C. albicans* and *C. dubliniensis* was carried out using DIG-11-dUTP as described above in the section on chemiluminescent detection of amplification products. Internal probes SEQ ID NOs. 577 and 578 were immobilized on the bottom of individual microtiter plates and hybridization was carried out as described above in the above section on chemiluminescent detection of amplification products. Luminometer data showed that the amplicon from *C. albicans* hybridized only to probe SEQ ID NO. 577 while the amplicon from *C. dubliniensis* hybridized only to probe SEQ ID NO. 578, thereby demonstrating that each probe was species-specific.

EXAMPLE 9:

Specific identification of *Entamoeba histolytica*. Upon analysis of *tuf* (elongation factor 1 alpha) sequence data, it was possible to find four regions where

Entamoeba histolytica sequences remained conserved while other parasitical and eukaryotic species have diverged. Primers TEntG38 (SEQ ID NO. 703), TEntG442 (SEQ ID NO. 704), TEntG534 (SEQ ID NO. 705), and TEntG768 (SEQ ID NO. 706) were designed so that SEQ ID NO. 703 could be paired with the three other primers. On PTC-200 thermocyclers (MJ Research), the cycling conditions for initial sensitivity and specificity testing were 3 min. at 94 °C for initial denaturation, then forty cycles of two steps consisting of 1 second at 95 °C and 30 seconds at 55 °C, followed by terminal extension at 72 °C for 2 minutes. Detection of the PCR products was made by electrophoresis in agarose gels (2 %) containing 0.25 µg/ml of ethidium bromide. The three primer pairs could detect the equivalent of less than 200 *E. histolytica* genome copies. Specificity was tested using 0.5 ng of purified genomic DNA from a panel of microorganisms including *Babesia bovis*, *Babesia microtti*, *Candida albicans*, *Crithidia fasciculata*, *Leishmania major*, *Leishmania hertigi* and *Neospora caninum*. Only *E. histolytica* DNA could be amplified, thereby suggesting that the assay was species-specific.

EXAMPLE 10:

Sensitive identification of *Chlamydia trachomatis*. Upon analysis of *tuf* sequence data, it was possible to find two regions where *Chlamydia trachomatis* sequences remained conserved while other species have diverged. Primers Ctr82 (SEQ ID NO. 554) and Ctr249 (SEQ ID NO. 555) were designed. With the PTC-200 thermocyclers (MJ Research), the optimal cycling conditions for maximum sensitivity and specificity were determined to be 3 min. at 94 °C for initial denaturation, then forty cycles of two steps consisting of 1 second at 95 °C and 30 seconds at 60 °C, followed by terminal extension at 72 °C for 2 minutes. Detection of the PCR products was made by electrophoresis in agarose gels (2 %) containing 0.25 µg/ml of ethidium bromide. The assay could detect the equivalent of 8 *C. trachomatis* genome copies. Specificity was tested with 0.1 ng of purified genomic DNA from a panel of microorganisms including 22 species commonly encountered

in the vaginal flora (*Bacillus subtilis*, *Bacteroides fragilis*, *Candida albicans*, *Clostridium difficile*, *Corynebacterium cervicis*, *Corynebacterium urealyticum*, *Enterococcus faecalis*, *Enterococcus faecium*, *Escherichia coli*, *Fusobacterium nucleatum*, *Gardnerella vaginalis*, *Haemophilus influenzae*, *Klebsiella oxytoca*, *Lactobacillus acidophilus*, *Peptococcus niger*, *Peptostreptococcus prevotii*, *Porphyromonas asaccharolytica*, *Prevotella melaninogenica*, *Propionibacterium acnes*, *Staphylococcus aureus*, *Streptococcus acidominimus*, and *Streptococcus agalactiae*). Only *C. trachomatis* DNA could be amplified, thereby suggesting that the assay was species-specific.

EXAMPLE 11:

Genus-specific detection and identification of enterococci. Upon analysis of *tuf* sequence data and comparison with the repertory of *tuf* sequences, it was possible to find two regions where *Enterococcus* sequences remained conserved while other genera have diverged (Annex XVII). Primer pair Encg313dF and Encg599c (SEQ ID NOs. 1137 and 1136) was tested for its specificity by using purified genomic DNA from a panel of bacteria listed in Table 10. Using the PTC-200 thermocycler (MJ Research), the optimal cycling conditions for maximum sensitivity and specificity were determined to be 3 min. at 94 °C for initial denaturation, then forty cycles of two steps consisting of 1 second at 95 °C and 30 seconds at 55 °C, followed by terminal extension at 72 °C for 2 minutes. Detection of the PCR products was made by electrophoresis in agarose gels (2 %) containing 0.25 µg/ml of ethidium bromide. Visualization of the PCR products was made under UV at 254 nm. The 18 enterococcal species listed in Table 10 were all amplified efficiently. The only other species amplified were *Abiotrophia adiacens*, *Gemella haemolysans* and *Gemella morbillorum*, three gram-positive species. Sensitivity tested with several strains of *E. casseliflavus*, *E. faecium*, *E. faecalis*, *E. flavescens* and *E. gallinarum* and with one strain of each other *Enterococcus* species listed in Table 10 ranged from 1 to 10 copies of genomic DNA. The sequence variation

within the 308-bp amplicon was sufficient so that internal probes could be used to speciate the amplicon and differentiate enterococci from *Abiotrophia adiacens*, *Gemella haemolysans* and *Gemella morbillorum*, thereby allowing to achieve excellent specificity. Species-specific internal probes were generated for each of the clinically important species, *E. faecalis* (SEQ ID NO. 1174), *E. faecium* (SEQ ID NO. 602), and the group including *E. casseliflavus*, *E. flavescens* and *E. gallinarum* (SEQ ID NO. 1122) (Annex XVIII). The species-specific internal probes were able to differentiate their respective *Enterococcus* species from all other *Enterococcus* species. These assays are sensitive, specific and ubiquitous for those five *Enterococcus* species.

EXAMPLE 12:

Identification of the major bacterial platelets contaminants using *tuf* sequences with a multiplex PCR test. Blood platelets preparations need to be monitored for bacterial contaminations. The *tuf* sequences of 17 important bacterial contaminants of platelets were aligned. As shown in Annex XIX, analysis of these sequences allowed the design of PCR primers. Since in the case of contamination of platelet concentrates, detecting all species (not just the more frequently encountered ones) is desirable, perfect specificity of primers was not an issue in the design. However, sensitivity is important. That is why, to avoid having to put too much degeneracy, only the most frequent contaminants were included in primer design, knowing that the selected primers would anyway be able to amplify more species than the 17 used in the design because they target highly conserved regions of *tuf* sequences. Oligonucleotide sequences which are conserved in these 17 major bacterial contaminants of platelet concentrates were chosen (oligos Tplaq 769 and Tplaq 991, respectively SEQ ID NOs. 636 and 637) thereby permitting the detection of these bacterial species. However, sensitivity was slightly deficient with staphylococci. To ensure maximal sensitivity in the detection of all the more frequent bacterial contaminants, a multiplex assay also including oligonucleotide

primers targetting the *Staphylococcus* genera (oligos Stag 422, SEQ ID NO. 553; and Stag 765, SEQ ID NO. 575) was developed. The bacterial species detected with the assay are listed in Table 14.

The primer pairs, oligos SEQ ID NO. 636 and SEQ ID NO. 637 that give an amplification product of 245 pb, and oligos SEQ ID NO. 553 and SEQ ID NO. 575 that give an amplification product of 368 pb, were used simultaneously in the multiplex PCR assay. Detection of these PCR products was made on the LightCycler thermocycler (Idaho Technology) using SYBR[®] Green I (Molecular Probe Inc.). SYBR[®] Green I is a fluorescent dye that binds specifically to double-stranded DNA.

Fluorogenic detection of PCR products with the LightCycler was carried out using 1.0 μ M of both Tplaq primers (SEQ ID NOs. 636-637) and 0.4 μ M of both TStag primers (SEQ ID NOs. 553 and 575), 2.5 mM MgCl₂, BSA 7.5 μ M, dNTP 0.2 mM (Pharmacia), 10 mM Tris-HCl (pH 8.3), 50 mM KCl, 0.5 U Taq DNA polymerase (Boehringer Mannheim) coupled with TaqStart[™] antibody (Clontech), and 0.07 ng of genomic DNA sample in a final volume of 7 μ l. The optimal cycling conditions for maximum sensitivity and specificity were 1 minute at 94 °C for initial denaturation, then forty-five cycles of three steps consisting of 0 second at 95 °C, 5 seconds at 60 °C and 9 seconds at 72 °C. Amplification was monitored during each elongation cycle by measuring the level of SYBR[®] Green I. However, real analysis takes place after PCR. Melting curves are done for each sample and transformation of the melting peak allows determination of T_m. Thus primer-dimer and specific PCR product are discriminated. With this assay, all prominent bacterial contaminants of platelet concentrates listed in Annex XIX and Table 14 were detected. Sensitivity tests were performed on the 9 most frequent bacterial contaminants of platelets. The detection limit was less than 20 genome copies for *E. cloacae*, *B. cereus*, *S. choleraesuis* and *S. marcescens*; less than 15 genome copies for *P. aeruginosa*; and 2 to 3 copies were detected for *S. aureus*, *S.*

epidermidis, *E. coli* and *K. pneumoniae*. Further refinements of assay conditions should increase sensitivity levels.

EXAMPLE 13:

The resolving power of the *tuf* and *atpD* sequences databases is comparable to the biochemical methods for bacterial identification. The present gold standard for bacterial identification is mainly based on key morphological traits and batteries of biochemical tests. Here we demonstrate that the use of *tuf* and *atpD* sequences combined with simple phylogenetic analysis of databases formed by these sequences is comparable to the gold standard. In the process of acquiring data for the *tuf* sequences, we sequenced the *tuf* gene of a strain that was given to us labelled as *Staphylococcus hominis* ATCC 35982. That *tuf* sequence (SEQ ID NO. 192) was incorporated into the *tuf* sequences database and subjected to a basic phylogenetic analysis using the Pileup command from version 10 of the GCG package (Genetics Computer Group). This analysis indicated that SEQ ID NO. 192 is not associated with other *S. hominis* strains but rather with the *S. warneri* strains. The ATCC 35982 strain was sent to the reference laboratory of the Laboratoire de santé publique du Québec (LSPQ). They used the classic identification scheme for staphylococci (Kloos and Schleifer, 1975., J. Clin. Microbiol. 1:82-88). Their results shown that although the colonial morphology could correspond to *S. hominis*, the more precise biochemical assays did not. These assays included discriminant mannitol, mannose and ribose acidification tests as well as rapid and dense growth in deep thioglycolate agar. The LSPQ report identified strain ATCC 35982 as *S. warneri* which confirms our database analysis. The same thing happened for *S. warneri* (SEQ ID NO. 187) which had initially been identified as *S. haemolyticus* by a routine clinical laboratory using a low resolving power automated system (MicroScan, AutoScan-4™). Again, the *tuf* and LSPQ analysis agreed on its identification as *S. warneri*. In numerous other instances, in the course of acquiring *tuf* and *atpD* sequence data from various species and genera,

analysis of our *tuf* and/or *atpD* sequence databases permitted the exact identification of mislabelled or erroneously identified strains. These results clearly demonstrate the usefulness and the high resolving power of our sequence-based identification assays using the *tuf* and *atpD* sequences databases.

EXAMPLE 14:

Detection of group B streptococci from clinical specimens.

Introduction

Streptococcus agalactiae, the group B streptococcus (GBS), is responsible for a severe illness affecting neonate infants. The bacterium is passed from the healthy carrier mother to the baby during delivery. To prevent this infection, it is recommended to treat expectant mothers susceptible of carrying GBS in their vaginal/anal flora. Carrier status is often a transient condition and rigorous monitoring requires cultures and classic bacterial identification weeks before delivery. To improve the detection and identification of GBS we developed a rapid, specific and sensitive PCR test fast enough to be performed right at delivery.

Materials and Methods

GBS clinical specimens. A total of 66 duplicate vaginal/anal swabs were collected from 41 consenting pregnant women admitted for delivery at the Centre Hospitalier Universitaire de Québec, Pavillon Saint-François d'Assise following the CDC recommendations. The samples were obtained either before or after rupture of membranes. The swab samples were tested at the Centre de Recherche en Infectiologie de l'Université Laval within 24 hours of collection. Upon receipt, one swab was cut and then the tip of the swab was added to GNS selective broth for identification of group B streptococci (GBS) by the standard culture methods

recommended by the CDC. The other swab was processed following the instruction of the IDI DNA extraction kit (Infectio Diagnostics (IDI) Inc.) prior to PCR amplification.

Oligonucleotides. PCR primers, Tsag340 (SEQ ID NO. 549) and Tsag552 (SEQ ID NO. 550) complementary to the regions of the *tuf* gene unique for GBS were designed based upon a multiple sequence alignment using our repertory of *tuf* sequences. Oligo primer analysis software (version 5.0) (National Biosciences) was used to analyse primers annealing temperature, secondary structure potential as well as mispriming and dimerization potential. The primers were synthesized using a model 391 DNA synthesizer (Applied Biosystems).

A pair of fluorescently labeled adjacent hybridization probes Sag465-F (SEQ ID NO. 583) and Sag436-C (SEQ ID NO. 582) were synthesized and purified by Operon Technologies. They were designed to meet the recommendations of the manufacturer (Idaho Technology) and based upon multiple sequence alignment analysis using our repertory of *tuf* sequences to be specific and ubiquitous for GBS. These adjacent probes, which are separated by one nucleotide, allow fluorescence resonance energy transfer (FRET), generating an increased fluorescence signal when both hybridized simultaneously to their target sequences. The probe SEQ ID NO. 583 was labeled with FITC in 3 prime while SEQ ID NO. 582 was labeled with Cy5 in 5 prime. The Cy5-labeled probes contained a 3'-blocking phosphate group to prevent extension of the probes during the PCR reactions.

PCR amplification. Conventional amplifications were performed either from 2 μ l of a purified genomic DNA preparation or cell lysates of vaginal/anal specimens. The 20 μ l PCR mixture contained 0.4 μ M of each GBS-specific primer (SEQ ID NOs. 549-550), 200 μ M of each deoxyribonucleotide (Pharmacia Biotech), 10 mM Tris-HCl (pH 9.0), 50 mM KCl, 0.1% Triton X-100, 2.5 mM $MgCl_2$, 3.3 mg/ml bovine serum albumin (BSA) (Sigma), and 0.5 U of *Taq* polymerase (Promega) combined with the TaqStartTM antibody (Clontech). The TaqStartTM antibody, which is a neutralizing monoclonal antibody of *Taq* DNA

polymerase, was added to all PCR reactions to enhance the efficiency of the amplification. The PCR mixtures were subjected to thermal cycling (3 min at 95 °C and then 40 cycles of 1 s at 95 °C, and 30 s at 62 °C with a 2-min final extension at 72 °C) with a PTC-200 DNA Engine thermocycler (MJ research). The PCR-amplified reaction mixture was resolved by agarose gel electrophoresis.

The LightCycler™ PCR amplifications were performed with 1 µl of a purified genomic DNA preparation or cell lysates of vaginal/anal specimens. The 10µl amplification mixture consisted of 0.4 µM each GBS-specific primer (SEQ ID NOs. 549-550), 200 µM each dNTP, 0.2 µM each fluorescently labeled probe (SEQ ID NOs. 582-583), 300 µg/ml BSA (Sigma), and 1 µl of 10x PC2 buffer (containing 50 mM Tris-HCl (pH 9.1), 16 mM ammonium sulfate, 3.5 mM Mg²⁺, and 150 µg/ml BSA) and 0.5 U KlenTaq1™ (AB Peptides) coupled with TaqStart™ antibody (Clontech). KlenTaq1™ is a highly active and more heat-stable DNA polymerase without 5'-exonuclease activity. This prevents hydrolysis of hybridized probes by the 5' to 3' exonuclease activity. A volume of 7 µl of the PCR mixture was transferred into a composite capillary tube (Idaho Technology). The tubes were then centrifuged to move the reaction mixture to the tips of the capillaries and then cleaned with optical-grade methanol. Subsequently the capillaries were loaded into the carousel of a LC32 LightCycler™ (Idaho Technology), an instrument that combines rapid-cycle PCR with fluorescence analysis for continuous monitoring during amplification. The PCR reaction mixtures were subjected to a denaturation step at 94 °C for 3 min followed by 45 cycles of 0 s at 94 °C, 20 s at 64 °C and 10 s at 72 °C with a temperature transition rate of 20 °C/s. Fluorescence signals were obtained at each cycle by sequentially positioning each capillary on the carousel at the focus of optical elements affiliated to the built-in fluorimeter for 100 milliseconds. Complete amplification and analysis required about 35 min.

Specificity and sensitivity tests. The specificity of the conventional and LightCycler™ PCR assays was verified by using purified genomic DNA (0.1 ng/reaction) from a battery of ATCC reference strains representing 35 clinically

relevant gram-positive species (*Abiotrophia defectiva* ATCC 49176, *Bifidobacterium breve* ATCC 15700, *Clostridium difficile* ATCC 9689, *Corynebacterium urealyticum* ATCC 43042, *Enterococcus casseliflavus* ATCC 25788, *Enterococcus durans* ATCC 19432, *Enterococcus faecalis* ATCC 29212, *Enterococcus faecium* ATCC 19434, *Enterococcus gallinarum* ATCC 49573, *Enterococcus raffinosus* ATCC 49427, *Lactobacillus reuteri* ATCC 23273, *Lactococcus lactis* ATCC 19435, *Listeria monocytogenes* ATCC 15313, *Peptococcus niger* ATCC 27731, *Peptostreptococcus anaerobius* ATCC 27337, *Peptostreptococcus prevotii* ATCC 9321, *Staphylococcus aureus* ATCC 25923, *Staphylococcus epidermidis* ATCC 14990, *Staphylococcus haemolyticus* ATCC 29970, *Staphylococcus saprophyticus* ATCC 15305, *Streptococcus agalactiae* ATCC 27591, *Streptococcus anginosus* ATCC 33397, *Streptococcus bovis* ATCC 33317, *Streptococcus constellatus* ATCC 27823, *Streptococcus dysgalactiae* ATCC 43078, *Streptococcus gordonii* ATCC 10558, *Streptococcus mitis* ATCC 33399, *Streptococcus mutans* ATCC 25175, *Streptococcus oralis* ATCC 35037, *Streptococcus parauberis* ATCC 6631, *Streptococcus pneumoniae* ATCC 6303, *Streptococcus pyogenes* ATCC 19615, *Streptococcus salivarius* ATCC 7073, *Streptococcus sanguinis* ATCC 10556, *Streptococcus uberis* ATCC 19436). These microbial species included 15 species of streptococci and many members of the normal vaginal and anal floras. In addition, 40 GBS isolates of human origin, whose identification was confirmed by a latex agglutination test (Streptex, Murex), were also used to evaluate the ubiquity of the assay.

For determination of the sensitivities (i.e., the minimal number of genome copies that could be detected) for conventional and LightCycler™ PCR assays, serial 10-fold or 2-fold dilutions of purified genomic DNA from 5 GBS ATCC strains were used.

Results

Evaluation of the GBS-specific conventional and LightCycler™ PCR assays. The specificity of the two assays demonstrated that only DNAs from GBS

strains could be amplified. Both PCR assays did not amplify DNAs from any other bacterial species tested including 14 streptococcal species other than GBS as well as phylogenetically related species belonging to the genera *Enterococcus*, *Peptostreptococcus* and *Lactococcus*. Important members of the vaginal or anal flora, including coagulase-negative staphylococci, *Lactobacillus* sp., and *Bacteriodes* sp. were also negative with the GBS-specific PCR assay. The LightCycler™ PCR assays detected only GBS DNA by producing an increased fluorescence signal which was interpreted as a positive PCR result. Both PCR methods were able to amplify all of 40 GBS clinical isolates, showing a perfect correlation with the phenotypic identification methods.

The sensitivity of the assay was determined by using purified genomic DNA from the 5 ATCC strains of GBS. The detection limit for all of these 5 strains was one genome copy of GBS. The detection limit of the assay with the LightCycler™ was 3.5 fg of genomic DNA (corresponding to 1-2 genome copies of GBS). These results confirmed the high sensitivity of our GBS-specific PCR assay.

Direct Detection of GBS from vaginal/anal specimens. Among 66 vaginal/anal specimens tested, 11 were positive for GBS by both culture and PCR. There was one sample positive by culture only. The sensitivity of both PCR methods with vaginal/anal specimens for identifying colonization status in pregnant women at delivery was 91.7% when compared to culture results. The specificity and positive predictive values were both 100% and the negative predictive value was 97.8%. The time for obtaining results was approximately 45 min for LightCycler™ PCR, approximately 100 min for conventional PCR and 48 hours for culture.

Conclusion

We have developed two PCR assays (conventional and LightCycler™) for the detection of GBS, which are specific (i.e., no amplification of DNA from a variety of bacterial species other than GBS) and sensitive (i.e., able to detect around 1

genome copy for several reference ATCC strains of GBS). Both PCR assays are able to detect GBS directly from vaginal/anal specimens in a very short turnaround time. Using the real-time PCR assay on LightCycler™, we can detect GBS carriage in pregnant women at delivery within 45 minutes.

EXAMPLE 15:

Simultaneous detection and identification of *Streptococcus pyogenes* and its pyrogenic exotoxin A. The rapid detection of *Streptococcus pyogenes* and of its pyrogenic exotoxin A is of clinical importance. We developed a multiplex assay which permits the detection of strains of *S. pyogenes* carrying the pyrogenic toxin A gene, which is associated with scarlet fever and other pathologies. In order to specifically detect *S. pyogenes*, nucleotide sequences of the pyrrolidone carboxyl peptidase (*pcp*) gene were aligned to design PCR primers Spy291 (SEQ ID NO. 1211) and Spy473 (SEQ ID NO. 1210). Next, we designed primers for the specific detection of the pyrogenic exotoxin A. Nucleotide sequences of the *speA* gene, carried on the bacteriophage T12, were aligned as shown in Annex XXIII to design PCR primers Spytx814 (SEQ ID NO. 994) and Spytx 927 (SEQ ID NO. 995).

The primer pairs: oligos SEQ ID NOs. 1210-1211, yielding an amplification product of 207 bp, and oligos SEQ ID NOs. 994-995, yielding an amplification product of 135 bp, were used in a multiplex PCR assay.

PCR amplification was carried out using 0.4 μ M of both pairs of primers, 2.5 mM $MgCl_2$, BSA 0.05 μ M, dNTP 0.2 μ M (Pharmacia), 10mM Tris-HCl (pH 9.0), 0.1% Triton X-100, 2.5 mM $MgCl_2$, 0.5 U *Taq* DNA polymerase (Promega) coupled with TaqStart™ antibody (Clontech Laboratories Inc.), and 1 μ l of genomic DNA sample in a final volume of 20 μ l. PCR amplification was performed using a PTC-200 thermal cycler (MJ Research). The optimal cycling conditions for maximum specificity and sensitivity were 3 minutes at 94 °C for

initial denaturation, then forty cycles of two steps consisting of 1 second at 95 °C and 30 seconds at 63 °C, followed by a final step of 2 minutes at 72 °C. Detection of the PCR products was made by electrophoresis in agarose gels (2 %) containing 0.25 µg/ml of ethidium bromide. Visualization of the PCR products was made under UV at 254 nm.

The detection limit was less than 5 genome copies for both *S. pyogenes* and its pyrogenic exotoxin A. The assay was specific for pyrogenic exotoxin A-producing *S. pyogenes*: strains of the 27 other species of *Streptococcus* tested, as well as 20 strains of various gram-positive and gram-negative bacterial species were all negative.

A similar approach was used to design an alternative set of *speA*-specific primers (SEQ ID NOs. 996 to 998, see Annex XXIV). In addition, another set of primers based on the *tuf* gene (SEQ ID NOs. 999 to 1001, see Annex XXV) could be used to specifically detect *Streptococcus pyogenes*.

EXAMPLE 16:

Real-time detection and identification of Shiga toxin-producing bacteria. Shiga toxin-producing *Escherichia coli* and *Shigella dysenteriae* cause bloody diarrhea. Currently, identification relies mainly on the phenotypic identification of *S. dysenteriae* and *E. coli* serotype O157:H7. However, other serotypes of *E. coli* are increasingly found to be producers of type 1 and/or type 2 Shiga toxins. Two pairs of PCR primers targeting highly conserved regions present in each of the Shiga toxin genes *stx₁* and *stx₂* were designed to amplify all variants of those genes (see Annexes XXVI and XXVII). The first primer pair, oligonucleotides 1SLT224 (SEQ ID NO. 1081) and 1SLT385 (SEQ ID NO. 1080), yields an amplification product of 186 bp from the *stx₁* gene. For this amplicon, the 1SLTB1-Fam (SEQ ID NO. 1084) molecular beacon was designed for the specific detection of *stx₁*

using the fluorescent label 6-carboxy-fluorescein. The 1SltS1-FAM (SEQ ID NO. 2012) molecular scorpion was also designed as an alternate way for the specific detection of *stx*₁. A second pair of PCR primers, oligonucleotides 2SLT537 (SEQ ID NO. 1078) and 2SLT678b (SEQ ID NO. 1079), yields an amplification product of 160 bp from the *stx*₂ gene. Molecular beacon 2SLTB1-Tet (SEQ ID NO. 1085) was designed for the specific detection of *stx*₂ using the fluorescent label 5-tetrachloro-fluorescein. Both primer pairs were combined in a multiplex PCR assay.

PCR amplification was carried out using 0.8 μ M of primer pair SEQ ID NOs. 1080-1081, 0.5 μ M of primer pair SEQ ID NOs. 1078-1079, 0.3 μ M of each molecular beacon, 8 mM MgCl₂, 490 μ g/mL BSA, 0.2 mM dNTPs (Pharmacia), 50 mM Tris-HCl, 16 mM NH₄SO₄, 1X TaqMaster (Eppendorf), 2.5 U KlenTaq1 DNA polymerase (AB Peptides) coupled with TaqStartTM antibody (Clontech Laboratories Inc.), and 1 μ l of genomic DNA sample in a final volume of 25 μ l. PCR amplification was performed using a SmartCycler thermal cycler (Cepheid). The optimal cycling conditions for maximum sensitivity and specificity were 60 seconds at 95 °C for initial denaturation, then 45 cycles of three steps consisting of 10 seconds at 95 °C, 15 seconds at 56 °C and 5 seconds at 72 °C. Detection of the PCR products was made in real-time by measuring the fluorescent signal emitted by the molecular beacon when it hybridizes to its target at the end of the annealing step at 56 °C.

The detection limit was the equivalent of less than 5 genome copies. The assay was specific for the detection of both toxins, as demonstrated by the perfect correlation between PCR results and the phenotypic characterization performed using antibodies specific for each Shiga toxin type. The assay was successfully performed on several Shiga toxin-producing strains isolated from various geographic areas of the world, including 10 O157:H7 *E. coli*, 5 non-O157:H7 *E. coli* and 4 *S. dysenteriae*.

EXAMPLE 17:

Development of a PCR assay for the detection and identification of staphylococci at genus and species levels and its associated *mecA* gene. The *Staphylococcus*-specific PCR primers described in Example 7 (SEQ ID NOs. 553 and 575) were used in multiplex with the *mecA*-specific PCR primers and the *S. aureus*-specific primers described in our assigned US patent no. 5,994,066 (SEQ ID NOs. 261 and 262 for *mecA* and SEQ ID NOs. 152 and 153 for *S. aureus* in the said patent). Sequence alignment analysis of 10 publicly available *mecA* gene sequences allowed to design an internal probe specific to *mecA* (SEQ ID NO. 1177). An internal probe was also designed for the *S. aureus*-specific amplicon (SEQ ID NO 1234). PCR amplification and agarose gel electrophoresis of the amplified products were performed as described in Example 7, with the exception that 0.4 μ M (each) of the two *Staphylococcus*-specific primers (SEQ ID NOs. 553 and 575) and 0.4 μ M (each) of the *mecA*-specific primers and 0.4 μ M (each) of the *S. aureus*-specific primers were used in the PCR mixture. The specificity of the multiplex assay with 40-cycle PCR protocols was verified by using purified genomic DNA from five methicillin-resistant and fifteen methicillin-sensitive staphylococcal strains. The sensitivity of the multiplex assay with 40-cycle PCR protocols was determined by using purified genomic DNA from twenty-three methicillin-resistant and twenty-eight methicillin-sensitive staphylococcal strains. The detection limit was 2 to 10 genome copies of genomic DNA, depending on the staphylococcal species tested. Furthermore, the *mecA*-specific internal probe, the *S. aureus*-specific internal probe and the coagulase-negative staphylococci-specific internal probe (described in Example 7) were able to recognize twenty-three methicillin-resistant staphylococcal strains and twenty-eight methicillin-sensitive staphylococcal strains with high sensitivity and specificity.

The format of the assay is not limited to the one described above. A person skilled in the art could adapt the assay for different formats such as PCR with real-time detection using molecular beacon probes. Molecular beacon probes designed to be used in this assay include, but are not limited to, SEQ ID NO. 1232 for detection of the *S. aureus*-specific amplicon, SEQ ID NO. 1233 for detection of coagulase-negative staphylococci and SEQ ID NO. 1231 for detection of *mecA*.

Alternatively, a multiplex PCR assay containing the *Staphylococcus*-specific PCR primers described in Example 7 (SEQ ID NOs. 553 and 575) and the *mecA*-specific PCR primers described in our assigned US patent no. 5,994,066 (SEQ ID NOs. 261 and 262 in the said patent) were developed. PCR amplification and agarose gel electrophoresis of the amplified products were performed as described in Example 7, with the exception that 0.4 μ M (each) of the *Staphylococcus*-specific primers (SEQ ID NOs. 553 and 575) and 0.4 μ M (each) of the *mecA*-specific primers described in our assigned US patent no. 5,994,066 (SEQ ID NOs. 261 and 262 in the said patent) were used in the PCR mixture. The sensitivity of the multiplex assay with 40-cycle PCR protocols was determined by using purified genomic DNA from two methicillin-resistant and five methicillin-sensitive staphylococcal strains. The detection limit was 2 to 5 copies of genomic DNA, depending on the staphylococcal species tested. The specificity of the multiplex PCR assay coupled with capture-probe hybridization was tested with two strains of methicillin-resistant *S. aureus*, two strains of methicillin-sensitive *S. aureus* and seven strains of methicillin-sensitive coagulase-negative staphylococci. The *mecA*-specific internal probe (SEQ ID NO. 1177) and the *S. aureus*-specific internal probe (SEQ ID NO. 587) described in Example 7 were able to recognize all the strains with high specificity showing a perfect correlation with susceptibility to methicillin. The sensitivity of the PCR assay coupled with capture-probe hybridization was tested with one strain of methicillin-resistant *S. aureus*. The detection limit was around 10 copies of genomic DNA.

EXAMPLE 18:

Sequencing of *pbp1a*, *pbp2b* and *pbp2x* genes of *Streptococcus pneumoniae*.

Penicillin resistance in *Streptococcus pneumoniae* involves the sequential alteration of up to five penicillin-binding proteins (PBPs) 1A, 1B, 2A, 2X and 2B in such a way that their affinity is greatly reduced toward the antibiotic molecule. The altered PBP genes have arisen as the result of interspecies recombination events from related streptococcal species. Among the PBPs usually found in *S. pneumoniae*, PBPs 1A, 2B, and 2X play the most important role in the development of penicillin resistance. Alterations in PBP 2B and 2X mediate low-level resistance to penicillin while additional alterations in PBP 1A play a significant role in full penicillin resistance.

In order to generate a database for *pbp* sequences that can be used for design of primers and/or probes for the specific and ubiquitous detection of β -lactam resistance in *S. pneumoniae*, *pbp1a*, *pbp2b* and *pbp2x* DNA fragments sequenced by us or selected from public databases (GenBank and EMBL) from a variety of *S. pneumoniae* strains were used to design oligonucleotide primers. This database is essential for the design of specific and ubiquitous primers and/or probes for detection of β -lactam resistance in *S. pneumoniae* since the altered PBP 1A, PBP 2B and PBP 2X of β -lactam resistant *S. pneumoniae* are encoded by mosaic genes with numerous sequence variations among resistant isolates. The PCR primers were located in conserved regions of *pbp* genes and were able to amplify *pbp1a*, *pbp2b*, and *pbp2x* sequences of several strains of *S. pneumoniae* having various levels of resistance to penicillin and third-generation cephalosporins. Using primer pairs SEQ ID NOs. 1125 and 1126, SEQ ID NOs. 1142 and 1143, SEQ ID NOs. 1146 and 1147, it was possible to amplify and determine *pbp1a* sequences SEQ ID NOs. 1004-1018, 1648, 2056-2060 and 2062-2064, *pbp2b* sequences SEQ ID NOs. 1019-1033, and *pbp2x* sequences SEQ ID NOs. 1034-1048. Six other PCR primers

(SEQ ID NOs. 1127-1128, 1144-1145, 1148-1149) were also designed and used to complete the sequencing of *pbp1a*, *pbp2b* and *pbp2x* amplification products. The described primers (SEQ ID NOs. 1125 and 1126, SEQ ID NOs. 1142 and 1143, SEQ ID NOs. 1146 and 1147, SEQ ID NOs. 1127-1128, 1144-1145, 1148-1149) represent a powerful tool for generating new *pbp* sequences for design of primers and/or probes for detection of β -lactam resistance in *S. pneumoniae*.

EXAMPLE 19:

Sequencing of *hexA* genes of *Streptococcus* species. The *hexA* sequence of *S. pneumoniae* described in our assigned US patent no. 5,994,066 (SEQ ID NO. 31 in the said patent, SEQ ID NO. 1183 in the present application) allowed the design of a PCR primer (SEQ ID NO. 1182) which was used with primer Spn1401 described in our assigned US patent no. 5,994,066 (SEQ ID NO. 156 in the said patent, SEQ ID NO. 1179 in the present application) to generate a database for *hexA* sequences that can be used to design primers and/or probes for the specific identification and detection of *S. pneumoniae* (Annex XLII). Using primers SEQ ID NO. 1179 and SEQ ID NO. 1182 (Annex XLII), it was possible to amplify and determine the *hexA* sequence from *S. pneumoniae* (4 strains) (SEQ ID NOs. 1184-1187), *S. mitis* (three strains) (SEQ ID NOs. 1189-1191) and *S. oralis* (SEQ ID NO. 1188).

EXAMPLE 20:

Development of multiplex PCR assays coupled with capture probe hybridization for the detection and identification of *Streptococcus pneumoniae* and its penicillin resistance genes.

Two different assays were developed to identify *S. pneumoniae* and its susceptibility to penicillin.

ASSAY I:

Bacterial strains. The specificity of the multiplex PCR assay was verified by using a panel of ATCC (American Type Culture Collection) reference strains consisting of 33 gram-negative and 67 gram-positive bacterial species (Table 13).

In addition, a total of 98 strains of *S. pneumoniae*, 16 strains of *S. mitis* and 3 strains of *S. oralis* from the American Type Culture Collection, the microbiology laboratory of the Centre Hospitalier Universitaire de Québec, Pavillon Centre Hospitalier de l'Université Laval (CHUL), (Ste-Foy, Québec, Canada), the Laboratoire de santé publique du Québec, (Sainte-Anne-de-Bellevue, Québec, Canada), the Sunnybrook and Women's College Health Sciences Centre (Toronto, Canada), the Infectious Diseases Section, Department of Veterans Affairs Medical Center, (Houston, USA) were also tested to further validate the *Streptococcus pneumoniae*-specific PCR assay. The penicillin MICs (minimal inhibitory concentrations) were measured by the broth dilution method according to the recommended protocol of NCCLS.

PCR primers and internal probes. The analysis of *hexA* sequences from a variety of streptococcal species from the publicly available *hexA* sequence and from the database described in Example 19 (SEQ ID NOs. 1184-1191) allowed the selection of a PCR primer specific to *S. pneumoniae*, SEQ ID NO. 1181. This primer was used with the *S. pneumoniae*-specific primer SEQ ID NO. 1179 to generate an amplification product of 241 bp (Annex XLII). The PCR primer SEQ ID NO. 1181 is located 127 nucleotides downstream on the *hexA* sequence compared to the original *S. pneumoniae*-specific PCR primer Spn1515 described in our assigned US patent no. 5,994,066 (SEQ ID NO. 157 in the said patent). These modifications were done to ensure the design of the *S. pneumoniae*-specific internal probe according to the new *hexA* sequences of several streptococcal species from the database described in Example 19 (SEQ ID NOs. 1184-1191).

The analysis of *pbp1a* sequences from *S. pneumoniae* strains with various levels of penicillin resistance from public databases and from the database described in Example 18 allowed the identification of amino acid substitutions Ile-459 to Met and Ser-462 to Ala that occur in isolates with high-level penicillin resistance (MICs $\geq 1\mu\text{g/ml}$), and amino acid substitutions Ser-575 to Thr, Gln-576 to Gly and Phe-577 to Tyr that are common to all penicillin-resistant isolates with MICs $\geq 0.25\mu\text{g/ml}$. As shown in Annex XXXI, PCR primer pair SEQ ID NOs. 1130 and 1131 were designed to detect high-level penicillin resistance (MICs $\geq 1\mu\text{g/ml}$), whereas PCR primer pair SEQ ID NOs. 1129 and 1131 were designed to detect intermediate- and high-level penicillin resistance (MICs $\geq 0.25\mu\text{g/ml}$).

The analysis of *hexA* sequences from the publicly available *hexA* sequence and from the database described in Example 19 allowed the design of an internal probe specific to *S. pneumoniae* (SEQ ID NO. 1180) (Annex XLII). The range of mismatches between the *S. pneumoniae*-specific 241-bp amplicon was from 2 to 5, in the middle of the 19-bp probe. The analysis of *pbp1a* sequences from public databases and from the database described in Example 18 allowed the design of five internal probes containing all possible mutations to detect the high-level penicillin resistance 383-bp amplicon (SEQ ID NOs. 1197, 1217-1220). Alternatively, two other internal probes (SEQ ID NOs. 2024-2025) can also be used to detect the high-level penicillin resistance 383-bp amplicon. Five internal probes containing all possible mutations to detect the 157-bp amplicon which includes intermediate- and high-level penicillin resistance were also designed (SEQ ID NOs. 1094, 1192-1193, 1214 and 1216). Design and synthesis of primers and probes, and detection of the probe hybridization were performed as described in Example 7. Annex XXXI illustrates one of the internal probe for detection of the high-level penicillin resistance 383-bp amplicon (SEQ ID NO. 1197) and one of the internal probe for detection of the intermediate- and high-level penicillin resistance 157-bp amplicon (SEQ ID NO. 1193).

PCR amplification. For all bacterial species, amplification was performed from purified genomic DNA using a PTC-200 thermocycler (MJ Research). 1 μ l of genomic DNA at 0.1 ng/ μ l, or 1 μ l of a bacterial lysate, was transferred to a 19 μ l PCR mixture. Each PCR reaction contained 50 mM KCl, 10 mM Tris-HCl (H 9.0), 0.1% Triton X-100, 2.5 mM MgCl₂, 0.1 μ M (each) of the *S. pneumoniae*-specific primers SEQ ID NO. 1179 and SEQ ID NO. 1181, 0.2 μ M of primer SEQ ID NO. 1129, 0.7 μ M of primer SEQ ID NO. 1131, and 0.6 μ M of primer SEQ ID NO. 1130, 0.05 mM bovine serum albumin (BSA), and 0.5 U *Taq* polymerase (Promega) coupled with TaqStartTM antibody. In order to generate Digoxigenin (DIG)-labeled amplicons for capture probe hybridization, 0.1X PCR DIG labeling four deoxynucleoside triphosphates mix (Boehringer Mannheim GmbH) was used for amplification.

For determination of the sensitivity of the PCR assays, 10-fold dilutions of purified genomic DNA were used to determine the minimal number of genome copies which can be detected.

Capture probe hybridization. The DIG-labeled amplicons were hybridized to the capture probes bound to 96-well plates. The plates were incubated with anti-DIG-alkaline phosphatase and the chemiluminescence was measured by using a luminometer (MLX, Dynex Technologies Inc.) after incubation with CSPD and recorded as Relative Light Unit (RLU). The RLU ratio of tested sample with and without captures probes was then calculated. A ratio ≥ 2.0 was defined as a positive hybridization signal. All reactions were performed in duplicate.

Results

Amplifications with the multiplex PCR assay. The specificity of the assay was assessed by performing 40-cycle PCR amplifications with the panel of gram-positive (67 species from 12 genera) and gram-negative (33 species from 17

genera) bacterial species listed in Table 13. All bacterial species tested other than *S. pneumoniae* were negative except *S. mitis* and *S. oralis*. Ubiquity tests were performed using a collection of 98 *S. pneumoniae* strains including high-level penicillin resistance (n=53), intermediate resistance (n=12) and sensitive (n=33) strains. There was a perfect correlation between PCR and standard susceptibility testing for 33 penicillin-sensitive isolates. Among 12 *S. pneumoniae* isolates with intermediate penicillin resistance based on susceptibility testing, 11 had intermediate resistance based on PCR, but one *S. pneumoniae* isolate with penicillin MIC of 0.25 µg/ml showed a high-level penicillin resistance based on genotyping. Among 53 isolates with high-level penicillin resistance based on susceptibility testing, 51 had high-level penicillin resistance based on PCR but two isolates with penicillin MIC > 1 µg/ml showed an intermediate penicillin resistance based on genotyping. In general, there was a good correlation between the genotype and classical culture method for bacterial identification and susceptibility testing.

The sensitivity of the *S. pneumoniae*-specific assay with 40-cycle PCR protocols was determined by using purified genomic DNA from 9 isolates of *S. pneumoniae*. The detection limit was around 10 copies of genomic DNA for all of them.

Post-PCR hybridization with internal probes. The specificity of the multiplex PCR assay coupled with capture-probe hybridization was tested with 98 strains of *S. pneumoniae*, 16 strains of *S. mitis* and 3 strains of *S. oralis*. The internal probe specific to *S. pneumoniae* (SEQ ID NO. 1180) detected all 98 *S. pneumoniae* strains but did not hybridize to the *S. mitis* and *S. oralis* amplicons. The five internal probes specific to the high-level resistance amplicon (SEQ ID NOs. 1197, 1217-1220) detected all amplification patterns corresponding to high-level resistance. The two *S. pneumoniae* strains with penicillin MIC > 1 µg/ml that showed an intermediate penicillin resistance based on PCR amplification were also intermediate resistance based on probe hybridization. Similarly, among 12 strains

with intermediate-penicillin resistance based on susceptibility testing, 11 showed intermediate-penicillin resistance based on hybridization with the five internal probes specific to the intermediate and high-level resistance amplicon (SEQ ID NOs. 1094, 1192-1193, 1214 and 1216). The strain described above having a penicillin MIC of 0.25 µg/ml which was high-level penicillin resistance based on PCR amplification was also high-level resistance based on probe hybridization. In summary, the combination of the multiplex PCR and hybridization assays results in a highly specific test for the detection of penicillin-resistant *Streptococcus pneumoniae*.

ASSAY II:

Bacterial strains. The specificity of the multiplex PCR assay was verified by using the same strains as those used for the development of Assay I. The penicillin MICs (minimal inhibitory concentrations) were measured by the broth dilution method according to the recommended protocol of NCCLS.

PCR primers and internal probes. The analysis of *pbpla* sequences from *S. pneumoniae* strains with various levels of penicillin resistance from public databases and from the database described in Example 18 allowed the design of two primers located in the constant region of *pbpla*. PCR primer pair (SEQ ID NOs. 2015 and 2016) was designed to amplify a 888-bp variable region of *pbpla* from all *S. pneumoniae* strains. A series of internal probes were designed for identification of the *pbpla* mutations associated with penicillin resistance in *S. pneumoniae*. For detection of high-level penicillin resistance (MICs $\geq 1\mu\text{g/ml}$), three internal probes were designed (SEQ ID NOs. 2017-2019). Alternatively, ten other internal probes were designed that can also be used for detection of high-level resistance within the 888-bp *pbpla* amplicon: (1) three internal probes for identification of the amino acid substitutions Thr-371 to Ser or Ala within the motif S370TMK (SEQ ID NOs. 2031-2033); (2) two internal probes for detection

of the amino acid substitutions Ile-459 to Met and Ser-462 to Ala near the motif S428RN (SEQ ID NOs. 1135 and 2026); (3) two internal probes for identification of the amino acid substitutions Asn-443 to Asp (SEQ ID NOs. 1134 and 2027); and (4) three internal probes for detection of all sequence variations within another region (SEQ ID NOs. 2028-2030). For detection of high-level and intermediate penicillin resistance (MICs ≥ 0.25 $\mu\text{g/ml}$), four internal probes were designed (SEQ ID NOs. 2020-2023). Alternatively, six other internal probes were designed for detection of the four consecutive amino acid substitutions T574SQF to A574TGY near the motif K557TG (SEQ ID NOs. 2034-2039) that can also be used for detection of intermediate- and high-level resistance within the 888-bp *pbpla* amplicon.

PCR amplification. For all bacterial species, amplification was performed from purified genomic DNA using a PTC-200 thermocycler (MJ Research). 1 μl of genomic DNA at 0.1 ng/ μl , or 1 μl of a bacterial lysate, was transferred to a 19 μl PCR mixture. Each PCR reaction contained 50 mM KCl, 10 mM Tris-HCl (pH 9.0), 0.1% Triton X-100, 2.5 mM MgCl_2 , 0.08 μM (each) of the *S. pneumoniae*-specific primers SEQ ID NO. 1179 and SEQ ID NO. 1181, 0.4 μM of the *pbpla*-specific primer SEQ ID NO. 2015, 1.2 μM of *pbpla*-specific primer SEQ ID NO. 2016, 0.05 mM bovine serum albumin (BSA), and 0.5 U *Taq* polymerase (Promega) coupled with TaqStartTM antibody. In order to generate Digoxigenin (DIG)-labeled amplicons for capture probe hybridization, 0.1X PCR DIG labeling four deoxynucleoside triphosphates mix (Boehringer Mannheim GmbH) was used for amplification.

For determination of the sensitivities of the PCR assays, 10-fold dilutions of purified genomic DNA were used to determine the minimal number of genome copies which can be detected.

Capture probe hybridization. The DIG-labeled amplicons were hybridized to the capture probes bound to 96-well plates as described for Assay I.

Results

Amplifications with the multiplex PCR assay. The specificity of the assay was assessed by performing 40-cycle PCR amplifications with the panel of gram-positive (67 species from 12 genera) and gram-negative (33 species from 17 genera) bacterial species listed in Table 13. All bacterial species tested other than *S. pneumoniae* were negative except *S. mitis* and *S. oralis*. Ubiquity tests were performed using a collection of 98 *S. pneumoniae* strains including high-level penicillin resistance (n=53), intermediate resistance (n=12) and sensitive (n=33) strains. All the above *S. pneumoniae* strains produced the 888-bp amplicon corresponding to *pbp1a* and the 241-bp fragment corresponding to *hexA*.

The sensitivity of the *S. pneumoniae*-specific assay with 40-cycle PCR protocols was determined by using purified genomic DNA from 9 isolates of *S. pneumoniae*. The detection limit was around 10 copies of genomic DNA for all of them.

Post-PCR hybridization with internal probes. The specificity of the multiplex PCR assay coupled with capture-probe hybridization was tested with 98 strains of *S. pneumoniae*, 16 strains of *S. mitis* and 3 strains of *S. oralis*. The internal probe specific to *S. pneumoniae* (SEQ ID NO. 1180) detected all 98 *S. pneumoniae* strains but did not hybridize to the *S. mitis* and *S. oralis* amplicons. The three internal probes (SEQ ID NOs 2017-2019) specific to high-level resistance detected all the 43 strains with high-level penicillin resistance based on susceptibility testing. Among 12 isolates with intermediate-penicillin resistance based on susceptibility testing, 11 showed intermediate-penicillin resistance based on hybridization with 4 internal probes (SEQ ID NOs. 2020-2023) and one strain

having penicillin MIC of 0.25 µg/ml was misclassified as high-level penicillin resistance. In summary, the combination of the multiplex PCR and hybridization assays results in a highly specific test for the detection of penicillin-resistant *Streptococcus pneumoniae*.

EXAMPLE 21:

Sequencing of the vancomycin resistance *vanA*, *vanC1*, *vanC2* and *vanC3* genes.

The publicly available sequences of the *vanH-vanA-vanX-vanY* locus of transposon Tn1546 from *E. faecalis*, *vanC1* sequence from one strain of *E. gallinarum*, *vanC2* and *vanC3* sequences from a variety of *E. casseliflavus* and *E. flavescens* strains, respectively, allowed the design of PCR primers able to amplify the *vanA*, *vanC1*, *vanC2* and *vanC3* sequences of several *Enterococcus* species. Using primer pairs van6877 and van9106 (SEQ ID NOs. 1150 and 1155), vanC1-122 and vanC1-1315 (SEQ ID NOs. 1110 and 1109), and vanC2C3-1 and vanC2C3-1064 (SEQ ID NOs. 1108 and 1107), it was possible to amplify and determine *vanA* sequences SEQ ID NOs. 1049-1057, *vanC1* sequences SEQ ID NOs. 1058-1059, *vanC2* sequences SEQ ID NOs. 1060-1063 and *vanC3* sequences SEQ ID NOs. 1064-1066, respectively. Four other PCR primers (SEQ ID NOs. 1151-1154) were also designed and used to complete the sequencing of *vanA* amplification products.

EXAMPLE 22:

Development of a PCR assay for the detection and identification of enterococci at genus and species levels and its associated resistance genes *vanA* and *vanB*.

The comparison of *vanA* and *vanB* sequences revealed conserved regions allowing the design of PCR primers specific to both *vanA* and *vanB* sequences (Annex XXXVIII). The PCR primer pair vanAB459 and vanAB830R (SEQ ID NOs. 1112 and 1111) was used in multiplex with the *Enterococcus*-specific primers Encg313dF and Encg599c (SEQ ID NOs. 1137 and 1136) described in Example

11. Sequence alignment analysis of *vanA* and *vanB* sequences revealed regions suitable for the design of internal probes specific to *vanA* (SEQ ID NO. 1170) and *vanB* (SEQ ID NO. 1171). PCR amplification and agarose gel electrophoresis of the amplified products were performed as described in Example 11. The optimal cycling conditions for maximum sensitivity and specificity were found to be 3 min. at 94 °C, followed by forty cycles of two steps consisting of 1 second at 95 °C and 30 seconds at 62 °C, plus a terminal extension at 72 °C for 2 minutes. The specificity of the multiplex assay with 40-cycle PCR was verified by using 0.1 nanogram of purified genomic DNA from a panel of bacteria listed in Table 10. The sensitivity of the multiplex assay with 40-cycle PCR was verified with three strains of *E. casseliflavus*, eight strains of *E. gallinarum*, two strains of *E. flavescens*, two vancomycin-resistant strains of *E. faecalis* and one vancomycin-sensitive strain of *E. faecalis*, three vancomycin-resistant strains of *E. faecium*, one vancomycin-sensitive strain of *E. faecium* and one strain of each of the other enterococcal species listed in Table 10. The detection limit was 1 to 10 copies of genomic DNA, depending on the enterococcal species tested. The *vanA*- and *vanB*-specific internal probes (SEQ ID NOs. 1170 and 1171), as well as the *E. faecalis*- and *E. faecium*-specific internal probes (SEQ ID NOs. 1174 and 602) and the internal probe specific to the group including *E. casseliflavus*, *E. gallinarum* and *E. flavescens* (SEQ ID NO. 1122) described in Example 11, were able to recognize vancomycin-resistant enterococcal species with high sensitivity, specificity and ubiquity showing a perfect correlation between the genotypic and phenotypic analysis.

The format of the assay is not limited to the one described above. A person skilled in the art could adapt the assay for different formats such as PCR with real-time detection using molecular beacon probes. Molecular beacon probes designed to be used in this assay include, but are not limited to, SEQ ID NO. 1236 for the detection of *E. faecalis*, SEQ ID NO. 1235 for the detection of *E. faecium*, SEQ ID NO. 1240 for the detection of *vanA*, and SEQ ID NO. 1241 for the detection of *vanB*.

EXAMPLE 23:

Development of a multiplex PCR assay for detection and identification of vancomycin-resistant *Enterococcus faecalis*, *Enterococcus faecium* and the group including *Enterococcus gallinarum*, *Enterococcus casseliflavus*, and *Enterococcus flavescens*. The analysis of *vanA* and *vanB* sequences revealed conserved regions allowing design of a PCR primer pair (SEQ ID NOs. 1089 and 1090) specific to *vanA* sequences (Annex XXVIII) and a PCR primer pair (SEQ ID NOs. 1095 and 1096) specific to *vanB* sequences (Annex XXIX). The *vanA*-specific PCR primer pair (SEQ ID NOs. 1089 and 1090) was used in multiplex with the *vanB*-specific PCR primer pair described in our assigned US patent 5,994,066 (SEQ ID NOs. 1095 and 1096 in the present patent and SEQ ID NOs. 231 and 232 in the said patent). The comparison of *vanC1*, *vanC2* and *vanC3* sequences revealed conserved regions allowing design of PCR primers (SEQ ID NOs. 1101 and 1102) able to generate a 158-bp amplicon specific to the group including *E. gallinarum*, *E. casseliflavus* and *E. flavescens* (Annex XXX). The *vanC*-specific PCR primer pair (SEQ ID NOs. 1101 and 1102) was used in multiplex with the *E. faecalis*-specific PCR primer pair described in our assigned US patent 5,994,066 (SEQ ID NOs. 40 and 41 in the said patent) and with the *E. faecium*-specific PCR primer pair described in our patent publication WO98/20157 (SEQ ID NOs. 1 and 2 in the said publication). For both multiplexes, the optimal cycling conditions for maximum sensitivity and specificity were found to be 3 min. at 94 °C, followed by forty cycles of two steps consisting of 1 second at 95 °C and 30 seconds at 58 °C, plus a terminal extension at 72 °C for 2 minutes. Detection of the PCR products was made by electrophoresis in agarose gels (2 %) containing 0.25 µg/ml of ethidium bromide. The *vanA*-specific PCR primer pair (SEQ ID NOs. 1089 and 1090), the *vanB*-specific primer pair (SEQ ID NOs. 1095 and 1096) and the *vanC*-specific primer pair (SEQ ID NOs. 1101 and 1102) were tested for their specificity by using 0.1 nanogram of purified genomic DNA from a panel of 5 vancomycin-

sensitive *Enterococcus* species, 3 vancomycin-resistant *Enterococcus* species, 13 other gram-positive bacteria and one gram-negative bacterium. Specificity tests were performed with the *E. faecium*-specific PCR primer pair described in our patent publication WO98/20157 (SEQ ID NOs. 1 and 2 in the said publication) and with the *E. faecalis*-specific PCR primer pair described in our assigned US patent 5,994,066 (SEQ ID NOs. 40 and 41 in the said patent) on a panel of 37 gram-positive bacterial species. All *Enterococcus* strains were amplified with high specificity showing a perfect correlation between the genotypic and phenotypic analysis. The sensitivity of the assays was determined for several strains of *E. gallinarum*, *E. casseliflavus*, *E. flavescens* and vancomycin-resistant *E. faecalis* and *E. faecium*. Using each of the *E. faecalis*- and *E. faecium*-specific PCR primer pairs as well as *vanA*-, *vanB*- and *vanC*-specific PCR primers used alone or in multiplex as described above, the sensitivity ranged from 1 to 10 copies of genomic DNA.

The format of the assay is not limited to the one described above. A person skilled in the art could adapt the assay for different formats such as PCR with real-time detection using molecular beacon probes. Molecular beacon probes designed to be used in this assay include, but are not limited to, SEQ ID NO. 1238 for the detection of *E. faecalis*, SEQ ID NO. 1237 for the detection of *E. faecium*, SEQ ID NO. 1239 for the detection of *vanA*, and SEQ ID NO. 1241 for the detection of *vanB*.

Alternatively, another PCR assay was developed for the detection of vancomycin-resistant *E. faecium* and vancomycin-resistant *E. faecalis*. This assay included two multiplex: (1) the first multiplex contained the *vanA*-specific primer pair (SEQ ID NOs. 1090-1091) and the *vanB*-specific PCR primer pair described in our assigned US patent 5,994,066 (SEQ ID NOs. 1095 and 1096 in the present patent and SEQ ID NOs. 231 and 232 in the said patent), and (2) the second multiplex contained the *E. faecalis*-specific PCR primer pair described in our assigned US patent 5,994,066 (SEQ ID NOs. 40 and 41 in the said patent) and the *E. faecium*-specific PCR primer pair described in our patent publication WO98/20157 (SEQ ID NOs. 1

and 2 in the said publication). For both multiplexes, the optimal cycling conditions for maximum sensitivity and specificity were found to be 3 min. at 94 °C, followed by forty cycles of two steps consisting of 1 second at 95 °C and 30 seconds at 58 °C, plus a terminal extension at 72 °C for 2 minutes. Detection of the PCR products was made by electrophoresis in agarose gels (2 %) containing 0.25 µg/ml of ethidium-bromide. The two multiplexes were tested for their specificity by using 0.1 nanogram of purified genomic DNA from a panel of two vancomycin-sensitive *E. faecalis* strains, two vancomycin-resistant *E. faecalis* strains, two vancomycin-sensitive *E. faecium* strains, two vancomycin-resistant *E. faecium* strains, 16 other enterococcal species and 31 other gram-positive bacterial species. All the *E. faecium* and *E. faecalis* strains were amplified with high specificity showing a perfect correlation between the genotypic analysis and the susceptibility to glycopeptide antibiotics (vancomycin and teicoplanin). The sensitivity of the assay was determined for two vancomycin-resistant *E. faecalis* strains and two vancomycin-resistant *E. faecium* strains. The detection limit was 5 copies of genomic DNA for all the strains.

This multiplex PCR assay was coupled with capture-probe hybridization. Four internal probes were designed: one specific to the *vanA* amplicon (SEQ ID NO. 2292), one specific to the *vanB* amplicon (SEQ ID NO. 2294), one specific to the *E. faecalis* amplicon (SEQ ID NO. 2291) and one specific to the *E. faecium* amplicon (SEQ ID NO. 2287). Each of the internal probes detected their specific amplicons with high specificity and sensitivity.

EXAMPLE 24:

Universal amplification involving the EF-G (*fusA*) subdivision of *tuf* sequences. As shown in Figure 3, primers SEQ ID NOs. 1228 and 1229 were designed to amplify the region between the end of *fusA* and the beginning of *tuf* genes in the *str* operon. Genomic DNAs from a panel of 35 strains were tested for PCR amplification with those primers. In the initial experiment, the following strains showed a positive

result: *Abiotrophia adiacens* ATCC 49175, *Abiotrophia defectiva* ATCC 49176, *Bacillus subtilis* ATCC 27370, *Clostridium difficile* ATCC 9689, *Enterococcus avium* ATCC 14025, *Enterococcus casseliflavus* ATCC 25788, *Enterococcus cecorum* ATCC 43198, *Enterococcus faecalis* ATCC 29212, *Enterococcus faecium* ATCC 19434, *Enterococcus flavescens* ATCC 49996, *Enterococcus gallinarum* ATCC 49573, *Enterococcus solitarius* ATCC 49428, *Escherichia coli* ATCC 11775, *Haemophilus influenzae* ATCC 9006, *Lactobacillus acidophilus* ATCC 4356, *Peptococcus niger* ATCC 27731, *Proteus mirabilis* ATCC 25933, *Staphylococcus aureus* ATCC 43300, *Staphylococcus auricularis* ATCC 33753, *Staphylococcus capitis* ATCC 27840, *Staphylococcus epidermidis* ATCC 14990, *Staphylococcus haemolyticus* ATCC 29970, *Staphylococcus hominis* ATCC 27844, *Staphylococcus lugdunensis* ATCC 43809, *Staphylococcus saprophyticus* ATCC 15305, *Staphylococcus simulans* ATCC 27848, and *Staphylococcus warneri* ATCC 27836. This primer pair could amplify additional bacterial species; however, there was no amplification for some species, suggesting that the PCR cycling conditions could be optimized or the primers modified. For example, SEQ ID NO. 1227 was designed to amplify a broader range of species.

In addition to other possible primer combinations to amplify the region covering *fusA* and *tuf*, Figure 3 illustrates the positions of amplification primers SEQ ID NOs. 1221-1227 which could be used for universal amplification of *fusA* segments. All of the above mentioned primers (SEQ ID NOs. 1221-1229) could be useful for the universal and/or the specific detection of bacteria.

Moreover, different combinations of primers SEQ ID NOs. 1221-1229, sometimes in combination with *tuf* sequencing primer SEQ ID NO. 697, were used to sequence portions of the *str* operon, including the intergenic region. In this manner, the following sequences were generated: SEQ ID NOs. 1518-1526, 1578-1580, 1786-1821, 1822-1834, 1838-1843, 2184, 2187, 2188, 2214-2249, and 2255-2269.

EXAMPLE 25:

DNA fragment isolation from *Staphylococcus saprophyticus* by arbitrarily primed PCR. DNA sequences of unknown coding potential for the species-specific detection and identification of *Staphylococcus saprophyticus* were obtained by the method of arbitrarily primed PCR (AP-PCR).

AP-PCR is a method which can be used to generate specific DNA probes for microorganisms (Fani *et al.*, 1993, *Molecular Ecology* 2:243-250). A description of the AP-PCR protocol used to isolate a species-specific genomic DNA fragment from *Staphylococcus saprophyticus* follows. Twenty different oligonucleotide primers of 10 nucleotides in length (all included in the AP-PCR kit OPAD (Operon Technologies, Inc., Alameda, CA)) were tested systematically with DNAs from 5 bacterial strains of *Staphylococcus saprophyticus* as well as with bacterial strains of 27 other staphylococcal (non-*S. saprophyticus*) species. For all bacterial species, amplification was performed directly from one μL (0.1 ng/ μL) of purified genomic DNA. The 25 μL PCR reaction mixture contained 50 mM KCl, 10 mM Tris-HCl (pH 9.0), 0.1% Triton X-100, 2.5 mM MgCl_2 , 1.2 μM of only one of the 20 different AP-PCR primers OPAD, 200 μM of each of the four dNTPs, 0.5 U of *Taq* DNA polymerase (Promega Corp., Madison, Wis.) coupled with TaqStartTM antibody (Clontech Laboratories Inc., Palo Alto, CA). PCR reactions were subjected to cycling using a MJ Research PTC-200 thermal cycler as follows: 3 min at 96 °C followed by 42 cycles of 1 min at 94 °C for the denaturation step, 1 min at 31 °C for the annealing step and 2 min at 72 °C for the extension step. A final extension step of 7 min at 72 °C followed the 42 cycles to ensure complete extension of PCR products. Subsequently, twenty microliters of the PCR-amplified mixture were resolved by electrophoresis on a 1.5 % agarose gel containing 0.25 $\mu\text{g/ml}$ of ethidium bromide. The size of the amplification products was estimated by comparison with a 50-bp molecular weight ladder.

Amplification patterns specific for *Staphylococcus saprophyticus* were observed with the AP-PCR primer OPAD-16 (sequence: 5'-AACGGGCGTC-3'). Amplification with this primer consistently showed a band corresponding to a

DNA fragment of approximately 380 bp for all *Staphylococcus saprophyticus* strains tested but not for any of the other staphylococcal species tested.

The band corresponding to the 380 bp amplicon, specific and ubiquitous for *S. saprophyticus* based on AP-PCR, was excised from the agarose gel and purified using the QIAquickTM gel extraction kit (QIAGEN Inc.). The gel-purified DNA fragment was cloned into the T/A cloning site of the pCR 2.1TM plasmid vector (Invitrogen Inc.) using T4 DNA ligase (New England BioLabs). Recombinant plasmids were transformed into *E. coli* DH5 α competent cells using standard procedures. All reactions were performed according to the manufacturer's instructions. Plasmid DNA isolation was done by the method of Birnboim and Doly (Nucleic Acid Res., 1979, 7:1513-1523) for small-scale preparations. All plasmid DNA preparations were digested with the EcoRI restriction endonuclease to ensure the presence of the approximately 380 bp AP-PCR insert into the plasmid. Subsequently, a large-scale and highly purified plasmid DNA preparation was performed from two selected clones shown to carry the AP-PCR insert by using the QIAGEN plasmid purification kit (midi format). These large-scale plasmid preparations were used for automated DNA sequencing.

The 380 bp nucleotide sequence was determined for three strains of *S. saprophyticus* (SEQ ID NOs. 74, 1093, and 1198). Both strands of the AP-PCR insert from the two selected clones were sequenced by the dideoxynucleotide chain termination sequencing method with SP6 and T7 sequencing primers by using the Applied Biosystems automated DNA sequencer (model 373A) with their PRISMTM Sequenase^{RTM} Terminator Double-stranded DNA Sequencing Kit (Applied Biosystems, Foster City, CA).

Optimal species-specific amplification primers (SEQ ID NOs. 1208 and 1209) have been selected from the sequenced AP-PCR *Staphylococcus saprophyticus* DNA fragments with the help of the primer analysis software OligoTM 5.0 (National BioSciences Inc.). The selected primers were tested in PCR assays to verify their specificity and ubiquity. Data obtained with DNA preparations from reference ATCC strains of 49 gram-positive and 31 gram-negative bacterial

species, including 28 different staphylococcal species, indicate that the selected primer pairs are specific for *Staphylococcus saprophyticus* since no amplification signal has been observed with DNAs from the other staphylococcal or bacterial species tested. This assay was able to amplify efficiently DNA from all 60 strains of *S. saprophyticus* from various origins tested. The sensitivity level achieved for three *S. saprophyticus* reference ATCC strains was around 6 genome copies.

EXAMPLE 26:

Sequencing of prokaryotic *tuf* gene fragments. The comparison of publicly available *tuf* sequences from a variety of bacterial species revealed conserved regions, allowing the design of PCR primers able to amplify *tuf* sequences from a wide range of bacterial species. Using primer pair SEQ ID NOs. 664 and 697, it was possible to amplify and determine *tuf* sequences SEQ ID NOs.: 1-73, 75-241, 607-618, 621, 662, 675, 717-736, 868-888, 932, 967-989, 992, 1002, 1572-1575, 1662-1663, 1715-1733, 1835-1837, 1877-1878, 1880-1881, 2183, 2185, 2200, 2201, and 2270-2272.

EXAMPLE 27:

Sequencing of procaryotic *recA* gene fragments. The comparison of publicly available *recA* sequences from a variety of bacterial species revealed conserved regions, allowing the design of PCR primers able to amplify *recA* sequences from a wide range of bacterial species. Using primer pairs SEQ ID NOs. 921-922 and 1605-1606, it was possible to amplify and determine *recA* sequences SEQ ID NOs.: 990-991, 1003, 1288-1289, 1714, 1756-1763, 1866-1873 and 2202-2212.

EXAMPLE 28:

Specific detection and identification of *Escherichia coli/Shigella* sp. using *tuf* sequences. The analysis of *tuf* sequences from a variety of bacterial species allowed the selection of PCR primers (SEQ ID NOs. 1661 and 1665) and of an internal probe (SEQ ID NO. 2168) specific to *Escherichia coli/Shigella* sp. The strategy used to design the PCR primers was based on the analysis of a multiple sequence alignment of various *tuf* sequences. The multiple sequence alignment included the *tuf* sequences of *Escherichia coli/Shigella* sp. as well as *tuf* sequences from other species and bacterial genera, especially representatives of closely related species. A careful analysis of this alignment allowed the selection of oligonucleotide sequences which are conserved within the target species but which discriminate sequences from other species, especially from the closely related species, thereby permitting the species-specific and ubiquitous detection and identification of the target bacterial species.

The chosen primer pair, oligos SEQ ID NOs. 1661 and 1665, gives an amplification product of 219 bp. Standard PCR was carried out using 0.4 μ M of each primer, 2.5 mM MgCl₂, BSA 0.05 mM, 50 mM KCl, 10 mM Tris-HCl (pH 9.0), 0.1 % Triton X-100, dNTPs 0.2 mM (Pharmacia), 0.5 U *Taq* DNA polymerase (Promega) coupled with TaqStartTM antibody (Clontech Laboratories Inc.), 1 μ l of genomic DNA sample in a final volume of 20 μ l using a PTC-200 thermocycler (MJ Research). The optimal cycling conditions for maximum sensitivity and specificity were 3 minutes at 95 °C for initial denaturation, then forty cycles of two steps consisting of 1 second at 95 °C and 30 seconds at 60 °C, followed by terminal extension at 72 °C for 2 minutes. Detection of the PCR products was made by electrophoresis in agarose gels (2 %) containing 0.25 μ g/ml of ethidium bromide. Visualization of the PCR products was made under UV at 254 nm.

Specificity of the assay was tested by adding to the PCR reactions 0.1 ng of genomic DNA from each of the following bacterial species: *Escherichia coli* (7

strains), *Shigella sonnei*, *Shigella flexneri*, *Shigella dysenteriae*, *Salmonella typhimurium*, *Salmonella typhi*, *Salmonella enteritidis*, *Tatumella pyseos*, *Klebsiella pneumoniae* (2 strains), *Enterobacter aerogenes*, *Citrobacter farmeri*, *Campylobacter jejuni*, *Serratia marcescens*. Amplification was observed only for the *Escherichia coli* and *Shigella* sp. strains listed and *Escherichia fergusonii*. The sensitivity of the assay with 40-cycle PCR was verified with one strain of *E. coli* and three strains of *Shigella* sp. The detection limit for *E. coli* and *Shigella* sp. was 1 to 10 copies of genomic DNA, depending on the strains tested.

EXAMPLE 29:

Specific detection and identification of *Klebsiella pneumoniae* using *atpD* sequences. The analysis of *atpD* sequences from a variety of bacterial species allowed the selection of PCR primers specific to *K. pneumoniae*. The primer design strategy is similar to the strategy described in Example 28 except that *atpD* sequences were used in the alignment.

Two *K. pneumoniae*-specific primers were selected, (SEQ ID NOs. 1331 and 1332) which give an amplification product of 115 bp. Standard PCR was carried out on PTC-200 thermocyclers (MJ Research) using 0.4 μ M of each primer as described in Example 28. The optimal cycling conditions for maximum sensitivity and specificity were as follow: three minutes at 95 °C for initial denaturation, then forty cycles of two steps consisting of 1 second at 95 °C and 30 seconds at 55°C, followed by terminal extension at 72 °C for 2 minutes.

Specificity of the assay was tested by adding to the PCR reactions 0.1 ng of genomic DNA from each of the following bacterial species: *Klebsiella pneumoniae* (2 strains), *Klebsiella ornitholytica*, *Klebsiella oxytoca* (2 strains), *Klebsiella planticola*, *Klebsiella terrigena*, *Citrobacter freundii*, *Escherichia coli*, *Salmonella cholerasuis typhi*, *Serratia marcescens*, *Enterobacter aerogenes*, *Proteus vulgaris*,

Kluyvera ascorbata, *Kluyvera georgiana*, *Kluyvera cryocrescens* and *Yersinia enterocolitica*. Amplification was detected for the two *K. pneumoniae* strains, *K. planticola*, *K. terrigena* and the three *Kluyvera* species tested. Analysis of the multiple alignment sequence of the *atpD* gene allowed the design of an internal probe SEQ ID NO. 2167 which can discriminate *Klebsiella pneumoniae* from other *Klebsiella*-sp. and *Kluyvera* sp. The sensitivity of the assay with 40-cycle PCR was verified with one strain of *K. pneumoniae*. The detection limit for *K. pneumoniae* was around 10 copies of genomic DNA.

EXAMPLE 30:

Specific detection and identification of *Acinetobacter baumannii* using *atpD* sequences. The analysis of *atpD* sequences from a variety of bacterial species allowed the selection of PCR primers specific to *Acinetobacter baumannii*. The primer design strategy is similar to the strategy described in Example 28.

Two *A. baumannii*-specific primers were selected, SEQ ID NOs. 1690 and 1691, which give an amplification product of 233 bp. Standard PCR was carried out on PTC-200 thermocyclers (MJ Research) using 0.4 μ M of each primer as described in Example 28. The optimal cycling conditions for maximum sensitivity and specificity were as follow: three minutes at 95 °C for initial denaturation, then forty cycles of two steps consisting of 1 second at 95 °C and 30 seconds at 60°C, followed by terminal extension at 72 °C for 2 minutes.

Specificity of the assay was tested by adding to the PCR reactions 0.1 ng of genomic DNA from each of the following bacterial species: *Acinetobacter baumannii* (3 strains), *Acinetobacter anitratus*, *Acinetobacter lwöffi*, *Serratia marcescens*, *Enterobacter cloacae*, *Enterococcus faecalis*, *Pseudomonas aeruginosa*, *Psychrobacter phenylpyruvicus*, *Neisseria gonorrhoeae*, *Haemophilus haemoliticus*, *Yersinia enterocolitica*, *Proteus vulgaris*, *Eikenella corrodens*,

Escherichia coli. Amplification was detected only for *A. baumannii*, *A. anitratus* and *A. lwoffii*. The sensitivity of the assay with 40-cycle PCR was verified with two strains of *A. baumannii*. The detection limit for the two *A. baumannii* strains tested was 5 copies of genomic DNA. Analysis of the multiple alignment sequence of the *atpD* gene allowed the design of a *A. baumannii*-specific internal probe (SEQ ID NO. 2169).

EXAMPLE 31:

Specific detection and identification of *Neisseria gonorrhoeae* using *tuf* sequences.

The analysis of *tuf* sequences from a variety of bacterial species allowed the selection of PCR primers specific to *Neisseria gonorrhoeae*. The primer design strategy is similar to the strategy described in Example 28.

Two *N. gonorrhoeae*-specific primers were selected, SEQ ID NOs. 551 and 552, which give an amplification product of 139 bp. PCR amplification was carried out on PTC-200 thermocyclers (MJ Research) using 0.4 μ M of each primer as described in Example 28. The optimal cycling conditions for maximum sensitivity and specificity were as follow: three minutes at 95 °C for initial denaturation, then forty cycles of two steps consisting of 1 second at 95 °C and 30 seconds at 65°C, followed by terminal extension at 72 °C for 2 minutes.

Specificity of the assay was tested by adding into the PCR reactions, 0.1 ng of genomic DNA from each of the following bacterial species: *Neisseria gonorrhoeae* (19 strains), *Neisseria meningitidis* (2 strains), *Neisseria lactamica*, *Neisseria flavescens*, *Neisseria animalis*, *Neisseria canis*, *Neisseria cuniculi*, *Neisseria elongata*, *Neisseria mucosa*, *Neisseria polysaccharea*, *Neisseria sicca*, *Neisseria subflava*, *Neisseria weaveri*. Amplification was detected only for *N. gonorrhoeae*, *N. sicca* and *N. polysaccharea*. The sensitivity of the assay with 40-cycle PCR was verified with two strains of *N. gonorrhoeae*. The detection limit for the *N.*

gonorrhoeae strains tested was 5 copies of genomic DNA. Analysis of the multiple alignment sequence of the *tuf* gene allowed the design of an internal probe, SEQ ID NO. 2166, which can discriminate *N. gonorrhoeae* from *N. sicca* and *N. polysaccharea*.

EXAMPLE 32:

Sequencing of bacterial *gyrA* and *parC* gene fragments. Sequencing of bacterial *gyrA* and *parC* fragments. One of the major mechanism of resistance to quinolone in various bacterial species is mediated by target changes (DNA gyrase and/or topoisomerase IV). These enzymes control DNA topology and are vital for chromosome function and replication. Each of these enzymes is a tetramer composed of two subunits: GyrA and GyrB forming A₂B₂ complex in DNA gyrase; and ParC and ParE forming C₂E₂ complex in DNA topoisomerase IV. It has been shown that they are hotspots, called the quinolone-resistance-determining region (QRDR) for mutations within *gyrA* that encodes for the GyrA subunit of DNA gyrase and within *parC* that encodes the *parC* subunit of topoisomerase IV.

In order to generate a database for *gyrA* and *parC* sequences that can be used for design of primers and/or probes for the specific detection of quinolone resistance in various bacterial species, *gyrA* and *parC* DNA fragments selected from public database (GenBank and EMBL) from a variety of bacterial species were used to design oligonucleotide primers.

Using primer pair SEQ ID NOs. 1297 and 1298, it was possible to amplify and determine *gyrA* sequences from *Klebsiella oxytoca* (SEQ ID NO. 1764), *Klebsiella pneumoniae* subsp. *ozaneae* (SEQ ID NO. 1765), *Klebsiella planticola* (SEQ ID NO. 1766), *Klebsiella pneumoniae* (SEQ ID NO. 1767), *Klebsiella pneumoniae* subsp. *pneumoniae* (two strains) (SEQ ID NOs. 1768-1769), *Klebsiella*

pneumoniae subsp. *rhinoscleromatis* (SEQ ID NO. 1770), *Klebsiella terrigena* (SEQ ID NO. 1771), *Kluyvera ascorbata* (SEQ ID NO. 2013), *Kluyvera georgiana* (SEQ ID NO. 2014) and *Escherichia coli* (4 strains) (SEQ ID NOs. 2277-2280). Using primer pair SEQ ID NOs. 1291 and 1292, it was possible to amplify and determine *gyrA* sequences from *Legionella pneumophila* subsp. *pneumophila* (SEQ ID NO. 1772), *Proteus mirabilis* (SEQ ID NO. 1773), *Providencia rettgeri* (SEQ ID NO. 1774), *Proteus vulgaris* (SEQ ID NO. 1775) and *Yersinia enterocolitica* (SEQ ID NO. 1776). Using primer pair SEQ ID NOs. 1340 and 1341, it was possible to amplify and determine *gyrA* sequence from *Staphylococcus aureus* (SEQ ID NO. 1255).

Using primers SEQ ID NOs. 1318 and 1319, it was possible to amplify and determine *parC* sequences from *K. oxytoca* (two strains) (SEQ ID NOs. 1777-1778), *Klebsiella pneumoniae* subsp. *ozaenae* (SEQ ID NO. 1779), *Klebsiella planticola* (SEQ ID NO. 1780), *Klebsiella pneumoniae* (SEQ ID NO. 1781), *Klebsiella pneumoniae* subsp. *pneumoniae* (two strains) (SEQ ID NOs. 1782-1783), *Klebsiella pneumoniae* subsp. *rhinoscleromatis* (SEQ ID NO. 1784) and *Klebsiella terrigena* (SEQ ID NO. 1785).

EXAMPLE 33:

Development of a PCR assay for the specific detection and identification of *Staphylococcus aureus* and its quinolone resistance genes *gyrA* and *parC*. The analysis of *gyrA* and *parC* sequences from a variety of bacterial species revealed conserved regions allowing the design of PCR primers specific to the quinolone-resistance-determining region (QRDR) of *gyrA* and *parC* from *Staphylococcus aureus*. PCR primer pair SEQ ID NOs. 1340 and 1341 was designed to amplify the *gyrA* sequence of *S. aureus*, whereas PCR primer pair SEQ ID NOs. 1342 and 1343 was designed to amplify *S. aureus parC*. The comparison of *gyrA* and *parC* sequences from *S. aureus* strains with various levels of quinolone resistance

allowed the identification of amino acid substitutions Ser-84 to Leu, Glu-88 to Gly or Lys in the GyrA subunit of DNA gyrase encoded by *gyrA* and amino acid changes Ser-80 to Phe or Tyr and Ala-116 to Glu in the ParC subunit of topoisomerase IV encoded by *parC*. These amino acid substitutions in GyrA and ParC subunits occur in isolates with intermediate- or high-level quinolone resistance. Internal probes for the specific detection of wild-type *S. aureus gyrA* (SEQ ID NO. 1940) and wild-type *S. aureus parC* (SEQ ID NO. 1941) as well as internal probes for the specific detection of each of the *gyrA* (SEQ ID NOs. 1333-1335) and *parC* mutations identified in quinolone-resistant *S. aureus* (SEQ ID NOs. 1336-1339) were designed.

The *gyrA*- and *parC*-specific primer pairs (SEQ ID NOs. 1340-1341 and SEQ ID NOs. 1342-1343) were used in multiplex. PCR amplification was carried out on PTC-200 thermocyclers (MJ Research) using 0.3, 0.3, 0.6 and 0.6 μ M of each primers, respectively, as described in Example 28. The optimal cycling conditions for maximum sensitivity and specificity were 3 minutes at 95 °C for initial denaturation, then forty cycles of two steps consisting of 1 second at 95 °C and 30 seconds at 62 °C, followed by terminal extension at 72 °C for 2 minutes. Detection of the PCR products was made by electrophoresis in agarose gels (2 %) containing 0.25 μ g/ml of ethidium bromide. The specificity of the multiplex assay with 40-cycle PCR was verified by using 0.1 ng of purified genomic DNA from a panel of gram-positive bacteria. The list included the following: *Abiotrophia adiacens*, *Abiotrophia defectiva*, *Bacillus cereus*, *Bacillus mycoides*, *Enterococcus faecalis* (2 strains), *Enterococcus flavescens*, *Gemella morbillorum*, *Lactococcus lactis*, *Listeria innocua*, *Listeria monocytogenes*, *Staphylococcus aureus* (5 strains), *Staphylococcus auricularis*, *Staphylococcus capitis* subsp. *urealyticus*, *Staphylococcus carnosus*, *Staphylococcus chromogenes*, *Staphylococcus epidermidis* (3 strains), *Staphylococcus gallinarum*, *Staphylococcus haemolyticus* (2 strains), *Staphylococcus hominis*, *Staphylococcus hominis* subsp. *hominis*, *Staphylococcus lentus*, *Staphylococcus lugdunensis*, *Staphylococcus*

saccharolyticus, *Staphylococcus saprophyticus* (3 strains), *Staphylococcus simulans*, *Staphylococcus warneri*, *Staphylococcus xylosus*, *Streptococcus agalactiae*, *Streptococcus pneumoniae*. Strong amplification of both *gyrA* and *parC* genes was only detected for the *S. aureus* strains tested. The sensitivity of the multiplex assay with 40-cycle PCR was verified with one quinolone-sensitive and four quinolone-resistant strains of *S. aureus*. The detection limit was 2 to 10 copies of genomic DNA, depending on the strains tested.

Detection of the hybridization with the internal probes was performed as described in Example 7. The internal probes specific to wild-type *gyrA* and *parC* of *S. aureus* and to the *gyrA* and *parC* variants of *S. aureus* were able to recognize two quinolone-resistant and one quinolone-sensitive *S. aureus* strains showing a perfect correlation with the susceptibility to quinolones.

The complete assay for the specific detection of *S. aureus* and its susceptibility to quinolone contains the *Staphylococcus*-specific primers (SEQ ID NOs. 553 and 575) described in Example 7 and the multiplex containing the *S. aureus gyrA*- and *parC*-specific primer pairs (SEQ ID NOs. 1340-1341 and SEQ ID NOs. 1342-1343). Amplification is coupled with post-PCR hybridization with the internal probe specific to *S. aureus* (SEQ ID NO. 587) described in Example 7 and the internal probes specific to wild-type *S. aureus gyrA* and *parC* (SEQ ID NOs. 1940-1941) and to the *S. aureus gyrA* and *parC* variants (SEQ ID NOs. 1333-1338).

An assay was also developed for the detection of quinolone-resistant *S. aureus* using the SmartCycler (Cepheid). Real-time detection is based on the use of *S. aureus parC*-specific primers (SEQ ID NOs. 1342 and 1343) and the *Staphylococcus*-specific primers (SEQ ID NOs. 553 and 575) described in Example 7. Internal probes were designed for molecular beacon detection of the wild-type *S. aureus parC* (SEQ ID NO.1939), for detection of the Ser-80 to Tyr or

Phe amino acid substitutions in the ParC subunit encoded by *S. aureus parC* (SEQ ID NOs. 1938 and 1955) and for detection of *S. aureus* (SEQ ID NO. 2282).

EXAMPLE 34:

Development of a PCR assay for the detection and identification of *Klebsiella pneumoniae* and its quinolone resistance genes *gyrA* and *parC*. The analysis of *gyrA* and *parC* sequences from a variety of bacterial species from the public databases and from the database described in Example 32 revealed conserved regions allowing the design of PCR primers specific to the quinolone-resistance-determining region (QRDR) of *gyrA* and *parC* from *K. pneumoniae*. PCR primer pair SEQ ID NOs. 1936 and 1937, or pair SEQ ID NOs. 1937 and 1942, were designed to amplify the *gyrA* sequence of *K. pneumoniae*, whereas PCR primer pair SEQ ID NOs. 1934 and 1935 was designed to amplify *K. pneumoniae parC* sequence. An alternative pair, SEQ ID NOs. 1935 and 1936, can also amplify *K. pneumoniae parC*. The comparison of *gyrA* and *parC* sequences from *K. pneumoniae* strains with various levels of quinolone resistance allowed the identification of amino acid substitutions Ser-83 to Tyr or Phe and Asp-87 to Gly or Ala and Asp-87 to Asn in the GyrA subunit of DNA gyrase encoded by *gyrA* and amino acid changes Ser-80 to Ile or Arg and Glu-84 to Gly or Lys in the ParC subunit of topoisomerase IV encoded by *parC*. These amino acid substitutions in the GyrA and ParC subunits occur in isolates with intermediate- or high-level quinolone resistance. Internal probes for the specific detection of wild-type *K. pneumoniae gyrA* (SEQ ID NO. 1943) and wild-type *K. pneumoniae parC* (SEQ ID NO. 1944) as well as internal probes for the specific detection of each of the *gyrA* (SEQ ID NOs. 1945-1949) and *parC* mutations identified in quinolone-resistant *K. pneumoniae* (SEQ ID NOs. 1950-1953) were designed.

Two multiplex using the *K. pneumoniae gyrA*- and *parC*-specific primer pairs were used: the first multiplex contained *K. pneumoniae gyrA*-specific primers (SEQ ID

NOs. 1937 and 1942) and *K. pneumoniae* *parC*-specific primers (SEQ ID NOs. 1934 and 1935) and the second multiplex contained *K. pneumoniae* *gyrA/parC*-specific primer (SEQ ID NOs. 1936), *K. pneumoniae* *gyrA*-specific primer (SEQ ID NO. 1937) and *K. pneumoniae* *parC*-specific primer (SEQ ID NO. 1935). Standard PCR was carried out on PTC-200 thermocyclers (MJ Research) using for the first multiplex 0.6, 0.6, 0.4, 0.4 μ M of each primer, respectively, and for the second multiplex 0.8, 0.4, 0.4 μ M of each primer, respectively. PCR amplification and agarose gel electrophoresis of the amplified products were performed as described in Example 28. The optimal cycling conditions for maximum sensitivity and specificity were 3 minutes at 95 °C for initial denaturation, then forty cycles of two steps consisting of 1 second at 95 °C and 30 seconds at 62 °C, followed by terminal extension at 72 °C for 2 minutes. The specificity of the two multiplex assays with 40-cycle PCR was verified by using 0.1 ng of purified genomic DNA from a panel of gram-negative bacteria. The list included: *Acinetobacter baumannii*, *Citrobacter freundii*, *Eikenella corrodens*, *Enterobacter aerogenes*, *Enterobacter cancerogenes*, *Enterobacter cloacae*, *Escherichia coli* (10 strains), *Haemophilus influenzae*, *Klebsiella pneumoniae*, *Klebsiella ornitholytica*, *Klebsiella oxytoca* (2 strains), *Klebsiella planticola*, *Klebsiella terrigena*, *Kluyvera ascorbata*, *Kluyvera cryocrescens*, *Kluyvera georgiana*, *Neisseria gonorrhoeae*, *Proteus mirabilis*, *Proteus vulgaris*, *Pseudomonas aeruginosa*, *Salmonella choleraesuis* subsp. *typhimurium*, *Salmonella enteritidis*, *Serratia liquefaciens*, *Serratia marcescens* and *Yersinia enterocolytica*. For both multiplex, strong amplification of both *gyrA* and *parC* was observed only for the *K. pneumoniae* strain tested. The sensitivity of the two multiplex assays with 40-cycle PCR was verified with one quinolone-sensitive strain of *K. pneumoniae*. The detection limit was around 10 copies of genomic DNA.

The complete assay for the specific detection of *K. pneumoniae* and its susceptibility to quinolone contains the *Klebsiella*-specific primers (SEQ ID NOs. 1331 and 1332) described in Example 29 and either the multiplex containing the *K.*

pneumoniae gyrA- and *parC*-specific primers (SEQ ID NOs. 1935, 1936, 1937) or the multiplex containing the *K. pneumoniae gyrA*- and *parC*-specific primers (SEQ ID NOs. 1934, 1937, 1939, 1942). Amplification is coupled with post-PCR hybridization with the internal probe specific to *K. pneumoniae* (SEQ ID NO. 2167) described in Example 29 and the internal probes specific to wild-type *K. pneumoniae gyrA* and *parC* (SEQ ID NOs. 1943, 1944) and to the *K. pneumoniae gyrA* and *parC* variants (SEQ ID NOs. 1945-1949 and 1950-1953).

An assay was also developed for the detection of quinolone-resistant *K. pneumoniae* using the SmartCycler (Cepheid). Real-time detection is based on the use of resistant *K. pneumoniae gyrA*-specific primers (SEQ ID NOs. 1936 and 1937) and the *K. pneumoniae*-specific primers (SEQ ID NOs. 1331 and 1332) described in Example 29. Internal probes were designed for molecular beacon detection of the wild-type *K. pneumoniae gyrA* (SEQ ID NO. 2251), for detection of the Ser-83 to Tyr or Phe and/or Asp-87 to Gly or Asn in the GyrA subunit of DNA gyrase encoded by *gyrA* (SEQ ID NOs. 2250) and for detection of *K. pneumoniae* (SEQ ID NO. 2281).

EXAMPLE 35:

Development of a PCR assay for detection and identification of *S. pneumoniae* and its quinolone resistance genes *gyrA* and *parC*. The analysis of *gyrA* and *parC* sequences from a variety of bacterial species revealed conserved regions allowing the design of PCR primers able to amplify the quinolone-resistance-determining region (QRDR) of *gyrA* and *parC* from all *S. pneumoniae* strains. PCR primer pair SEQ ID NOs. 2040 and 2041 was designed to amplify the QRDR of *S. pneumoniae gyrA*, whereas PCR primer pair SEQ ID NOs. 2044 and 2045 was designed to amplify the QRDR of *S. pneumoniae parC*. The comparison of *gyrA* and *parC* sequences from *S. pneumoniae* strains with various levels of quinolone resistance allowed the identification of amino acid substitutions Ser-81 to Phe or

Tyr in the GyrA subunit of DNA gyrase encoded by *gyrA* and amino acid changes Ser-79 to Phe in the ParC subunit of topoisomerase IV encoded by *parC*. These amino acid substitutions in the GyrA and ParC subunits occur in isolates with intermediate- or high-level quinolone resistance. Internal probes for the specific detection of each of the *gyrA* (SEQ ID NOs. 2042 and 2043) and *parC* (SEQ ID NO. 2046) mutations identified in quinolone-resistant *S. pneumoniae* were designed.

For all bacterial species, amplification was performed from purified genomic DNA. 1 μ l of genomic DNA at 0.1 ng/ μ L was transferred directly to a 19 μ l PCR mixture. Each PCR reaction contained 50 mM KCl, 10 mM Tris-HCl (pH 9.0), 0.1% Triton X-100, 2.5 mM MgCl₂, 0.4 μ M (each) of the above primers SEQ ID NOs. 2040, 2041, 2044 and 2045, 0.05 mM bovine serum albumin (BSA) and 0.5 U *Taq* polymerase coupled with TaqStart™ antibody. The optimal cycling conditions for maximum sensitivity and specificity were 3 minutes at 95 °C for initial denaturation, then forty cycles of two steps consisting of 1 second at 95 °C and 30 seconds at 58 °C, followed by terminal extension at 72 °C for 2 minutes. In order to generate Digoxigenin (DIG)-labeled amplicons for capture probe hybridization, 0.1X PCR DIG labeling four deoxynucleoside triphosphates mix (Boehringer Mannheim GmbH) was used for amplification.

The DIG-labeled amplicons were hybridized to the capture probes bound to 96-well plates. The plates were incubated with anti-DIG-alkaline phosphatase and the chemiluminescence was measured by using a luminometer (MLX, Dynex Technologies Inc.) after incubation with CSPD and recorded as Relative Light Unit (RLU). The RLU ratio of tested sample with and without captures probes was then calculated. A ratio ≥ 2.0 was defined as a positive hybridization signal. All reactions were performed in duplicate.

The specificity of the multiplex assay with 40-cycle PCR was verified by using 0.1 ng of purified genomic DNA from a panel of bacteria listed in Table 13. Strong amplification of both *gyrA* and *parC* was detected only for the *S. pneumoniae* strains tested. Weak amplification of both *gyrA* and *parC* genes was detected for *Staphylococcus simulans*. The detection limit tested with purified genomic DNA from 5 strains of *S. pneumoniae* was 1 to 10 genome copies. In addition, 5 quinolone-resistant and 2 quinolone-sensitive clinical isolates of *S. pneumoniae* were tested to further validate the developed multiplex PCR coupled with capture probe hybridization assays. There was a perfect correlation between detection of *S. pneumoniae gyrA* and *parC* mutations and the susceptibility to quinolone.

The complete assay for the specific detection of *S. pneumoniae* and its susceptibility to quinolone contains the *S. pneumoniae*-specific primers (SEQ ID NOs. 1179 and 1181) described in Exemple 20 and the multiplex containing the *S. pneumoniae gyrA*-specific and *parC*-specific primer pairs (SEQ ID NOS. 2040 and 2041 and SEQ ID NOs. 2044 and 2045). Amplification is coupled with post-PCR hybridization with the internal probe specific to *S. pneumoniae* (SEQ ID NO. 1180) described in Example and the internal probes specific to each of the *S. pneumoniae gyrA* and *parC* variants (SEQ ID NOs. 2042, 2043 and 2046).

EXAMPLE 36:

Detection of extended-spectrum TEM-type β -lactamases in *Escherichia coli*. The analysis of TEM sequences which confer resistance to third-generation cephalosporins and to β -lactamase inhibitors allowed the identification of amino acid substitutions Met-69 to Ile or Leu or Val, Ser-130 to Gly, Arg-164 to Ser or His, Gly-238 to Ser, Glu-240 to Lys and Arg-244 to Ser or Cys or Thr or His or Leu. PCR primers SEQ ID NOs. 1907 and 1908 were designed to amplify TEM sequences. Internal probes for the specific detection of wild-type TEM (SEQ ID NO. 2141) and for each of the amino acid substitutions (SEQ ID NOs. 1909-1926) identified in TEM variants were designed to detect resistance to third-generation

cephalosporins and to β -lactamase inhibitors. Design and synthesis of primers and probes, and detection of the hybridization were performed as described in Example 7.

For all bacterial species, amplification was performed from purified genomic DNA. One μ l of genomic DNA at 0.1 ng/ μ l was transferred directly to a 19 μ l PCR mixture. Each PCR reaction contained 50 mM KCl, 10 mM Tris-HCl (pH 9.0); 0.1% Triton X-100, 2.5 mM MgCl₂, 0.4 μ M of the TEM-specific primers SEQ ID NOs. 1907 and 1908, 200 μ M (each) of the four deoxynucleoside triphosphates, 0.05 mM bovine serum albumin (BSA) and 0.5 U *Taq* polymerase (Promega) coupled with TaqStartTM antibody. PCR amplification and agarose gel analysis of the amplified products were performed as described in Example 28. The optimal cycling conditions for maximum sensitivity and specificity were 3 minutes at 95 °C for initial denaturation, then forty cycles of three steps consisting of 5 seconds at 95 °C, 30 seconds at 55 °C and 30 seconds at 72 °C, followed by terminal extension at 72 °C for 2 minutes.

The specificity of the TEM-specific primers with 40-cycle PCR was verified by using 0.1 ng of purified genomic from the following bacteria: three third-generation cephalosporin-resistant *Escherichia coli* strains (one with TEM-10, one with TEM-28 and the other with TEM-49), two third-generation cephalosporin-sensitive *Escherichia coli* strain (one with TEM-1 and the other without TEM), one third-generation cephalosporin-resistant *Klebsiella pneumoniae* strain (with TEM-47), and one β -lactamase-inhibitor-resistant *Proteus mirabilis* strain (with TEM-39). Amplification with the TEM-specific primers was detected only for strains containing TEM.

The sensitivity of the assay with 40-cycle PCR was verified with three *E. coli* strains containing TEM-1 or TEM-10 or TEM-49, one *K. pneumoniae* strain containing TEM-47 and one *P. mirabilis* strain containing TEM-39. The detection

limit was 5 to 100 copies of genomic DNA, depending on the TEM-containing strains tested.

The TEM-specific primers SEQ ID NOs. 1907 and 1908 were used in multiplex with the *Escherichia coli/Shigella sp.*-specific primers SEQ ID NOs. 1661 and 1665 described in Example 28 to allow the complete identification of *Escherichia coli/Shigella sp.* and the susceptibility to β -lactams. PCR amplification with 0.4 μ M of each of the primers and agarose gel analysis of the amplified products was performed as described above.

The specificity of the multiplex with 40-cycle PCR was verified by using 0.1 ng of purified genomic DNA from the following bacteria: three third-generation cephalosporin-resistant *Escherichia coli* strains (one with TEM-10, one with TEM-28 and the other with TEM-49), two third-generation cephalosporin-sensitive *Escherichia coli* strain (one with TEM-1 and the other without TEM), one third-generation cephalosporin-resistant *Klebsiella pneumoniae* strain (with TEM-47), and one β -lactamase-inhibitor-resistant *Proteus mirabilis* strain (with TEM-39). The multiplex was highly specific to *Escherichia coli* strains containing TEM.

The complete assay for detection of TEM-type β -lactamases in *E. coli* includes PCR amplification using the multiplex containing the TEM-specific primers (SEQ ID NOs. 1907 and 1908) and the *Escherichia coli/Shigella sp.*-specific primers (SEQ ID NOs. 1661 and 1665) coupled with post PCR-hybridization with the internal probes specific to wild-type TEM (SEQ ID NO. 2141) and to the TEM variants (SEQ ID NOs. 1909-1926).

EXAMPLE 37:

Detection of extended-spectrum SHV-type β -lactamases in *Klebsiella pneumoniae*.

The comparison of SHV sequences, which confer resistance to third-generation

cephalosporins and to β -lactamase inhibitors, allowed the identification of amino acid substitutions Ser-130 to Gly, Asp-179 to Ala or Asn, Gly-238 to Ser, and Glu-240 to Lys. PCR primer pair SEQ ID NOs. 1884 and 1885 was designed to amplify SHV sequences. Internal probes for the specific identification of wild-type SHV (SEQ ID NO. 1896) and for each of the amino acid substitutions (SEQ ID NOs. 1886-1895 and 1897-1898) identified in SHV variants were designed to detect resistance to third-generation cephalosporins and to β -lactamase inhibitors. Design and synthesis of primers and probes, and detection of the hybridization were performed as described in Example 7.

For all bacterial species, amplification was performed from purified genomic DNA. One μ l of genomic DNA at 0.1ng/ μ l was transferred directly to a 19 μ l PCR mixture. Each PCR reaction contained 50 mM KCl, 10 mM Tris-HCl (pH 9.0), 0.1% Triton X-100, 2.5 mM $MgCl_2$, 0.4 μ M of the SHV-specific primers SEQ ID NO. 1884 and 1885, 200 μ M (each) of the four deoxynucleoside triphosphates, 0.05 mM bovine serum albumin (BSA) and 0.5 U *Taq* polymerase (Promega) coupled with TaqStartTM antibody. PCR amplification and agarose gel analysis of the amplified products were performed as described in Example 28. The optimal cycling conditions for maximum sensitivity and specificity were 3 minutes at 95 °C for initial denaturation, then forty cycles of three steps consisting of 5 seconds at 95 °C, 30 seconds at 55 °C and 30 seconds at 72 °C, followed by terminal extension at 72 °C for 2 minutes.

The specificity of the SHV-specific primers with 40-cycle PCR was verified by using 0.1 ng of purified genomic from the following bacteria: two third-generation cephalosporin-resistant *Klebsiella pneumoniae* strains (one with SHV-2a and the other with SHV-12), one third-generation cephalosporin-sensitive *Klebsiella pneumoniae* strain (with SHV-1), two third-generation cephalosporin-resistant *Escherichia coli* strains (one with SHV-8 and the other with SHV-7), and two third-generation cephalosporin-sensitive *Escherichia coli* strains (one with SHV-1

and the other without any SHV). Amplification with the SHV-specific primers was detected only for strains containing SHV.

The sensitivity of the assay with 40-cycle PCR was verified with four strains containing SHV. The detection limit was 10 to 100 copies of genomic DNA, depending on the SHV-containing strains tested.

The amplification was coupled with post-PCR hybridization with the internal probes specific for identification of wild-type SHV (SEQ ID NO. 1896) and for each of the amino acid substitutions (SEQ ID NOs. 1886-1895 and 1897-1898) identified in SHV variants. The specificity of the probes was verified with six strains containing various SHV enzymes, one *Klebsiella pneumoniae* strain containing SHV-1, one *Klebsiella pneumoniae* strain containing SHV-2a, one *Klebsiella pneumoniae* strain containing SHV-12, one *Escherichia coli* strain containing SHV-1, one *Escherichia coli* strain containing SHV-7 and one *Escherichia coli* strain containing SHV-8. The probes correctly detected each of the SHV genes and their specific mutations. There was a perfect correlation between the SHV genotype of the strains and the susceptibility to β -lactam antibiotics.

The SHV-specific primers SEQ ID NOs. 1884 and 1885 were used in multiplex with the *K. pneumoniae*-specific primers SEQ ID NOs. 1331 and 1332 described in Example 29 to allow the complete identification of *K. pneumoniae* and the susceptibility to β -lactams. PCR amplification with 0.4 μ M of each of the primers and agarose gel analysis of the amplified products were performed as described above.

The specificity of the multiplex with 40-cycle PCR was verified by using 0.1 ng of purified genomic DNA from the following bacteria: three *K. pneumoniae* strains containing SHV-1, one *Klebsiella pneumoniae* strain containing SHV-2a, one

Klebsiella pneumoniae strain containing SHV-12, one *K. rhinoscleromatis* strain containing SHV-1, one *Escherichia coli* strain without SHV. The multiplex was highly specific to *Klebsiella pneumoniae* strain containing SHV.

EXAMPLE 38:

Development of a PCR assay for the detection and identification of *Neisseria gonorrhoeae* and its associated tetracycline resistance gene *tetM*. The analysis of publicly available *tetM* sequences revealed conserved regions allowing the design of PCR primers specific to *tetM* sequences. The PCR primer pair SEQ ID NOs. 1588 and 1589 was used in multiplex with the *Neisseria gonorrhoeae*-specific primers SEQ ID NOs. 551 and 552 described in Example 31. Sequence alignment analysis of *tetM* sequences revealed regions suitable for the design of an internal probe specific to *tetM* (SEQ ID NO. 2254). PCR amplification was carried out on PTC-200 thermocyclers (MJ Research) using 0.4 μ M of each primer pair as described in Example 28. The optimal cycling conditions for maximum sensitivity and specificity were as follow: three minutes at 95 °C for initial denaturation, then forty cycles of two steps consisting of 1 second at 95 °C and 30 seconds at 60°C, followed by terminal extension at 72 °C for 2 minutes.

The specificity of the multiplex PCR assay with 40-cycle PCR was verified by using 0.1 ng of purified genomic DNA from the following bacteria: two tetracycline-resistant *Escherichia coli* strains (one containing the tetracycline-resistant gene *tetB* and the other containing the tetracycline-resistant gene *tetC*), one tetracycline-resistant *Pseudomonas aeruginosa* strain (containing the tetracycline-resistant gene *tetA*), nine tetracycline-resistant *Neisseria gonorrhoeae* strains, two tetracycline-sensitive *Neisseria meningitidis* strains, one tetracycline-sensitive *Neisseria polysaccharea* strain, one tetracycline-sensitive *Neisseria sicca* strain and one tetracycline-sensitive *Neisseria subflava* strain. Amplification with both the *tetM*-specific and *Neisseria gonorrhoeae*-specific primers was detected

only for *N. gonorrhoeae* strains containing *tetM*. There was a weak amplification signal using *Neisseria gonorrhoeae*-specific primers for the following species: *Neisseria sicca*, *Neisseria polysaccharea* and *Neisseria meningitidis*. There was a perfect correlation between the *tetM* genotype and the tetracycline susceptibility pattern of the *Neisseria gonorrhoeae* strains tested. The internal probe specific to *N. gonorrhoeae* SEQ ID NO. 2166 described in Example 31 can discriminate *Neisseria gonorrhoeae* from the other *Neisseria* sp.

The sensitivity of the assay with 40-cycle PCR was verified with two tetracycline resistant strains of *N. gonorrhoeae*. The detection limit was 5 copies of genomic DNA for both strains.

EXAMPLE 39:

Development of a PCR assay for the detection and identification of *Shigella* sp. and their associated trimethoprim resistance gene *dhfrIa*. The analysis of publicly available *dhfrIa* and other *dhfr* sequences revealed regions allowing the design of PCR primers specific to *dhfrIa* sequences. The PCR primer pair (SEQ ID NOs. 1459 and 1460) was used in multiplex with the *Escherichia coli/Shigella* sp.-specific primers SEQ ID NOs. 1661 and 1665 described in Example 28. Sequence alignment analysis of *dhfrIa* sequences revealed regions suitable for the design of an internal probe specific to *dhfrIa* (SEQ ID NO. 2253). PCR amplification and agarose gel analysis of the amplified products were performed as described in Example 28 with an annealing temperature of 60 °C. The specificity of the multiplex assay with 40-cycle PCR was verified by using 0.1 ng of purified genomic DNA from a panel of bacteria. The list included the following trimethoprim-sensitive strains, *Salmonella typhimurium*, *Salmonella typhi*, *Salmonella enteritidis*, *Tatumella ptyseos*, *Klebsiella pneumoniae*, *Enterobacter aerogenes*, *Citrobacter farmeri*, *Campylobacter jejuni*, *Serratia marcescens*, *Shigella dysenteriae*, *Shigella flexneri*, *Shigella sonnei*, six trimethoprim-resistant *Escherichia coli* strains (containing *dhfrIa* or *dhfrV* or *dhfrVII* or *dhfrXII* or

dhfrXIII or *dhfrXV*), four trimethoprim-resistant strains containing *dhfrIa* (*Shigella sonnei*, *Shigella flexneri*, *Shigella dysenteriae* and *Escherichia coli*). There was a perfect correlation between the *dhfrIa* genotype and the trimethoprim susceptibility pattern of the *Escherichia coli* and *Shigella* sp. strains tested. The *dhfrIa* primers were specific to the *dhfrIa* gene and did not amplify any of the other trimethoprim-resistant *dhfr* genes tested. The sensitivity of the multiplex assay with 40-cycle PCR was verified with three strains of trimethoprim-resistant strains of *Shigella* sp. The detection limit was 5 to 10 genome copies of DNA, depending on the *Shigella* sp. strains tested.

EXAMPLE 40:

Development of a PCR assay for the detection and identification of *Acinetobacter baumannii* and its associated aminoglycoside resistance gene *aph(3')-VIa*. The comparison of publicly available *aph(3')-VIa* sequence revealed regions allowing the design of PCR primers specific to *aph(3')-VIa*. The PCR primer pair (SEQ ID NOs. 1404 and 1405) was used in multiplex with the *Acinetobacter baumannii*-specific primers SEQ ID NOs. 1692 and 1693 described in Example 30. Analysis of the *aph(3')-VIa* sequence revealed region suitable for the design of an internal probe specific to *aph(3')-VIa* (SEQ ID NO. 2252). PCR amplification and agarose gel analysis of the amplified products were performed as described in Example 28. The specificity of the multiplex assay with 40-cycle PCR was verified by using 0.1 ng of purified genomic DNA from a panel of bacteria including: two aminoglycoside-resistant *A. baumannii* strains (containing *aph(3')-VIa*), one aminoglycoside-sensitive *A. baumannii* strain, one of each of the following aminoglycoside-resistant bacteria, one *Serratia marcescens* strain containing the aminoglycoside-resistant gene *aacC1*, one *Serratia marcescens* strain containing the aminoglycoside-resistant gene *aacC4*, one *Enterobacter cloacae* strain containing the aminoglycoside-resistant gene *aacC2*, one *Enterococcus faecalis* containing the aminoglycoside-resistant gene *aacA-aphD*, one *Pseudomonas*

aeruginosa strain containing the aminoglycoside-resistant gene *aac6IIa* and one of each of the following aminoglycoside-sensitive bacterial species, *Acinetobacter anitratus*, *Acinetobacter lwoffii*, *Psychobacter phenylpyruvian*, *Neisseria gonorrhoeae*, *Haemophilus haemolyticus*, *Haemophilus influenzae*, *Yersinia enterocolitica*, *Proteus vulgaris*, *Eikenella corrodens*, *Escherichia coli*. There was a perfect correlation between the *aph(3')-VIa* genotype and the aminoglycoside susceptibility pattern of the *A. baumannii* strains tested. The *aph(3')-VIa*-specific primers were specific to the *aph(3')-VIa* gene and did not amplify any of the other aminoglycoside-resistant genes tested. The sensitivity of the multiplex assay with 40-cycle PCR was verified with two strains of aminoglycoside-resistant strains of *A. baumannii*. The detection limit was 5 genome copies of DNA for both *A. baumannii* strains tested.

EXAMPLE 41:

Specific identification of *Bacteroides fragilis* using *atpD* (V-type) sequences. The comparison of *atpD* (V-type) sequences from a variety of bacterial species allowed the selection of PCR primers for *Bacteroides fragilis*. The strategy used to design the PCR primers was based on the analysis of a multiple sequence alignment of various *atpD* sequences from *B. fragilis*, as well as *atpD* sequences from the related species *B. dispar*, bacterial genera and archaea, especially representatives with phylogenetically related *atpD* sequences. A careful analysis of this alignment allowed the selection of oligonucleotide sequences which are conserved within the target species but which discriminate sequences from other species, especially from closely related species *B. dispar*, thereby permitting the species-specific and ubiquitous detection and identification of the target bacterial species.

The chosen primer pair, SEQ ID NOs. 2134-2135, produces an amplification product of 231 bp. Standard PCR was carried out on PTC-200 thermocyclers (MJ Research Inc.) using 0.4 μ M of each primers pair as described in Example 28. The

optimal cycling conditions for maximum sensitivity and specificity were as follows: three minutes at 95°C for initial denaturation, then forty cycles of two steps consisting of 1 second at 95°C and 30 seconds at 60°C, followed by terminal extension at 72°C for 2 minutes.

The format of this assay is not limited to the one described above. A person skilled in the art could adapt the assay for different formats such as PCR with real-time detection using molecular beacon probes. Molecular beacon probes designed to be used in this assay include, but are not limited to, SEQ ID NO. 2136 for the detection of the *B. fragilis* amplicon.

EXAMPLE 42:

Evidence for horizontal gene transfer in the evolution of the elongation factor Tu in Enterococci.

ABSTRACT

The elongation factor Tu, encoded by *tuf* genes, is a GTP binding protein that plays a central role in protein synthesis. One to three *tuf* genes per genome are present depending on the bacterial species. Most low G+C gram-positive bacteria carry only one *tuf* gene. We have designed degenerate PCR primers derived from consensus sequences of the *tuf* gene to amplify partial *tuf* sequences from 17 enterococcal species and other phylogenetically related species. The amplified DNA fragments were sequenced either by direct sequencing or by sequencing cloned inserts containing putative amplicons. Two different *tuf* genes (*tufA* and *tufB*) were found in 11 enterococcal species, including *Enterococcus avium*, *E. casseliflavus*, *E. dispar*, *E. durans*, *E. faecium*, *E. gallinarum*, *E. hirae*, *E. malodoratus*, *E. mundtii*, *E. pseudoavium*, and *E. raffinosus*. For the other six enterococcal species (*E. cecorum*, *E. columbae*, *E. faecalis*, *E. sulfureus*, *E.*

saccharolyticus, and *E. solitarius*), only the *tufA* gene was present. Based on 16S rRNA gene sequence analysis, the 11 species having two *tuf* genes all share a common ancestor, while the six species having only one copy diverged from the enterococcal lineage before that common ancestor. The presence of one or two copies of the *tuf* gene in enterococci was confirmed by Southern hybridization.

Phylogenetic analysis of *tuf* sequences demonstrated that the enterococcal *tufA* gene branches with the *Bacillus*, *Listeria* and *Staphylococcus* genera, while the enterococcal *tufB* gene clusters with the genera *Streptococcus* and *Lactococcus*. Primary structure analysis showed that four amino acid residues within the sequenced regions are conserved and unique to the enterococcal *tufB* genes and the *tuf* genes of streptococci and *L. lactis*. The data suggest that an ancestral streptococcus or a streptococcus-related species may have horizontally transferred a *tuf* gene to the common ancestor of the 11 enterococcal species which now carry two *tuf* genes.

INTRODUCTION

The elongation factor Tu (EF-Tu) is a GTP binding protein playing a central role in protein synthesis. It mediates the recognition and transport of aminoacyl-tRNAs and their positioning to the A-site of the ribosome. The highly conserved function and ubiquitous distribution render the elongation factor a valuable phylogenetic marker among eubacteria and even throughout the archaeobacterial and eukaryotic kingdoms. The *tuf* genes encoding elongation factor Tu are present in various copy numbers per bacterial genome. Most gram-negative bacteria contain two *tuf* genes. As found in *Escherichia coli*, the two genes, while being almost identical in sequence, are located in different parts of the bacterial chromosome. However, recently completed microbial genomes revealed that only one *tuf* gene is found in *Helicobacter pylori* as well as in some obligate parasitic bacteria, such as *Borrelia burgdorferi*, *Rickettsia prowazekii*, and *Treponema pallidum*, and in some cyanobacteria. In most gram-positive bacteria studied so far, only one *tuf* gene was found. However, Southern hybridization showed that there are two *tuf* genes in

some clostridia as well as in *Streptomyces coelicolor* and *S. lividans*. Up to three *tuf*-like genes have been identified in *S. ramocissimus*.

Although massive prokaryotic gene transfer is suggested to be one of the factors responsible for the evolution of bacterial genomes, the genes encoding components of the translation machinery are thought to be highly conserved and difficult to be transferred horizontally due to the complexity of their interactions. However, a few recent studies demonstrated evidence that horizontal gene transfer has also occurred in the evolution of some genes coding for the translation apparatus, namely, 16S rRNA and some aminoacyl-tRNA synthetases. No further data suggest that such a mechanism is involved in the evolution of the elongation factors. Previous studies concluded that the two copies of *tuf* genes in the genomes of some bacteria resulted from an ancient event of gene duplication. Moreover, a study of the *tuf* gene in *R. prowazekii* suggested that intrachromosomal recombination has taken place in the evolution of the genome of this organism.

To date, little is known about the *tuf* genes of enterococcal species. In this study, we analyzed partial sequences of *tuf* genes in 17 enterococcal species, namely, *E. avium*, *E. casseliflavus*, *E. cecorum*, *E. columbae*, *E. dispar*, *E. durans*, *E. faecalis*, *E. faecium*, *E. gallinarum*, *E. hirae*, *E. malodoratus*, *E. mundtii*, *E. pseudoavium*, *E. raffinosus*, *E. saccharolyticus*, *E. solitarius*, and *E. sulfureus*. We report here the presence of two divergent copies of *tuf* genes in 11 of these enterococcal species. The 6 other species carried a single *tuf* gene. The evolutionary implications are discussed.

MATERIALS AND METHODS

Bacterial strains. Seventeen enterococcal strains and other gram-positive bacterial strains obtained from the American Type Culture Collection (ATCC, Manassas, Va.) were used in this study (Table 16). All strains were grown on sheep blood agar or in brain-heart infusion broth prior to DNA isolation.

DNA isolation. Bacterial DNAs were prepared using the G NOME DNA extraction kit (Bio101, Vista, Calif.) as previously described.

Sequencing of putative *tuf* genes. In order to obtain the *tuf* gene sequences of enterococci and other gram-positive bacteria, two sequencing approaches were used: 1) sequencing of cloned PCR products and 2) direct sequencing of PCR products. A pair of degenerate primers (SEQ ID NOs. 664 and 697) were used to amplify an 886-bp portion of the *tuf* genes from enterococcal species and other gram-positive bacteria as previously described. For *E. avium*, *E. casseliflavus*, *E. dispar*, *E. durans*, *E. faecium*, *E. gallinarum*, *E. hirae*, *E. mundtii*, *E. pseudoavium*, and *E. raffinosus*, the amplicons were cloned using the Original TA cloning kit (Invitrogen, Carlsbad, Calif.) as previously described. Five clones for each species were selected for sequencing. For *E. cecorum*, *E. faecalis*, *E. saccharolyticus*, and *E. solitarius* as well as the other gram-positive bacteria, the sequences of the 886-bp amplicons were obtained by direct sequencing. Based on the results obtained from the earlier rounds of sequencing, two pairs of primers were designed for obtaining the partial *tuf* sequences from the other enterococcal species by direct sequencing. One pair of primers (SEQ ID NOs. 543 and 660) were used to amplify the enterococcal *tuf* gene fragments from *E. columbae*, *E. malodoratus*, and *E. sulfureus*. Another pair of primers (SEQ ID NOs. 664 and 661) were used to amplify the second *tuf* gene fragments from *E. avium*, *E. malodoratus*, and *E. pseudoavium*.

Prior to direct sequencing, PCR products were electrophoresed on 1% agarose gel at 120V for 2 hours. The gel was then stained with 0.02% methylene blue for 30 minutes and washed twice with autoclaved distilled water for 15 minutes. The gel slices containing PCR products of the expected sizes were cut out and purified with the QIAquick gel extraction kit (QIAGEN Inc., Mississauga, Ontario, Canada) according to the manufacturer's instructions. PCR mixtures for sequencing were prepared as described previously. DNA sequencing was carried out with the Big Dye™ Terminator Ready Reaction cycle sequencing kit using a 377 DNA sequencer (PE Applied Biosystems, Foster City, Calif.). Both strands of the

amplified DNA were sequenced. The sequence data were verified using the Sequencer™ 3.0 software (Gene Codes Corp., Ann Arbor, Mich.).

Sequence analysis and phylogenetic study. Nucleotide sequences of the *tuf* genes and their respective flanking regions for *E. faecalis*, *Staphylococcus aureus*, and *Streptococcus pneumoniae*, were retrieved from the TIGR microbial genome database and *S. pyogenes* from the University of Oklahoma database. DNA sequences and deduced protein sequences obtained in this study were compared with those in all publicly available databases using the BLAST and FASTA programs. Unless specified, sequence analysis was conducted with the programs from GCG package (Version 10; Genetics Computer Group, Madison, Wisc.). Sequence alignment of the *tuf* genes from 74 species representing all three kingdoms of life (Tables 16 and 17) were carried out by use of Pileup and corrected upon visual analysis. The N- and C-termini extremities of the sequences were trimmed to yield a common block of 201 amino acids sequences and equivocal residues were removed. Phylogenetic analysis was performed with the aid of PAUP 4.0b4 written by Dr. David L. Swofford (Sinauer Associates, Inc., Publishers, Sunderland, Mass.). The distance matrix and maximum parsimony were used to generate phylogenetic trees and bootstrap resampling procedures were performed using 500 and 100 replications in each analysis, respectively.

Protein structure analysis. The crystal structures of (i) *Thermus aquaticus* EF-Tu in complex with Phe-tRNA^{Phe} and a GTP analog and (ii) *E. coli* EF-Tu in complex with GDP served as templates for constructing the equivalent models for enterococcal EF-Tu. Homology modeling of protein structure was performed using the SWISS-MODEL server and inspected using the SWISS-PDB viewer version 3.1.

Southern hybridization. In a previous study, we amplified and cloned an 803-bp PCR product of the *tuf* gene fragment from *E. faecium*. Two divergent sequences of the inserts, which we assumed to be *tufA* and *tufB* genes, were obtained. The recombinant plasmid carrying either *tufA* or *tufB* sequence was used to generate two probes labeled with Digoxigenin (DIG)-11-dUTP by PCR

incorporation following the instructions of the manufacturer (Boehringer Mannheim, Laval, Québec, Canada). Enterococcal genomic DNA samples (1-2 µg) were digested to completion with restriction endonucleases *Bgl*II and *Xba*I as recommended by the supplier (Amersham Pharmacia Biotech, Mississauga, Ontario, Canada). These restriction enzymes were chosen because no restriction sites were observed within the amplified *tuf* gene fragments of most enterococci. Southern blotting and filter hybridization were performed using positively charged nylon membranes (Boehringer Mannheim) and QuikHyb hybridization solution (Stratagene Cloning Systems, La Jolla, Calif.) according to the manufacturers' instructions with modifications. Twenty µl of each digestion were electrophoresed for 2 h at 120V on a 0.8% agarose gel. The DNA fragments were denatured with 0.5 M NaOH and transferred by Southern blotting onto a positively charged nylon membrane (Boehringer Mannheim). The filters were pre-hybridized for 15 min and then hybridized for 2 h in the QuikHyb solution at 68°C with either DIG-labeled probe. Posthybridization washings were performed twice with 0.5x SSC, 1% SDS at room temperature for 15 min and twice in the same solution at 60°C for 15 min. Detection of bound probes was achieved using disodium 3- (4-methoxyspiro (1,2-dioxetane-3,2'- (5'-chloro) tricyclo(3,3.1.1^{3,7}) decan)-4-yl) phenyl phosphate (CSPD) (Boehringer Mannheim) as specified by the manufacturer.

GenBank submission. The GenBank accession numbers for partial *tuf* gene sequences generated in this study are given in Table 16.

RESULTS

Sequencing and nucleotide sequence analysis. In this study, all gram-positive bacteria other than enterococci yielded a single *tuf* sequence of 886 bp using primers SEQ ID NOs. 664 and 697 (Table 16). Each of four enterococcal species including *E. cecorum*, *E. faecalis*, *E. saccharolyticus*, and *E. solitarius* also yielded one 886-bp *tuf* sequence. On the other hand, for *E. avium*, *E. casseliflavus*, *E. dispar*, *E. durans*, *E. faecium*, *E. gallinarum*, *E. hirae*, *E. mundtii*, *E. pseudoavium*,

and *E. raffinosus*, direct sequencing of the 886-bp fragments revealed overlapping peaks according to their sequence chromatograms, suggesting the presence of additional copies of the *tuf* gene. Therefore, the *tuf* gene fragments of these 10 species were cloned first and then sequenced. Sequencing data revealed that two different types of *tuf* sequences (*tufA* and *tufB*) are found in eight of these species including *E. casseliflavus*, *E. dispar*, *E. durans*, *E. faecium*, *E. gallinarum*, *E. hirae*, *E. mundtii*, and *E. raffinosus*. Five clones from *E. avium* and *E. pseudoavium* yielded only a single *tuf* sequence. These new sequence data allowed the design of new primers specific for the enterococcal *tufA* or *tufB* sequences. Primers SEQ ID NOs. 543 and 660 were designed to amplify only enterococcal *tufA* sequences and a 694-bp fragment was amplified from all 17 enterococcal species. The 694-bp sequences of *tufA* genes from *E. columbae*, *E. malodoratus*, and *E. sulfureus* were obtained by direct sequencing using these primers. Primers SEQ ID NOs. 664 and 661 were designed for the amplification of 730-bp portion of *tufB* genes and yielded the expected fragments from 11 enterococcal species, including *E. malodoratus* and the 10 enterococcal species in which heterogeneous *tuf* sequences were initially found. The sequences of the *tufB* fragments for *E. avium*, *E. malodoratus* and *E. pseudoavium* were determined by direct sequencing using the primers SEQ ID NOs. 664 and 661. Overall, *tufA* gene fragments were obtained from all 17 enterococcal species but *tufB* gene fragments were obtained with only 11 enterococcal species (Table 16).

The identities between *tufA* and *tufB* for each enterococcal species were 68-79% at the nucleotide level and 81 to 89% at the amino acid level. The *tufA* gene is highly conserved among all enterococcal species with identities varying from 87% to 99% for DNA and 93% to 99% for amino acid sequences, while the identities among *tufB* genes of enterococci varies from 77% to 92% for DNA and 91% to 99% for amino acid sequences, indicating their different origins and evolution (Table 18). Since *E. solitarius* has been transferred to the genus *Tetragenococcus*, which is also a low G+C gram-positive bacterium, our sequence comparison did not include this species as an enterococcus. G+C content of enterococcal *tufA*

sequences ranged from 40.8% to 43.1%, while that of enterococcal *tufB* sequences varied from 37.8% to 46.3%. Based on amino acid sequence comparison, the enterococcal *tufA* gene products share higher identities with those of *Abiotrophia adiacens*, *Bacillus subtilis*, *Listeria monocytogenes*, *S. aureus*, and *S. epidermidis*. On the other hand, the enterococcal *tufB* gene products share higher percentages of amino acid identity with the *tuf* genes of *S. pneumoniae*, *S. pyogenes* and *Lactococcus lactis* (Table 18).

In order to elucidate whether the two enterococcal *tuf* sequences encode genuine EF-Tu, the deduced amino acid sequences of both genes were aligned with other EF-Tu sequences available in SWISSPROT (Release 38). Sequence alignment demonstrated that both gene products are highly conserved and carry all conserved residues present in this portion of prokaryotic EF-Tu (Figure 4). Therefore, it appears that both gene products could fulfill the function of EF-Tu. The partial *tuf* gene sequences encode the portion of EF-Tu from residues 117 to 317, numbered as in *E. coli*. This portion makes up of the last four α -helices and two β -strands of domain I, the entire domain II and the N-terminal part of domain III on the basis of the determined structures of *E. coli* EF-Tu.

Based on the deduced amino acid sequences, the enterococcal *tufB* genes have unique conserved residues Lys129, Leu140, Ser230, and Asp234 (*E. coli* numbering) that are also conserved in streptococci and *L. lactis*, but not in the other bacteria (Figure 4). All these residues are located in loops except for Ser230. In other bacteria the residue Ser230 is substituted for highly conserved Thr, which is the 5th residue of the third β -strand of domain II. This region is partially responsible for the interaction between the EF-Tu and aminoacyl-tRNA by the formation of a deep pocket for any of the 20 naturally occurring amino acids. According to our three-dimensional model (data not illustrated), the substitution Thr230→Ser in domain II of EF-Tu may have little impact on the capability of the pocket to accommodate any amino acid. However, the high conservation of Thr230 comparing to the unique Ser substitution found only in streptococci and 11 enterococci could suggest a subtle functional role for this residue.

The *tuf* gene sequences obtained for *E. faecalis*, *S. aureus*, *S. pneumoniae* and *S. pyogenes* were compared with their respective incomplete genome sequence. Contigs with more than 99% identity were identified. Analysis of the *E. faecalis* genome data revealed that the single *E. faecalis tuf* gene is located within an *str* operon where *tuf* is preceded by *fus* that encodes the elongation factor G. This *str* operon is present in *S. aureus* and *B. subtilis* but not in the two streptococcal genomes examined. The 700-bp or so sequence upstream the *S. pneumoniae tuf* gene has no homology with any known gene sequences. In *S. pyogenes*, the gene upstream of *tuf* is similar to a cell division gene, *ftsW*, suggesting that the *tuf* genes in streptococci are not arranged in a *str* operon.

Phylogenetic analysis. Phylogenetic analysis of the *tuf* amino acid sequences with representatives of eubacteria, archeabacteria, and eukaryotes using neighbor-joining and maximum parsimony methods showed three major clusters representing the three kingdoms of life. Both methods gave similar topologies consistent with the rRNA gene data (data not shown). Within the bacterial clade, the tree is polyphyletic but *tufA* genes from all enterococcal species always clustered with those from other low G+C gram-positive bacteria (except for streptococci and lactococci), while the *tufB* genes of the 11 enterococcal species form a distinct cluster with streptococci and *L. lactis* (Figure 5). Duplicated genes from the same organism do not cluster together, thereby not suggesting evolution by recent gene duplication.

Southern hybridization. Southern hybridization of *BglII/XbaI* digested genomic DNA from 12 enterococcal species tested with the *tufA* probe (DIG-labeled *tufA* fragment from *E. faecium*) yielded two bands of different sizes in 9 species, which also carried two divergent *tuf* sequences according to their sequencing data. For *E. faecalis* and *E. solitarius*, a single band was observed indicating that one *tuf* gene is present (Figure 6). A single band was also found when digested genomic DNA from *S. aureus*, *S. pneumoniae*, and *S. pyogenes* were hybridized with the *tufA* probe (data not shown). For *E. faecium*, the presence of three bands can be explained by the existence of a *XbaI* restriction site in the

middle of the *tufA* sequence, which was confirmed by sequencing data. Hybridization with the *tufB* probe (DIG-labeled *tufB* fragment of *E. faecium*) showed a banding profile similar to the one obtained with the *tufA* probe (data not shown).

DISCUSSION

In this study, we have shown that two divergent copies of genes encoding the elongation factor Tu are present in some enterococcal species. Sequence data revealed that both genes are highly conserved at the amino acid level. One copy (*tufA*) is present in all enterococcal species, while the other (*tufB*) is present only in 11 of the 17 enterococcal species studied. Based on 16S rRNA sequence analysis, these 11 species are members of three different enterococcal subgroups (*E. avium*, *E. faecium*, and *E. gallinarum* species groups) and a distinct species (*E. dispar*). Moreover, 16S rDNA phylogeny suggests that these 11 species possessing 2 *tuf* genes all share a common ancestor before they further evolved to become the modern species. Since the six other species having only one copy diverged from the enterococcal lineage before that common ancestor, it appears that the presence of one *tuf* gene in these six species is not attributable to gene loss.

Two clusters of low G+C gram-positive bacteria were observed in the phylogenetic tree of the *tuf* genes: one contains a majority of low G+C gram-positive bacteria and the other contains lactococci and streptococci. This is similar to the finding on the basis of phylogenetic analysis of the 16S rRNA gene and the *hrcA* gene coding for a unique heat-shock regulatory protein. The enterococcal *tufA* genes branched with most of the low G+C gram-positive bacteria, suggesting that they originated from a common ancestor. On the other hand, the enterococcal *tufB* genes branched with the genera *Streptococcus* and *Lactococcus* that form a distinct lineage separated from other low G+C gram-positive bacteria (Figure 5). The finding that these EF-Tu proteins share some conserved amino acid residues unique to this branch also supports the idea that they may share a common ancestor. Although these conserved residues might result from convergent

evolution upon a specialized function, such convergence at the sequence level, even for a few residues, seems to be rare, making it an unlikely event. Moreover, no currently known selective pressure, if any, would account for keeping one versus two *tuf* genes in bacteria. The G+C contents of enterococcal *tufA* and *tufB* sequences are similar, indicating that they both originated from low G+C gram-positive bacteria, in accordance with the phylogenetic analysis.

The *tuf* genes are present in various copy numbers in different bacteria. Furthermore, the two *tuf* genes are normally associated with characteristic flanking genes. The two *tuf* gene copies commonly encountered within gram-negative bacteria are part of the bacterial *str* operon and tRNA-*tufB* operon, respectively. The arrangement of *tufA* in the *str* operon was also found in a variety of bacteria, including *Thermotoga maritima*, the most ancient bacteria sequenced so far, *Aquifex aeolicus*, cyanobacteria, *Bacillus* sp., *Micrococcus luteus*, *Mycobacterium tuberculosis*, and *Streptomyces* sp. Furthermore, the tRNA-*tufB* operon has also been identified in *Aquifex aeolicus*, *Thermus thermophilus*, and *Chlamydia trachomatis*. The two widespread *tuf* gene arrangements argue in favor of their ancient origins. It is noteworthy that most obligate intracellular parasites, such as *Mycoplasma* sp., *R. prowazekii*, *B. burgdorferi*, and *T. pallidum*, contain only one *tuf* gene. Their flanking sequences are distinct from the two conserved patterns as a result of selection for effective propagation by an extensive reduction in genome size by intragenomic recombination and rearrangement.

Most gram-positive bacteria with low G+C content sequenced to date contain only a single copy of the *tuf* gene as a part of the *str* operon. This is the case for *B. subtilis*, *S. aureus* and *E. faecalis*. PCR amplification using a primer targeting a conserved region of the *fus* gene and the *tufA*-specific primer SEQ ID NO. 660, but not the *tufB*-specific primer SEQ ID NO. 661, yielded the expected amplicons for all 17 enterococcal species tested, indicating the presence of the *fus-tuf* organization in all enterococci (data not shown). However, in the genomes of *S. pneumoniae* and *S. pyogenes*, the sequences flanking the *tuf* genes varies although the *tuf* gene itself remains highly conserved. The enterococcal *tufB* genes are

clustered with streptococci, but at present we do not have enough data to identify the genes flanking the enterococcal *tufB* genes. Furthermore, the functional role of the enterococcal *tufB* genes remains unknown. One can only postulate that the two divergent gene copies are expressed under different conditions.

The amino acid sequence identities between the enterococcal *tufA* and *tufB* genes are lower than either i) those between the enterococcal *tufA* and the *tuf* genes from other low G+C gram-positive bacteria (streptococci and lactococci excluded) or ii) those between the enterococcal *tufB* and streptococcal and lactococcal *tuf* genes. These findings suggest that the enterococcal *tufA* genes share a common ancestor with other low G+C gram-positive bacteria via the simple scheme of vertical evolution, while the enterococcal *tufB* genes are more closely related to those of streptococci and lactococci. The facts that some enterococci possess an additional *tuf* gene and that the single streptococcal *tuf* gene is not clustered with other low G+C gram-positive bacteria cannot be explained by the mechanism of gene duplication or intrachromosomal recombination. According to sequence and phylogenetic analysis, we propose that the presence of the additional copy of the *tuf* genes in 11 enterococcal species is due to horizontal gene transfer. The common ancestor of the 11 enterococcal species now carrying *tufB* genes acquired a *tuf* gene from an ancestral streptococcus or a streptococcus-related species during enterococcal evolution through gene transfer before the diversification of modern enterococci. Further study of the flanking regions of the gene may provide more clues for the origin and function of this gene in enterococci.

Recent studies of genes and genomes have demonstrated that considerable horizontal transfer occurred in the evolution of aminoacyl-tRNA synthetases in all three kingdoms of life. The heterogeneity of 16S rRNA is also attributable to horizontal gene transfer in some bacteria, such as *Streptomyces*, *Thermomonospora chromogena* and *Mycobacterium celatum*. In this study, we provide the first example in support of a likely horizontal transfer of the *tuf* gene encoding the elongation factor Tu. This may be an exception since stringent functional constraints do not allow for frequent horizontal transfer of the *tuf* gene as with

other genes. However, enterococcal *tuf* genes should not be the only such exception as we have noticed that the phylogeny of *Streptomyces tuf* genes is equally or more complex than that of enterococci. For example, the three *tuf*-like genes in a high G+C gram-positive bacterium, *S. ramocissimus*, branched with the *tuf* genes of phylogenetically divergent groups of bacteria (Figure 5). Another example may be the *tuf* genes in clostridia, which represent a phylogenetically very broad range of organisms and form a plethora of lines and groups of various complexities and depths. Four species belonging to three different clusters within the genus *Clostridium* have been shown by Southern hybridization to carry two copies of the *tuf* gene. Further sequence data and phylogenetic analysis may help interpreting the evolution of the elongation factor Tu in these gram-positive bacteria. Since the *tuf* genes and 16S rRNA genes are often used for phylogenetic study, the existence of duplicate genes originating from horizontal gene transfer may alter the phylogeny of microorganisms when the laterally acquired copy of the gene is used for such analysis. Hence, caution should be taken in interpreting phylogenetic data. In addition, the two *tuf* genes in enterococci have evolved separately and are distantly related to each other phylogenetically. The enterococcal *tufB* genes are less conserved and unique to the 11 enterococcal species only. We previously demonstrated that the enterococcal *tufA* genes could serve as a target to develop a DNA-based assay for identification of enterococci. The enterococcal *tufB* genes would also be useful in identification of these 11 enterococcal species.

EXAMPLE 43:

Elongation Factor Tu (*tuf*) and the F-ATPase beta-subunit (*atpD*) as phylogenetic tools for species of the family *Enterobacteriaceae*.

SUMMARY

The phylogeny of enterobacterial species commonly found in clinical samples was analyzed by comparing partial sequences of their elongation factor Tu (*tuf*) genes and their F-ATPase beta-subunit (*atpD*) genes. A 884-bp fragment for *tuf* and a 884- or 871-bp fragment for *atpD* were sequenced for 88 strains of 72 species from 25 enterobacterial genera. The *atpD* sequence analysis revealed a specific indel to *Pantoea* and *Tatumella* species showing for the first time a tight phylogenetic affiliation between these two genera. Comprehensive *tuf* and *atpD* phylogenetic trees were constructed and are in agreement with each other. Monophyletic genera are *Yersinia*, *Pantoea*, *Edwardsiella*, *Cedecea*, *Salmonella*, *Serratia*, *Proteus*, and *Providencia*. Analogous trees were obtained based on available 16S rDNA sequences from databases. *tuf* and *atpD* phylogenies are in agreement with the 16S rDNA analysis despite the smaller resolution power for the latter. In fact, distance comparisons revealed that *tuf* and *atpD* genes provide a better resolution for pairs of species belonging to the family *Enterobacteriaceae*. However, 16S rDNA distances are better resolved for pairs of species belonging to different families. In conclusion, *tuf* and *atpD* conserved genes are sufficiently divergent to discriminate different species inside the family *Enterobacteriaceae* and offer potential for the development of diagnostic tests based on DNA to identify enterobacterial species.

INTRODUCTION

Members of the family *Enterobacteriaceae* are facultatively anaerobic gram-negative rods, catalase-positive and oxydase-positive (Brenner, 1984). They are found in soil, water, plants, and in animals from insects to man. Many enterobacteria are opportunistic pathogens. In fact, members of this family are responsible for about 50 % of nosocomial infections in the United States (Brenner, 1984). Therefore, this family is of considerable clinical importance.

Major classification studies on the family *Enterobacteriaceae* are based on phenotypic traits (Brenner *et al.*, 1999; Brenner *et al.*, 1980; Dickey & Zumoff,

1988; Farmer III *et al.*, 1980; Farmer III *et al.*, 1985b; Farmer III *et al.*, 1985a) such as biochemical reactions and physiological characteristics. However, phenotypically distinct strains may be closely related by genotypic criteria and may belong to the same genospecies (Bercovier *et al.*, 1980; Hartl & Dykhuizen, 1984). Also, phenotypically close strains (biogroups) may belong to different genospecies, like *Klebsiella pneumoniae* and *Enterobacter aerogenes* (Brenner, 1984) for example. Consequently, identification and classification of certain species may be ambiguous with techniques based on phenotypic tests (Janda *et al.*, 1999; Kitch *et al.*, 1994; Sharma *et al.*, 1990).

More advances in the classification of members of the family *Enterobacteriaceae* have come from DNA-DNA hybridization studies (Brenner *et al.*, 1993; Brenner *et al.*, 1986; Brenner, *et al.*, 1980; Farmer III, *et al.*, 1980; Farmer III, *et al.*, 1985b; Izard *et al.*, 1981; Steigerwalt *et al.*, 1976). Furthermore, the phylogenetic significance of bacterial classification based on 16S rDNA sequences has been recognized by many workers (Stackebrandt & Goebel, 1994; Wayne *et al.*, 1987). However, members of the family *Enterobacteriaceae* have not been subjected to extensive phylogenetic analysis of 16S rDNA (Sproer *et al.*, 1999). In fact, this molecule was not thought to solve taxonomic problems concerning closely related species because of its very high degree of conservation (Brenner, 1992; Sproer, *et al.*, 1999). Another drawback of the 16S rDNA gene is that it is found in several copies within the genome (seven in *Escherichia coli* and *Salmonella typhimurium*) (Hill & Harnish, 1981). Due to sequence divergence between the gene copies, direct sequencing of PCR products is often not suitable to achieve a representative sequence (Cilia *et al.*, 1996; Hill & Harnish, 1981). Other genes such as *gap* and *ompA* (Lawrence *et al.*, 1991), *rpoB* (Mollet *et al.*, 1997), and *infB* (Hedegaard *et al.*, 1999) were used to resolve the phylogeny of enterobacteria. However, none of these studies covered an extensive number of species.

tuf and *atpD* are the genes encoding the elongation factor Tu (EF-Tu) and the F-ATPase beta-subunit, respectively. EF-Tu is involved in peptide chain formation (Ludwig *et al.*, 1990). The two copies of the *tuf* gene (*tufA* and *tufB*) found in enterobacteria (Sela *et al.*, 1989) share high identity level (99 %) in *Salmonella typhimurium* and in *E. coli*. The recombination phenomenon could explain sequence homogenization between the two copies (Abdulkarim & Hughes, 1996; Grunberg-Manago, 1996). F-ATPase is present on the plasma membranes of eubacteria (Nelson & Taiz, 1989). It functions mainly in ATP synthesis (Nelson & Taiz, 1989) and the beta-subunit contains the catalytic site of the enzyme. EF-Tu and F-ATPase are highly conserved throughout evolution and shows functional constancy (Amann *et al.*, 1988; Ludwig, *et al.*, 1990). Recently, phylogenies based on protein sequences from EF-Tu and F-ATPase beta-subunit showed good agreement with each other and with the rDNA data (Ludwig *et al.*, 1993).

We elected to sequence 884-bp fragments of *tuf* and *atpD* from 88 clinically relevant enterobacterial strains representing 72 species from 25 genera. These sequences were used to create phylogenetic trees that were compared with 16S rDNA trees. These trees revealed good agreement with each others and demonstrated the high resolution of *tuf* and *atpD* phylogenies at the species level.

MATERIALS AND METHODS

Bacterial strains and genomic material. All bacterial strains used in this study were obtained from the American Type Culture Collection (ATCC) or the Deutsche Sammlung von Mikroorganismen und Zellkulturen GmbH (DSMZ). These enterobacteria can all be recovered from clinical specimens, but not all are pathogens. Whenever possible, we choose type strains. Identification of all strains was confirmed by classical biochemical tests using the automated system MicroScan WalkAway-96 system equipped with a Negative BP Combo Panel Type 15 (Dade Behring Canada). Genomic DNA was purified using the G NOME

DNA kit (Bio 101). Genomic DNA from *Yersinia pestis* was kindly provided by Dr. Robert R. Brubaker. Strains used in this study and their descriptions are shown in Table 19.

PCR primers. The eubacterial *tuf* and *atpD* gene sequences available from public databases were analyzed using the GCG package (version 8.0) (Genetics Computer Group). Based on multiple sequence alignments, two highly conserved regions were chosen for each genes, and PCR primers were derived from these regions with the help of Oligo primer analysis software (version 5.0) (National Biosciences). A second 5' primer was design to amplify the gene *atpD* for few enterobacteria difficult to amplifiy with the first primer set. When required, the primers contained inosines or degeneracies to account for variable positions. Oligonucleotide primers were synthesized with a model 394 DNA/RNA synthesizer (PE Applied Biosystems). PCR primers used in this study are listed in Table 20.

DNA sequencing. An 884-bp portion of the *tuf* gene and an 884-bp portion (or alternatively an 871-bp portion for a few enterobacterial strains) of the *atpD* gene were sequenced for all enterobacteria listed in the first strain column of Table 19. Amplification was performed with 4 ng of genomic DNA. The 40- μ l PCR mixtures used to generate PCR products for sequencing contained 1.0 μ M each primer, 200 μ M each deoxyribonucleoside triphosphate (Pharmacia Biotech), 10 mM Tris-HCl (pH 9.0 at 25 °C), 50 mM KCl, 0.1 % (w/v) Triton X-100, 2.5 mM MgCl₂, 0.05 mM BSA, 0.3 U of *Taq* DNA polymerase (Promega) coupled with TaqStartTM antibody (Clontech Laboratories). The TaqStartTM neutralizing monoclonal antibody for *Taq* DNA polymerase was added to all PCR mixtures to enhance efficiency of amplification (Kellogg *et al.*, 1994). The PCR mixtures were subjected to thermal cycling (3 min at 95 °C and then 35 cycles of 1 min at 95 °C, 1 min at 55 °C for *tuf* or 50 °C for *atpD*, and 1 min at 72 °C, with a 7-min final extension at 72 °C) using a PTC-200 DNA Engine thermocycler (MJ Research).

PCR products having the predicted sizes were recovered from an agarose gel stained for 15 min with 0.02 % of methylene blue followed by washing in sterile distilled water for 15 min twice (Flores *et al.*, 1992). Subsequently, PCR products having the predicted sizes were recovered from gels using the QIAquick gel extraction kit (QIAGEN).

Both strands of the purified amplicons were sequenced using the ABI Prism BigDye Terminator Cycle Sequencing Ready Reaction Kit (PE Applied Biosystems) on an automated DNA sequencer (Model 377). Amplicons from two independent PCR amplifications were sequenced for each strain to ensure the absence of sequencing errors attributable to nucleotide misincorporations by the *Taq* DNA polymerase. Sequence assembly was performed with the aid of Sequencher 3.0 software (Gene Codes).

Phylogenetic analysis. Multiple sequence alignments were performed using PileUp from the GCG package (Version 10.0) (Genetics Computer Group) and checked by eye with the editor SeqLab to edit sequences if necessary and to note which regions were to be excluded for phylogenetic analysis. *Vibrio cholerae* and *Shewanella putrefaciens* were used as outgroups. Bootstrap subsets (750 sets) and phylogenetic trees were generated with the Neighbor Joining algorithm from Dr. David Swofford's PAUP (Phylogenetic Analysis Using Parsimony) Software version 4.0b4 (Sinauer Associates) and with tree-bisection branch-swapping. The distance model used was Kimura (1980) two-parameter. Relative rate test was performed with the aid of Phyltest program version 2.0 (c).

RESULTS AND DISCUSSION

DNA amplification, sequencing and sequence alignments

A PCR product of the expected size of 884 bp was obtained for *tuf* and of 884 or 871 bp for *atpD* from all bacterial strains tested. After subtracting for biased

primer regions and ambiguous single strand data, sequences of at least 721 bp for *tuf* and 713 bp for *atpD* were submitted to phylogenetic analyses. These sequences were aligned with *tuf* and *atpD* sequences available in databases to verify that the nucleotide sequences indeed encoded a part of tested genes. Gaps were excluded to perform phylogenetic analysis.

Signature sequences

From the sequence alignments obtained from both tested genes, only one insertion was observed. This five amino acids insertion is located between the positions 325 and 326 of *atpD* gene of *E. coli* strain K-12 (Saraste *et al.*, 1981) and can be considered a signature sequence of *Tatumella ptyseos* and *Pantoea* species (Fig. 7). The presence of a conserved indel of defined length and sequence and flanked by conserved regions could suggest a common ancestor, particularly when members of a given taxa share this indel (Gupta, 1998). To our knowledge, high relatedness between the genera *Tatumella* and *Pantoea* is demonstrated for the first time.

Enterobacter agglomerans ATCC 27989 sequence does not possess the five amino acid indel (Fig. 7). This indel could represent a useful marker to help resolve the *Enterobacter agglomerans* and *Pantoea* classification. Indeed, the transfer of *Enterobacter agglomerans* to *Pantoea agglomerans* was proposed in 1989 by Gavini *et al.* (Gavini *et al.*, 1989). However, some strains are provisionally classified as *Pantoea* sp. until their interrelatedness is elucidated (Gavini, *et al.*, 1989). Since the transfer was proposed, the change of nomenclature has not yet been made for all *Enterobacter agglomerans* in the ATCC database. The absence of the five amino acids indel suggests that some strains of *Enterobacter agglomerans* most likely do not belong to the genus *Pantoea*.

Phylogenetic trees based on partial *tuf* sequences, *atpD* sequences, and published 16S rDNA data of members of the *Enterobacteriaceae*.

Representative trees constructed from *tuf* and *atpD* sequences with the neighbor-joining method are shown in Fig. 8. The phylogenetic trees generated from partial *tuf* sequences and *atpD* sequences are very similar. Nevertheless, *atpD* tree shows more monophyletic groups corresponding to species that belong to the same genus.

These groups are more consistent with the actual taxonomy. For both genes, some genera are not monophyletic. These results support previous phylogenies based on the genes *gap* and *ompA* (Lawrence, *et al.*, 1991), *rpoB* (Mollet, *et al.*, 1997), and *infB* (Hedegaard, *et al.*, 1999) which all showed that the genera *Escherichia* and *Klebsiella* are polyphyletic. There were few differences in branching between *tuf* and *atpD* genes.

Even though *Pantoea agglomerans* and *Pantoea dispersa* indels were excluded for phylogenetic analysis, these two species grouped together and were distant from *Enterobacter agglomerans* ATCC 27989, adding another evidence that the latter species is heterogenous and that not all members of this species belong to the genus *Pantoea*. In fact, the *E. agglomerans* strain ATCC 27989 exhibits branch lengths similar to others *Enterobacter* species with both genes. Therefore, we suggest that this strain belong to the genus *Enterobacter* until further reclassification of that genus.

tuf and *atpD* trees exhibit very short genetic distances between taxa belonging to the same genetic species including species segregated for clinical considerations. This first concern *E. coli* and *Shigella* species that were confirmed to be the same genetic species by hybridization studies (Brenner *et al.*, 1972; Brenner *et al.*, 1972; Brenner *et al.*, 1982) and phylogenies based on 16S rDNA (Wang *et al.*, 1997) and *rpoB* genes (Mollet, *et al.*, 1997). Hybridization studies (Bercovier, *et al.*, 1980) and phylogeny based on 16S rDNA genes (Ibrahim *et al.*, 1994) demonstrated also that *Yersinia pestis* and *Y. pseudotuberculosis* are the same genetic species. Among

Yersinia pestis and *Y. pseudotuberculosis*, the three *Klebsiella pneumoniae* subspecies, *E. coli-Shigella* species, and *Salmonella choleraesuis* subspecies, *Salmonella* is a less tightly knit species than the other genetic species. The same is true for *E. coli* and *Shigella* species.

~~*Escherichia fergusonii* is very close to *E. coli-Shigella* genetic species. This~~ observation is corroborated by 16S rDNA phylogeny (McLaughlin *et al.*, 2000) but not by DNA hybridization values. In fact, *E. fergusonii* is only 49% to 63% related to *E. coli-Shigella* (Farmer III, *et al.*, 1985b). It was previously observed that very recently diverged species may not be recognizable based on 16S rDNA sequences although DNA hybridization established them as different species (Fox *et al.*, 1992). Therefore, *E. fergusonii* could be a new “quasi-species”.

atpD phylogeny revealed *Salmonella* subspecies divisions consistent with the actual taxonomy. This result was already observed by Christensen *et al.* (Christensen & Olsen, 1998). Nevertheless, *tuf* partial sequences discriminate less than *atpD* between *Salmonella* subspecies.

Overall, *tuf* and *atpD* phylogenies exhibit enough divergence between species to ensure efficient discrimination. Therefore, it could be easy to distinguish phenotypically close enterobacteria belonging to different genetic species such as *Klebsiella pneumoniae* and *Enterobacter aerogenes*.

Phylogenetic relationships between *Salmonella*, *E. coli* and *C. freundii* are not well defined. 16S rDNA and 23S rDNA sequence data reveals a closer relationship between *Salmonella* and *E. coli* than between *Salmonella* and *C. freundii* (Christensen *et al.*, 1998), while DNA homology studies (Selander *et al.*, 1996) and *infB* phylogeny (Hedegaard, *et al.*, 1999) showed that *Salmonella* is more closely related to *C. freundii* than to *E. coli*. In that regard, *tuf* and *atpD* phylogenies are coherent with 16S rDNA and 23S rDNA sequence analysis.

Phylogenetic analyses were also performed using amino acids sequences. *tuf* tree based on amino acids is characterized by a better resolution between taxa outgroup and taxa ingroup (enterobacteria) than tree based on nucleic acids whereas *atpD* trees based on amino acids and nucleic acids give almost the same resolution between taxa outgroup and ingroup (data not shown).

Relative rate test (or two cluster test (Takezaki *et al.*, 1995)) evaluates if evolution is constant between two taxa. Before to apply the test, the topology of a tree is determined by tree-building method without the assumption of rate constancy. Therefore, two taxa (or two groups of taxa) are compared with a third taxon that is an outgroup of the first two taxa (Takezaki, *et al.*, 1995). Few pairs of taxa that exhibited a great difference between their branch lengths at particular nodes were chosen to perform the test. This test reveals that *tuf* and *atpD* are not constant in their evolution within the family *Enterobacteriaceae*. For *tuf*, for example, the hypothesis of rate constancy is rejected (Z value higher than 1.96) between *Yersinia* species. The same is true for *Proteus* species. For *atpD*, for example, evolution is not constant between *Proteus* species, between *Proteus* species and *Providencia* species, and between *Yersinia* species and *Escherichia coli*. For 16S rDNA, for example, evolution is not constant between two *E. coli*, between *E. coli* and *Enterobacter aerogenes*, and between *E. coli* and *Proteus vulgaris*. These results suggest that *tuf*, *atpD* and 16S rDNA could not serve as a molecular clock for the entire family *Enterobacteriaceae*.

Since the number and the nature of taxa can influence topology of trees, phylogenetic trees from *tuf* and *atpD* were reconstructed using sequences corresponding to strains for which 16S rDNA genes were published in GenEMBL. These trees were similar to those generated using 16S rDNA (Fig. 9). Nevertheless, 16S rDNA tree gave poorer resolution power than *tuf* and *atpD* gene trees. Indeed, these latter exhibited less multifurcation (polytomy) than the 16S rDNA tree.

Comparison of distances based on *tuf*, *atpD*, and 16S rDNA data.

tuf, *atpD*, and 16S rDNA distances (i.e. the number of differences per nucleotide site) were compared with each other for each pair of strains. We found that the *tuf* and *atpD* distances were respectively 2.268 ± 0.965 and 2.927 ± 0.896 times larger than 16S rDNA distances (Fig. 10a and b). *atpD* distances were 1.445 ± 0.570 times larger than *tuf* distances (Fig. 10c). Figure 10 also shows that the *tuf*, *atpD*, and 16S rDNA distances between members of different species of the same genus (0.053 ± 0.034 , 0.060 ± 0.020 , and 0.024 ± 0.010 , respectively) were in mean smaller than the distances between members of different genera belonging to the same family (0.103 ± 0.053 , 0.129 ± 0.051 , and 0.044 ± 0.013 , respectively). However, the overlap exhibits with standard deviations add to a focus of evidences that some enterobacterial genera are not well defined (Brenner, 1984). In fact, many distances for pairs of species especially belonging to the genera *Escherichia*, *Shigella*, *Enterobacter*, *Citrobacter*, *Klebsiella*, and *Kluyvera* overlap distances for pairs of species belonging to the same genus (Fig. 10). For example, distances for pairs composed by species of *Citrobacter* and species of *Klebsiella* overlap distances for pairs composed by two *Citrobacter* or by two *Klebsiella*.

Observing the distance distributions, 16S rDNA distances reveal a clear separation between the families *Enterobacteriaceae* and *Vibrionaceae* despite the fact that the family *Vibrionaceae* is genetically very close to the *Enterobacteriaceae* (Fig. 10a and b). Nevertheless, *tuf* and *atpD* show higher discriminating power below the family level (Fig. 10a and b).

There were some discrepancies in the relative distances for the same pairs of taxa between the two genes studied. First, distances between *Yersinia* species are at least two times lower for *atpD* than for *tuf* (Fig. 10c). Also, distances at the family level (between *Enterobacteriaceae* and *Vibrionaceae*) show that *Enterobacteriaceae* is a tighter knit family with *atpD* gene (*Proteus* genus

excepted) than with *tuf* gene. Both genes well delineate taxa belonging to the same species. There is one exception with *atpD*: *Klebsiella planticola* and *K. ornithinolithica* belong to the same genus but fit with taxa belonging to the same species (Fig. 10a and c). These two species are also very close genotypically with *tuf* gene. This suggest that *Klebsiella planticola* and *K. ornithinolithica* could be two newborn species. *tuf* and *atpD* genes exhibit little distances between *Escherichia fergusonii* and *E. coli-Shigella* species. Unfortunately, comparison with 16S rDNA could not be achieved because the *E. fergusonii* 16S rDNA sequence is not yet accessible in GenEMBL database. Therefore, the majority of phenotypically close enterobacteria could be easily discriminated genotypically using *tuf* and *atpD* gene sequences.

In conclusion, *tuf* and *atpD* genes exhibit phylogenies consistent with 16S rDNA genes phylogeny. For example, they reveal that the family *Enterobacteriaceae* is monophyletic. Moreover, *tuf* and *atpD* distances provide a higher discriminating power than 16S rDNA distances. In fact, *tuf* and *atpD* genes discriminate well between different genospecies and are conserved between strains of the same genetic species in such a way that primers and molecular probes for diagnostic purposes could be designed. Preliminary studies support these observations and diagnostic tests based on *tuf* and *atpD* sequence data to identify enterobacteria are currently under development.

EXAMPLE 44:

Testing new pairs of PCR primers selected from two species-specific genomic DNA fragments which are objects of our assigned US patent 6,001,564

Objective: The goal of these experiments is to demonstrate that it is relatively easy for a person skilled in the art to find other PCR primer pairs from the species-specific

fragments used as targets for detection and identification of a variety of microorganisms. In fact, we wish to prove that the PCR primers previously tested by our group and which are objects of the present patent application are not the only possible good choices for diagnostic purposes. For this example, we used diagnostic targets described in our assigned US patent 6,001,564.

Experimental strategy: We have selected randomly two species-specific genomic DNA fragments for this experiment. The first one is the 705-bp fragment specific to *Staphylococcus epidermidis* (SEQ ID NO: 36 from US patent 6,001,564) while the second one is the 466-bp fragment specific to *Moraxella catarrhalis* (SEQ ID NO: 29 from US patent 6,001,564). Subsequently, we have selected from these two fragments a number of PCR primer pairs other than those previously tested. We have chosen 5 new primer pairs from each of these two sequences which are well dispersed along the DNA fragment (Figures 11 and 12). We have tested these primers for their specificity and compared them with the original primers previously tested. For the specificity tests, we have tested all bacterial species closely related to the target species based on phylogenetic analysis with three conserved genes (rRNA genes, *tuf* and *atpD*). The rationale for selecting a restricted number of bacterial species to evaluate the specificity of the new primer pairs is based on the fact that the lack of specificity of a DNA-based assay is attributable to the detection of closely related species which are more similar at the nucleotide level. Based on the phylogenetic analysis, we have selected (i) species from the closely related genus *Staphylococcus*, *Enterococcus*, *Streptococcus* and *Listeria* to test the specificity of the *S. epidermidis*-specific PCR assays and (ii) species from the closely related genus *Moraxella*, *Kingella* and *Neisseria* to test the specificity of the *M. catarrhalis*-specific PCR assays.

Materials and methods

Bacterial strains. All bacterial strains used for these experiments were obtained from the American Type Culture Collection (ATCC, Rockville, MD).

Genomic DNA isolation. Genomic DNA was purified from the ATCC reference strains by using the G-nome DNA kit (Bio 101 Inc., Vista, CA).

Oligonucleotide design and synthesis. PCR primers were designed with the help of the OligoTM primer analysis software Version 4.0 (National Biosciences Inc., Plymouth, Minn.) and synthesized using a model 391 DNA synthesizer (Applied Biosystems, Foster City, CA).

PCR assays. All PCR assays were performed by using genomic DNA purified from reference strains obtained from the ATCC. One μ l of purified DNA preparation (containing 0.01 to 1 ng of DNA per μ l) was added directly into the PCR reaction mixture. The 20 μ L PCR reactions contained final concentrations of 50 mM KCl, 10 mM Tris-HCl (pH 9.0), 0.1% Triton X-100, 2.5 mM MgCl₂, 0.4 μ M of each primer, 200 μ M of each of the four dNTPs and 0.5 unit of *Taq* DNA polymerase (Promega, Madison, WI) combined with the TaqStartTM antibody (Clontech Laboratories Inc., Palo Alto, CA). An internal control was integrated into all amplification reactions to verify the efficiency of the amplification reaction as well as to ensure that significant PCR inhibition was absent. Primers amplifying a region of 252 bp from a control plasmid added to each amplification reaction were used to provide the internal control. PCR reactions were then subjected to thermal cycling (3 min at 95°C followed by 30 cycles of 1 second at 95°C for the denaturation step and 30 seconds at 50 to 65°C for the annealing-extension step) using a PTC-200 thermal cycler (MJ Research Inc., Watertown, MA). PCR amplification products were then analyzed by standard agarose gel (2%) electrophoresis. Amplification products were visualized in agarose gels containing 0.25 μ g/mL of ethidium bromide under UV at 254 nm.

Results

Tables 21 and 22 show the results of specificity tests with the 5 new primer pairs selected from SEQ ID NO: 29 (specific to *M. catarrhalis* from US patent 6,001,564) and SEQ ID NO: 36 (specific to *S. epidermidis* from US patent 6,001,564), respectively. In order to evaluate the performance of these new primers pairs, we compared them in parallel with the original primer pairs previously tested:

For *M. catarrhalis*, all of the 5 selected PCR primer pairs were specific for the target species because none of the closely related species could be amplified (Table 21). In fact, the comparison with the original primer pair SEQ ID NO: 118 + SEQ ID NO: 119 (from US patent 6,001,564) revealed that all new pairs showed identical results in terms of specificity and sensitivity thereby suggesting their suitability for diagnostic purposes.

For *S. epidermidis*, 4 of the 5 selected PCR primer pairs were specific for the target species (Table 22). It should be noted that for 3 of these four primer pairs the annealing temperature had to be increased from 55 °C to 60 or 65 °C to attain specificity for *S. epidermidis*. Again the comparison with the original primer pair SEQ ID NO: 145 + SEQ ID NO: 146 (from US patent 6,001,564) revealed that these four primer pairs were as good as the original pair. Increasing the annealing temperature for the PCR amplification is well known by persons skilled in the art to be a very effective way to improve the specificity of a PCR assay (Persing *et al.*, 1993, Diagnostic Molecular Microbiology: Principles and Applications, American Society for Microbiology, Washington, D.C.; Ehrlich and Greenberg, 1994, PCR-based Diagnostics in Infectious Disease, Blackwell Scientific Publications, Boston, MA). In fact, those skilled in the art are well aware of the fact that the annealing temperature is critical for the optimization of PCR assays. Only the primer pair VBsep3 + VBsep4 amplified bacterial species other than *S. epidermidis* including the staphylococcal species *S. capitis*, *S. cohnii*, *S. aureus*, *S. haemolyticus* and *S. hominis* (Table 22). For this non-specific primer pair, increasing the annealing temperature

from 55 to 65 °C was not sufficient to attain the desired specificity. One possible explanation for the fact that it appears slightly easier to select species-specific primers for *M. catarrhalis* than for *S. epidermidis* is that *M. catarrhalis* is more isolated in phylogenetic trees than *S. epidermidis*. The large number of coagulase negative staphylococcal species such as *S. epidermidis* is largely responsible for this phylogenetic clustering.

Conclusion

These experiment clearly show that it is relatively easy for a person skilled in the art to select, from the species-specific DNA fragments selected as target for identification, PCR primer pairs suitable for diagnostic purposes other than those previously tested. The amplification conditions can be optimize by modifying critical variables such as the annealing temperature to attain the desired specificity and sensitivity. Consequently, we consider that it is legitimate to claim any possible primer sequences selected from the species-specific fragment and that it would be unfair to grant only the claims dealing with the primer pairs previously tested. By extrapolation, these results strongly suggest that it is also relatively easy for a person skilled in the art to select, from the species-specific DNA fragments, DNA probes suitable for diagnostic purposes other than those previously tested.

EXAMPLE 45:

Testing modified versions of PCR primers derived from the sequence of several primers which are objects of US patent 6,001,564.

Objective: The purpose of this project is to verify the efficiency of amplification by modified PCR primers derived from primers previously tested. The types of primer modifications to be tested include (i) variation of the sequence at one or more nucleotide positions and (ii) increasing or reducing the length of the primers. For this example, we used diagnostic targets described in US patent 6,001,564.

Experimental strategy:

a) Testing primers with nucleotide changes

We have designed 13 new primers which are derived from the *S. epidermidis*-specific SEQ ID NO: 146 from US patent 6,001,564 (Table 23). These primers have been modified at one or more nucleotide positions. As shown in Table 23, the nucleotide changes were introduced all along the primer sequence. Furthermore, instead of modifying the primer at any nucleotide position, the nucleotide changes were introduced at the third position of each codon to better reflect potential genetic variations *in vivo*. It should be noted that no nucleotide changes were introduced at the 3' end of the oligonucleotide primers because those skilled in the art are well aware of the fact that mismatches at the 3' end should be avoided (Persing *et al.*, 1993, Diagnostic Molecular Microbiology: Principles and Applications, American Society for Microbiology, Washington, D.C.). All of these modified primers were tested in PCR assays in combination with SEQ ID NO: 145 from US patent 6,001,564 and the efficiency of the amplification was compared with the original primer pair SEQ ID NO: 145 + SEQ ID NO: 146 previously tested in US patent 6,001,564.

b) Testing shorter or longer versions of primers

We have designed shorter and longer versions of the original *S. epidermidis*-specific PCR primer pair SEQ ID NO: 145 + 146 from US patent 6,001,564 (Table 24) as well as shorter versions of the original *P. aeruginosa*-specific primer pair SEQ ID NO: 83 + 84 from US patent 6,001,564 (Table 25). As shown in Tables 24 and 25, both primers of each pair were shortened or lengthen to the same length. Again, those skilled in the art know that the melting temperature of both primers from a pair should be similar to avoid preferential binding at one primer binding site which is

detrimental in PCR (Persing *et al.*, 1993, Diagnostic Molecular Microbiology: Principles and Applications, American Society for Microbiology, Washington, D.C.; Ehrlich and Greenberg, 1994, PCR-based Diagnostics in Infectious Disease, Blackwell Scientific Publications, Boston, MA). All of these shorter or longer primer versions were tested in PCR assays and the efficiency of the amplification was compared with the original primer pair SEQ ID NOs 145 and 146.

Materials and methods

See the Materials and methods section of Example 44.

Results

a) Testing primers with nucleotide changes

The results of the PCR assays with the 13 modified versions of SEQ ID NO: 146 from US patent 6,001,564 are shown in Table 23. The 8 modified primers having a single nucleotide variation showed an efficiency of amplification identical to the original primer pair based on testing with 3 different dilutions of genomic DNA. The four primers having two nucleotide variations and primer VBmut12 having 3 nucleotide changes also showed PCR results identical to those obtained with the original pair. Finally, primer VBmut13 with four nucleotide changes showed a reduction in sensitivity by approximately one log as compared with the original primer pair. However, reducing the annealing temperature from 55 to 50 °C gave an efficiency of amplification very similar to that observed with the original primer pair (Table 23). In fact, reducing the annealing temperature of PCR cycles represents an effective way to reduce the stringency of hybridization for the primers and consequently allows the binding of probes with mismatches (Persing *et al.*, 1993, Diagnostic Molecular Microbiology: Principles and Applications, American Society for Microbiology, Washington, D.C.). Subsequently, we have confirmed the

specificity of the PCR assays with each of these 13 modified versions of SEQ ID NO: 146 from US patent 6,001,564 by performing amplifications from all bacterial species closely related to *S. epidermidis* which are listed in Table 22.

b) Testing shorter or longer versions of primers

For these experiments, two primer pairs were selected: i) SEQ ID NO: 145 + 146 from US patent 6,001,564 (specific to *S. epidermidis*) which are AT rich and ii) SEQ ID NO: 83 + 84 (specific to *P. aeruginosa*) which are GC rich. For the AT rich sequence, primers of 15 to 30 nucleotide in length were designed (Table 24) while for the GC rich sequences, primers of 13 to 19 nucleotide in length were designed (Table 25).

Table 24 shows that, for an annealing temperature of 55 °C, the 30-, 25-, 20- and 17-nucleotide versions of SEQ ID NO: 145 and 146 from US patent 6,001,564 all showed identical results as compared with the original primer pair except that the 17-nucleotide version amplified slightly less efficiently the *S. epidermidis* DNA. Reducing the annealing temperature from 55 to 45 °C for the 17-nucleotide version allowed to increase the amplification efficiency to a level very similar to that with the original primer pair (SEQ ID NO: 145 + 146 from US patent 6,001,564). Regarding the 15-nucleotide version, there was amplification of *S. epidermidis* DNA only when the annealing temperature was reduced to 45 °C. Under those PCR conditions the assay remained *S. epidermidis*-specific but the amplification signal with *S. epidermidis* DNA was slightly lower as compared with the original primer pair. Subsequently, we have further confirmed the specificity of the shorter or longer versions by amplifying DNA from all bacterial species closely related to *S. epidermidis* which are listed in Table 22.

Table 25 shows that, for an annealing temperature of 55 °C, all shorter versions of SEQ ID NO: 83 and 84 from US patent 6,001,564 showed identical PCR results as

compared with the original primer pair. As expected, these results show that it is simpler to reduce the length of GC rich as compared with AT rich. This is attributable to the fact that GC binding is more stable than AT binding.

Conclusion

a) Testing primers with nucleotide changes

The above experiments clearly show that PCR primers may be modified at one or more nucleotide positions without affecting the specificity and the sensitivity of the PCR assay. These results strongly suggest that a given oligonucleotide can detect variant genomic sequences from the target species. In fact, the nucleotide changes in the selected primers were purposely introduced at the third position of each codon to mimic nucleotide variation in genomic DNA. Thus we conclude that it is justified to claim "a variant thereof" for i) the SEQ IDs of the fragments and oligonucleotides which are object of the present patent application and ii) genomic variants of the target species.

b) Testing shorter or longer versions of primers

The above experiments clearly show that PCR primers may be shorter or longer without affecting the specificity and the sensitivity of the PCR assay. We have showed that oligonucleotides ranging in sizes from 13 to 30 nucleotides may be as specific and sensitive as the original primer pair from which they were derived. Consequently, these results suggest that it is not exaggerated to claim sequences having at least 12 nucleotide in length.

This invention has been described herein above, and it is readily apparent that modifications can be made thereto without departing from the spirit of this invention. These modifications are under the scope of this invention, as defined in the appended claims.

Table 1. Distribution (%) of nosocomial pathogens for various human infections in USA (1990-1992)¹.

Pathogen	UTI ²	SSI ³	BSI ⁴	Pneumonia	CSF ⁵
<i>Escherichia coli</i>	27	9	5	4	2
<i>Staphylococcus aureus</i>	2	21	17	21	2
<i>Staphylococcus epidermidis</i>	2	6	20	0	1
<i>Enterococcus faecalis</i>	16	12	9	2	0
<i>Enterococcus faecium</i>	1	1	0	0	0
<i>Pseudomonas aeruginosa</i>	12	9	3	18	0
<i>Klebsiella pneumoniae</i>	7	3	4	9	0
<i>Proteus mirabilis</i>	5	3	1	2	0
<i>Streptococcus pneumoniae</i>	0	0	3	1	18
Group B <i>Streptococci</i>	1	1	2	1	6
Other streptococci	3	5	2	1	3
<i>Haemophilus influenzae</i>	0	0	0	6	45
<i>Neisseria meningitidis</i>	0	0	0	0	14
<i>Listeria monocytogenes</i>	0	0	0	0	3
Other enterococci	1	1	0	0	0
Other staphylococci	2	8	13	2	0
<i>Candida albicans</i>	9	3	5	5	0
Other <i>Candida</i>	2	1	3	1	0
<i>Enterobacter</i> sp.	5	7	4	12	2
<i>Acinetobacter</i> sp.	1	1	2	4	2
<i>Citrobacter</i> sp.	2	1	1	1	0
<i>Serratia marcescens</i>	1	1	1	3	1
Other <i>Klebsiella</i>	1	1	1	2	1
Others	0	6	4	5	0

¹ Data recorded by the National Nosocomial Infections Surveillance (NNIS) from 80 hospitals (Emori and Gaynes, 1993, *Clin. Microbiol. Rev.*, 6:428-442).

² Urinary tract infection.

³ Surgical site infection.

⁴ Bloodstream infection.

⁵ Cerebrospinal fluid.

Table 2. Distribution (%) of bloodstream infection pathogens in Quebec (1995), Canada (1992), UK (1969-1988) and USA (1990-1992).

5	Organism	Quebec ¹	Canada ²	UK ³	USA ⁴	
				Community-acquired	Hospital-acquired	Hospital-acquired
	<i>E. coli</i>	15.6	53.8	24.8	20.3	5.0
10	<i>S. epidermidis</i> and other CoNS ⁵	25.8	-	0.5	7.2	31.0
	<i>S. aureus</i>	9.6	-	9.7	19.4	16.0
	<i>S. pneumoniae</i>	6.3	-	22.5	2.2	-
	<i>E. faecalis</i>	3.0	-	1.0	4.2	-
15	<i>E. faecium</i>	2.6	-	0.2	0.5	-
	<i>Enterococcus</i> sp.	-	-	-	9.0	-
	<i>H. influenzae</i>	1.5	-	3.4	0.4	-
	<i>P. aeruginosa</i>	1.5	8.2	1.0	8.2	3.0
	<i>K. pneumoniae</i>	3.0	11.2	3.0	9.2	4.0
20	<i>P. mirabilis</i>	-	3.9	2.8	5.3	1.0
	<i>S. pyogenes</i>	-	-	1.9	0.9	-
	<i>Enterobacter</i> sp.	4.1	5.5	0.5	2.3	4.0
	<i>Candida</i> sp.	8.5	-	-	1.0	8.0
	Others	18.5	17.4	28.7	18.9	19.0

25 ¹ Data obtained for 270 isolates collected at the Centre Hospitalier de l'Université Laval (CHUL) during a 5 month period (May to October 1995).

² Data from 10 hospitals throughout Canada representing 941 gram-negative isolates. (Chamberland *et al.*, 1992, *Clin. Infect. Dis.*, **15**:615-628).

30 ³ Data from a 20-year study (1969-1988) for nearly 4000 isolates. (Eykyn *et al.*, 1990, *J. Antimicrob. Chemother.*, Suppl. C, **25**:41-58).

⁴ Data recorded by the National Nosocomial Infections Surveillance (NNIS) from 80 hospitals (Emori and Gaynes, 1993, *Clin. Microbiol. Rev.*, **6**:428-442).

⁵ Coagulase-negative staphylococci.

Table 3. Distribution of positive and negative clinical specimens tested at the microbiology laboratory of the CHUL (February 1994 – January 1995).

5	Clinical specimens and/or sites	No. of samples tested (%)	% of positive specimens	% of negative specimens
	Urine	17,981 (54.5)	19.4	80.6
	Blood culture/marrow	10,010 (30.4)	6.9	93.1
	Sputum	1,266 (3.8)	68.4	31.6
10	Superficial pus	1,136 (3.5)	72.3	27.7
	Cerebrospinal fluid	553 (1.7)	1.0	99.0
	Synovial fluid	523 (1.6)	2.7	97.3
	Respiratory tract	502 (1.5)	56.6	43.4
	Deep pus	473 (1.4)	56.8	43.2
15	Ears	289 (0.9)	47.1	52.9
	Pleural and pericardial fluid	132 (0.4)	1.0	99.0
	Peritoneal fluid	101(0.3)	28.6	71.4
	Total:	32,966 (100.0)	20.0	80.0

Table 4. Example f microbial species for which *tuf* and/or *atpD* and/or *recA* nucleic acids and/ r sequences are used in the present invention.

5	Bacterial species	
	<i>Abiotrophia adiacens</i>	<i>Brevibacterium flavum</i>
	<i>Abiotrophia defectiva</i>	<i>Brevundimonas diminuta</i>
	<i>Achromobacter xylosoxidans</i> subsp. <i>denitrificans</i>	65 <i>Buchnera aphidicola</i>
10	<i>Acetobacterium woodii</i>	<i>Budvicia aquatica</i>
	<i>Acetobacter aceti</i>	<i>Burkholderia cepacia</i>
	<i>Acetobacter altoacetigenes</i>	<i>Burkholderia mallei</i>
	<i>Acetobacter polyoxogenes</i>	<i>Burkholderia pseudomallei</i>
	<i>Acholeplasma laidlawii</i>	70 <i>Buttiauxella agrestis</i>
15	<i>Acidothermus cellulolyticus</i>	<i>Butyrivibrio fibrisolvens</i>
	<i>Acidiphilum facilis</i>	<i>Campylobacter coli</i>
	<i>Acinetobacter baumannii</i>	<i>Campylobacter curvus</i>
	<i>Acinetobacter calcoaceticus</i>	<i>Campylobacter fetus</i> subsp. <i>fetus</i>
	<i>Acinetobacter lwoffii</i>	75 <i>Campylobacter fetus</i> subsp. <i>venerealis</i>
20	<i>Actinomyces meyeri</i>	<i>Campylobacter gracilis</i>
	<i>Aerococcus viridans</i>	<i>Campylobacter jejuni</i>
	<i>Aeromonas hydrophila</i>	<i>Campylobacter jejuni</i> subsp. <i>doylei</i>
	<i>Aeromonas salmonicida</i>	<i>Campylobacter jejuni</i> subsp. <i>jejuni</i>
	<i>Agrobacterium radiobacter</i>	80 <i>Campylobacter lari</i>
25	<i>Agrobacterium tumefaciens</i>	<i>Campylobacter rectus</i>
	<i>Alcaligenes faecalis</i> subsp. <i>faecalis</i>	<i>Campylobacter sputorum</i> subsp. <i>sputorum</i>
	<i>Allochromatium vinosum</i>	<i>Campylobacter upsaliensis</i>
	<i>Anabaena variabilis</i>	<i>Cedecea davisae</i>
	<i>Anacystis nidulans</i>	85 <i>Cedecea lapagei</i>
30	<i>Anaerorhabdus furcosus</i>	<i>Cedecea neteri</i>
	<i>Aquifex aeolicus</i>	<i>Chlamydia pneumoniae</i>
	<i>Aquifex pyrophilus</i>	<i>Chlamydia psittaci</i>
	<i>Arcanobacterium haemolyticum</i>	<i>Chlamydia trachomatis</i>
	<i>Archaeoglobus fulgidus</i>	90 <i>Chlorobium vibrioforme</i>
35	<i>Azotobacter vinelandii</i>	<i>Chloroflexus aurantiacus</i>
	<i>Bacillus anthracis</i>	<i>Chryseobacterium meningosepticum</i>
	<i>Bacillus cereus</i>	<i>Citrobacter amalonaticus</i>
	<i>Bacillus firmus</i>	<i>Citrobacter braakii</i>
	<i>Bacillus halodurans</i>	95 <i>Citrobacter farmeri</i>
40	<i>Bacillus megaterium</i>	<i>Citrobacter freundii</i>
	<i>Bacillus mycoides</i>	<i>Citrobacter koseri</i>
	<i>Bacillus pseudomycoides</i>	<i>Citrobacter sedlakii</i>
	<i>Bacillus stearothermophilus</i>	<i>Citrobacter werkmanii</i>
	<i>Bacillus subtilis</i>	100 <i>Citrobacter youngae</i>
45	<i>Bacillus thuringiensis</i>	<i>Clostridium acetobutylicum</i>
	<i>Bacillus weihenstephanensis</i>	<i>Clostridium beijerinckii</i>
	<i>Bacteroides distasonis</i>	<i>Clostridium bif fermentans</i>
	<i>Bacteroides fragilis</i>	<i>Clostridium botulinum</i>
	<i>Bacteroides forsythus</i>	105 <i>Clostridium difficile</i>
50	<i>Bacteroides ovatus</i>	<i>Clostridium innocuum</i>
	<i>Bacteroides vulgatus</i>	<i>Clostridium histolyticum</i>
	<i>Bartonella henselae</i>	<i>Clostridium novyi</i>
	<i>Bifidobacterium adolescentis</i>	<i>Clostridium septicum</i>
	<i>Bifidobacterium breve</i>	110 <i>Clostridium perfringens</i>
55	<i>Bifidobacterium dentium</i>	<i>Clostridium ramosum</i>
	<i>Bifidobacterium longum</i>	<i>Clostridium sordellii</i>
	<i>Blastochloris viridis</i>	<i>Clostridium tertium</i>
	<i>Borrelia burgdorferi</i>	<i>Clostridium tetani</i>
	<i>Bordetella pertussis</i>	115 <i>Comamonas acidovorans</i>
60	<i>Bordetella bronchiseptica</i>	<i>Corynebacterium accolens</i>
	<i>Brucella abortus</i>	<i>Corynebacterium bovis</i>
	<i>Brevibacterium linens</i>	<i>Corynebacterium cervicis</i>

Table 4. Example of microbial species for which *tuf* and/or *atpD* and/or *recA* nucleic acids and/or sequences are used in the present invention (continued).

Bacterial species (continued)	
5	<i>Corynebacterium diphtheriae</i>
	<i>Corynebacterium flavescens</i>
	<i>Corynebacterium genitalium</i>
	<i>Corynebacterium glutamicum</i>
10	<i>Corynebacterium jeikeium</i>
	<i>Corynebacterium kutscheri</i>
	<i>Corynebacterium minutissimum</i>
	<i>Corynebacterium mycetoides</i>
	<i>Corynebacterium pseudodiphtheriticum</i>
15	<i>Corynebacterium pseudogenitalium</i>
	<i>Corynebacterium pseudotuberculosis</i>
	<i>Corynebacterium renale</i>
	<i>Corynebacterium striatum</i>
	<i>Corynebacterium ulcerans</i>
20	<i>Corynebacterium urealyticum</i>
	<i>Corynebacterium xerosis</i>
	<i>Coxiella burnetii</i>
	<i>Cytophaga lytica</i>
	<i>Deinococcus radiodurans</i>
25	<i>Deinonema</i> sp.
	<i>Edwardsiella hoshinae</i>
	<i>Edwardsiella tarda</i>
	<i>Ehrlichia canis</i>
	<i>Ehrlichia risticii</i>
30	<i>Eikenella corrodens</i>
	<i>Enterobacter aerogenes</i>
	<i>Enterobacter agglomerans</i>
	<i>Enterobacter amnigenus</i>
	<i>Enterobacter asburiae</i>
35	<i>Enterobacter cancerogenus</i>
	<i>Enterobacter cloacae</i>
	<i>Enterobacter gergoviae</i>
	<i>Enterobacter hormaechei</i>
	<i>Enterobacter sakazakii</i>
40	<i>Enterococcus avium</i>
	<i>Enterococcus casseliflavus</i>
	<i>Enterococcus cecorum</i>
	<i>Enterococcus columbae</i>
	<i>Enterococcus dispar</i>
45	<i>Enterococcus durans</i>
	<i>Enterococcus faecalis</i>
	<i>Enterococcus faecium</i>
	<i>Enterococcus flavescens</i>
	<i>Enterococcus gallinarum</i>
50	<i>Enterococcus hirae</i>
	<i>Enterococcus malodoratus</i>
	<i>Enterococcus mundtii</i>
	<i>Enterococcus pseudoavium</i>
	<i>Enterococcus raffinosus</i>
55	<i>Enterococcus saccharolyticus</i>
	<i>Enterococcus solitarius</i>
	<i>Enterococcus sulfureus</i>
	<i>Erwinia amylovora</i>
	<i>Erwinia carotovora</i>
60	<i>Escherichia coli</i>
	<i>Escherichia fergusonii</i>
	<i>Escherichia hermannii</i>
	<i>Escherichia vulneris</i>
	<i>Eubacterium lentum</i>
65	<i>Eubacterium nodatum</i>
	<i>Ewingella americana</i>
	<i>Francisella tularensis</i>
	<i>Frankia alni</i>
	<i>Fervidobacterium islandicum</i>
70	<i>Fibrobacter succinogenes</i>
	<i>Flavobacterium ferrugineum</i>
	<i>Flexistipes sinusarabici</i>
	<i>Fusobacterium gonidiaformans</i>
	<i>Fusobacterium necrophorum</i> subsp. <i>necrophorum</i>
75	<i>Fusobacterium nucleatum</i> subsp. <i>polymorphum</i>
	<i>Gardnerella vaginalis</i>
	<i>Gemella haemolyans</i>
	<i>Gemella morbillorum</i>
	<i>Globicatella sanguis</i>
80	<i>Gloeobacter violaceus</i>
	<i>Gloeotheca</i> sp.
	<i>Gluconobacter oxydans</i>
	<i>Haemophilus actinomycetemcomitans</i>
	<i>Haemophilus aphrophilus</i>
85	<i>Haemophilus ducreyi</i>
	<i>Haemophilus haemolyticus</i>
	<i>Haemophilus influenzae</i>
	<i>Haemophilus parahaemolyticus</i>
	<i>Haemophilus parainfluenzae</i>
90	<i>Haemophilus paraphrophilus</i>
	<i>Haemophilus segnis</i>
	<i>Hafnia alvei</i>
	<i>Halobacterium marismortui</i>
	<i>Halobacterium salinarum</i>
95	<i>Haloferax volcanii</i>
	<i>Helicobacter pylori</i>
	<i>Herpetosiphon aurantiacus</i>
	<i>Kingella kingae</i>
	<i>Klebsiella ornithinolytica</i>
100	<i>Klebsiella oxytoca</i>
	<i>Klebsiella planticola</i>
	<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>
	<i>Klebsiella pneumoniae</i> subsp. <i>pneumoniae</i>
	<i>Klebsiella pneumoniae</i> subsp.
105	<i>rhinoscleromatis</i>
	<i>Klebsiella terrigena</i>
	<i>Kluyvera ascorbata</i>
	<i>Kluyvera cryocrescens</i>
	<i>Kluyvera georgiana</i>
110	<i>Kocuria kristinae</i>
	<i>Lactobacillus acidophilus</i>
	<i>Lactobacillus garvieae</i>
	<i>Lactobacillus paracasei</i>
	<i>Lactobacillus casei</i> subsp. <i>casei</i>
115	<i>Lactococcus garvieae</i>
	<i>Lactococcus lactis</i>
	<i>Lactococcus lactis</i> subsp. <i>lactis</i>
	<i>Leclercia adecarboxylata</i>
	<i>Legionella micdadei</i>

Table 4. Example of microbial species for which *tuf* and/or *atpD* and/or *recA* nucleic acids and/ or sequences are used in the present invention (continued).

5	Bacterial species (continued)	
	<i>Legionella pneumophila</i> subsp. <i>pneumophila</i>	<i>Neisseria gonorrhoeae</i>
	<i>Leminorella grimontii</i>	<i>Neisseria lactamica</i>
	<i>Leminorella richardii</i>	65 <i>Neisseria meningitidis</i>
10	<i>Leptospira biflexa</i>	<i>Neisseria mucosa</i>
	<i>Leptospira interrogans</i>	<i>Neisseria perflava</i>
	<i>Leuconostoc mesenteroides</i> subsp. <i>dextranicum</i>	<i>Neisseria pharyngis</i> var. <i>flava</i>
	<i>Listeria innocua</i>	70 <i>Neisseria polysaccharea</i>
15	<i>Listeria ivanovii</i>	<i>Neisseria sicca</i>
	<i>Listeria monocytogenes</i>	<i>Neisseria subflava</i>
	<i>Listeria seeligeri</i>	<i>Neisseria weaveri</i>
	<i>Macrococcus caseolyticus</i>	<i>Obesumbacterium proteus</i>
	<i>Magnetospirillum magnetotacticum</i>	75 <i>Ochrobactrum anthropi</i>
20	<i>Megamonas hypermegale</i>	<i>Pantoea agglomerans</i>
	<i>Methanobacterium thermoautotrophicum</i>	<i>Pantoea dispersa</i>
	<i>Methanococcus jannaschii</i>	<i>Paracoccus denitrificans</i>
	<i>Methanococcus vannielii</i>	<i>Pasteurella multocida</i>
	<i>Methanosarcina barkeri</i>	80 <i>Pectinatus frisingensis</i>
25	<i>Methanosarcina jannaschii</i>	<i>Peptococcus niger</i>
	<i>Methylobacillus flagellatum</i>	<i>Peptostreptococcus anaerobius</i>
	<i>Methylomonas clara</i>	<i>Peptostreptococcus asaccharolyticus</i>
	<i>Micrococcus luteus</i>	<i>Peptostreptococcus prevotii</i>
	<i>Micrococcus lylae</i>	85 <i>Phormidium ectocarpi</i>
30	<i>Mitsuokella multacidus</i>	<i>Pirellula marina</i>
	<i>Mobiluncus curtisii</i> subsp. <i>holmesii</i>	<i>Planobispora rosea</i>
	<i>Moellerella thermoacetica</i>	<i>Plesiomonas shigelloides</i>
	<i>Moellerella wisconsensis</i>	<i>Plectonema boryanum</i>
	<i>Moorella thermoacetica</i>	90 <i>Porphyromonas asaccharolytica</i>
35	<i>Moraxella catarrhalis</i>	<i>Porphyromonas gingivalis</i>
	<i>Moraxella osloensis</i>	<i>Pragia fontium</i>
	<i>Morganella morganii</i> subsp. <i>morganii</i>	<i>Prevotella buccalis</i>
	<i>Mycobacterium avium</i>	<i>Prevotella melaninogenica</i>
	<i>Mycobacterium bovis</i>	95 <i>Prevotella oralis</i>
40	<i>Mycobacterium gordonae</i>	<i>Prevotella ruminicola</i>
	<i>Mycobacterium kansasii</i>	<i>Prochlorothrix hollandica</i>
	<i>Mycobacterium leprae</i>	<i>Propionibacterium acnes</i>
	<i>Mycobacterium terrae</i>	<i>Propionigenium modestum</i>
	<i>Mycobacterium tuberculosis</i>	100 <i>Proteus mirabilis</i>
45	<i>Mycoplasma capricolum</i>	<i>Proteus penneri</i>
	<i>Mycoplasma gallisepticum</i>	<i>Proteus vulgaris</i>
	<i>Mycoplasma genitalium</i>	<i>Providencia alcalifaciens</i>
	<i>Mycoplasma hominis</i>	<i>Providencia rettgeri</i>
	<i>Mycoplasma pirum</i>	105 <i>Providencia rustigianii</i>
50	<i>Mycoplasma mycoides</i>	<i>Providencia stuartii</i>
	<i>Mycoplasma pneumoniae</i>	<i>Pseudomonas aeruginosa</i>
	<i>Mycoplasma pulmonis</i>	<i>Pseudomonas fluorescens</i>
	<i>Mycoplasma salivarium</i>	<i>Pseudomonas putida</i>
	<i>Myxococcus xanthus</i>	110 <i>Pseudomonas stutzeri</i>
55	<i>Neisseria animalis</i>	<i>Psychrobacter phenylpyruvicum</i>
	<i>Neisseria canis</i>	<i>Pyrococcus abyssi</i>
	<i>Neisseria cinerea</i>	<i>Rahnella aquatilis</i>
	<i>Neisseria cuniculi</i>	<i>Rickettsia prowazekii</i>
	<i>Neisseria elongata</i> subsp. <i>elongata</i>	115 <i>Rhizobium leguminosarum</i>
60	<i>Neisseria elongata</i> subsp. <i>intermedia</i>	<i>Rhizobium phaseoli</i>
	<i>Neisseria flava</i>	<i>Rhodobacter capsulatus</i>
	<i>Neisseria flavescens</i>	<i>Rhodobacter sphaeroides</i>

Table 4. Example of microbial species for which *tuf* and/or *atpD* and/or *recA* nucleic acids and/or sequences are used in the present invention (continued).

5	Bacterial species (continued)	
	<i>Rhodopseudomonas palustris</i>	
	<i>Rhodospirillum rubrum</i>	65
10	<i>Ruminococcus albus</i>	<i>Streptococcus gordonii</i>
	<i>Ruminococcus bromii</i>	<i>Streptococcus macacae</i>
	<i>Salmonella bongori</i>	<i>Streptococcus mitis</i>
	<i>Salmonella choleraesuis</i> subsp. <i>arizonae</i>	<i>Streptococcus mutans</i>
	<i>Salmonella choleraesuis</i> subsp. <i>choleraesuis</i>	<i>Streptococcus oralis</i>
15	<i>Salmonella choleraesuis</i> subsp. <i>diarizonae</i>	<i>Streptococcus parasanguinis</i>
	<i>Salmonella choleraesuis</i> subsp. <i>houtenae</i>	<i>Streptococcus pneumoniae</i>
	<i>Salmonella choleraesuis</i> subsp. <i>indica</i>	<i>Streptococcus pyogenes</i>
20	<i>Salmonella choleraesuis</i> subsp. <i>salamae</i>	<i>Streptococcus rattus</i>
	<i>Serpulina hyodysenteriae</i>	<i>Streptococcus salivarius</i>
	<i>Serratia ficaria</i>	<i>Streptococcus salivarius</i> subsp. <i>thermophilus</i>
	<i>Serratia fonticola</i>	<i>Streptococcus sanguinis</i>
25	<i>Serratia grimesii</i>	<i>Streptococcus sobrinus</i>
	<i>Serratia liquefaciens</i>	<i>Streptococcus suis</i>
	<i>Serratia marcescens</i>	<i>Streptococcus uberis</i>
	<i>Serratia odorifera</i>	<i>Streptococcus vestibularis</i>
	<i>Serratia plymuthica</i>	<i>Streptomyces anofaciens</i>
30	<i>Serratia rubidaea</i>	<i>Streptomyces aureofaciens</i>
	<i>Shewanella putrefaciens</i>	<i>Streptomyces cinnamomeus</i>
	<i>Shigella boydii</i>	<i>Streptomyces coelicolor</i>
	<i>Shigella dysenteriae</i>	<i>Streptomyces collinus</i>
	<i>Shigella flexneri</i>	<i>Streptomyces lividans</i>
35	<i>Shigella sonnei</i>	<i>Streptomyces netropsis</i>
	<i>Sinorhizobium meliloti</i>	<i>Streptomyces ramocissimus</i>
	<i>Spirochaeta aurantia</i>	<i>Streptomyces rimosus</i>
	<i>Staphylococcus aureus</i>	<i>Streptomyces venezuelae</i>
	<i>Staphylococcus aureus</i> subsp. <i>aureus</i>	90
	<i>Staphylococcus auricularis</i>	<i>Succinivibrio dextrinosolvens</i>
40	<i>Staphylococcus capitis</i> subsp. <i>capitis</i>	<i>Synechococcus</i> sp.
	<i>Staphylococcus cohnii</i> subsp. <i>cohnii</i>	<i>Synechocystis</i> sp.
	<i>Staphylococcus epidermidis</i>	<i>Tatumella ptyseos</i>
	<i>Staphylococcus haemolyticus</i>	<i>Taxobacter ocealeus</i>
45	<i>Staphylococcus hominis</i>	95
	<i>Staphylococcus hominis</i> subsp. <i>hominis</i>	<i>Tetragenococcus halophilus</i>
	<i>Staphylococcus lugdunensis</i>	<i>Thermoplasma acidophilum</i>
	<i>Staphylococcus saprophyticus</i>	<i>Thermotoga maritima</i>
	<i>Staphylococcus sciuri</i> subsp. <i>sciuri</i>	<i>Thermus aquaticus</i>
50	<i>Staphylococcus simulans</i>	<i>Thermus thermophilus</i>
	<i>Staphylococcus warneri</i>	100
	<i>Stigmatella aurantiaca</i>	<i>Thiobacillus ferrooxidans</i>
	<i>Stenotrophomonas maltophilia</i>	<i>Thiomonas cuprina</i>
	<i>Streptococcus acidominimus</i>	<i>Trabulsiella guamensis</i>
55	<i>Streptococcus agalactiae</i>	<i>Treponema pallidum</i>
	<i>Streptococcus anginosus</i>	<i>Ureaplasma urealyticum</i>
	<i>Streptococcus bovis</i>	105
	<i>Streptococcus cricetus</i>	<i>Veillonella parvula</i>
	<i>Streptococcus cristatus</i>	<i>Vibrio alginolyticus</i>
60	<i>Streptococcus downei</i>	<i>Vibrio anguillarum</i>
	<i>Streptococcus dysgalactiae</i>	<i>Vibrio cholerae</i>
	<i>Streptococcus equi</i> subsp. <i>equi</i>	<i>Vibrio mimicus</i>
	<i>Streptococcus ferus</i>	110
		<i>Wolinella succinogenes</i>
		<i>Xanthomonas citri</i>
		<i>Xanthomonas oryzae</i>
		<i>Xenorhabdus bovienii</i>
		<i>Xenorhabdus nematophilus</i>
		115
		<i>Yersinia bercovieri</i>
		<i>Yersinia enterocolitica</i>
		<i>Yersinia frederiksenii</i>
		<i>Yersinia intermedia</i>
		<i>Yersinia pestis</i>

Table 4. Example of microbial species for which *tuf* and/or *atpD* and/or *recA* nucleic acids and/ r sequences are used in the present invention (continued).

5

Bacterial species (continued)*Yersinia pseudotuberculosis**Yersinia rohdei**Yokenella regensburgei*

10

Zoogloea ramigera

Table 4. Example of microbial species for which *tuf* and/or *atpD* and/or *recA* nucleic acids and/or sequences are used in the present invention (continued).

5	Fungal species
	<i>Absidia corymbifera</i>
	<i>Absidia glauca</i>
	<i>Alternaria alternata</i>
10	<i>Arxula adenivorans</i>
	<i>Aspergillus flavus</i>
	<i>Aspergillus fumigatus</i>
	<i>Aspergillus nidulans</i>
	<i>Aspergillus niger</i>
15	<i>Aspergillus oryzae</i>
	<i>Aspergillus terreus</i>
	<i>Aspergillus versicolor</i>
	<i>Aureobasidium pullulans</i>
	<i>Basidiobolus ranarum</i>
20	<i>Bipolaris hawaiiensis</i>
	<i>Bilophila wadsworthia</i>
	<i>Blastoschizomyces capitatus</i>
	<i>Blastomyces dermatitidis</i>
	<i>Candida albicans</i>
25	<i>Candida catenulata</i>
	<i>Candida dubliniensis</i>
	<i>Candida famata</i>
	<i>Candida glabrata</i>
	<i>Candida guilliermondii</i>
30	<i>Candida haemulonii</i>
	<i>Candida inconspicua</i>
	<i>Candida kefyr</i>
	<i>Candida krusei</i>
	<i>Candida lambica</i>
35	<i>Candida lusitanae</i>
	<i>Candida norvegica</i>
	<i>Candida norvegensis</i>
	<i>Candida parapsilosis</i>
	<i>Candida rugosa</i>
40	<i>Candida spharica</i>
	<i>Candida tropicalis</i>
	<i>Candida utilis</i>
	<i>Candida viswanathii</i>
	<i>Candida zeylanoides</i>
45	<i>Cladophialophora carrionii</i>
	<i>Coccidioides immitis</i>
	<i>Coprinus cinereus</i>
	<i>Cryptococcus albidus</i>
	<i>Cryptococcus humicolus</i>
50	<i>Cryptococcus laurentii</i>
	<i>Cryptococcus neoformans</i>
	<i>Cunninghamella bertholletiae</i>
	<i>Curvularia lunata</i>
	<i>Emericella nidulans</i>
55	<i>Emmonsia parva</i>
	<i>Eremothecium gossypii</i>
	<i>Exophiala dermatitidis</i>
	<i>Exophiala jeanselmei</i>
	<i>Exophiala moniliae</i>
60	<i>Exserohilum rostratum</i>
	<i>Eremothecium gossypii</i>
	<i>Fonsecaea pedrosoi</i>
	<i>Fusarium moniliforme</i>
	<i>Fusarium oxysporum</i>
65	<i>Fusarium solani</i>
	<i>Geotrichum sp.</i>
	<i>Histoplasma capsulatum</i>
	<i>Hortaea werneckii</i>
	<i>Issatchenkia orientalis</i> Kudrjanzev
70	<i>Kluyveromyces lactis</i>
	<i>Malassezia furfur</i>
	<i>Malassezia pachydermatis</i>
	<i>Malbranchea filamentosa</i>
	<i>Metschnikowia pulcherrima</i>
75	<i>Microsporium audouinii</i>
	<i>Microsporium canis</i>
	<i>Mucor circinelloides</i>
	<i>Neurospora crassa</i>
	<i>Paecilomyces lilacinus</i>
80	<i>Paracoccidioides brasiliensis</i>
	<i>Penicillium marneffei</i>
	<i>Phialaphora verrucosa</i>
	<i>Pichia anomala</i>
	<i>Piedraia hortai</i>
85	<i>Podospora anserina</i>
	<i>Podospora curvicolla</i>
	<i>Puccinia graminis</i>
	<i>Pseudallescheria boydii</i>
	<i>Reclinomonas americana</i>
90	<i>Rhizomucor racemosus</i>
	<i>Rhizopus oryzae</i>
	<i>Rhodotorula minuta</i>
	<i>Rhodotorula mucilaginosa</i>
	<i>Saccharomyces cerevisiae</i>
95	<i>Saksenaea vasiformis</i>
	<i>Schizosaccharomyces pombe</i>
	<i>Scopulariopsis koningii</i>
	<i>Sordaria macrospora</i>
	<i>Sporobolomyces salmonicolor</i>
100	<i>Sporothrix schenckii</i>
	<i>Stephanosorus ciferrii</i>
	<i>Syncephalastrum racemosum</i>
	<i>Trichoderma reesei</i>
	<i>Trichophyton mentagrophytes</i>
105	<i>Trichophyton rubrum</i>
	<i>Trichophyton tonsurans</i>
	<i>Trichosporon cutaneum</i>
	<i>Ustilago maydis</i>
	<i>Wangiella dermatitidis</i>
110	<i>Yarrowia lipolytica</i>

Table 4. Example of microbial species for which *tuf* and/or *atpD* and/or *recA* nucleic acids and/or sequences are used in the present invention (continued).

Parasitical species	
5	<i>Babesia bigemina</i> <i>Babesia bovis</i> <i>Babesia microti</i> <i>Blastocystis hominis</i>
10	<i>Criohidia fasciculata</i> <i>Cryptosporidium parvum</i> <i>Entamoeba histolytica</i> <i>Giardia lamblia</i> <i>Kentrophoros sp.</i>
15	<i>Leishmania aethiopica</i> <i>Leishmania amazonensis</i> <i>Leishmania braziliensis</i> <i>Leishmania donovani</i> <i>Leishmania infantum</i>
20	<i>Leishmania enriettii</i> <i>Leishmania gerbilli</i> <i>Leishmania guyanensis</i> <i>Leishmania hertigi</i> <i>Leishmania major</i>
25	<i>Leishmania mexicana</i> <i>Leishmania panamensis</i> <i>Leishmania tarentolae</i> <i>Leishmania tropica</i> <i>Neospora caninum</i>
30	<i>Onchocerca volvulus</i> <i>Plasmodium berghei</i> <i>Plasmodium falciparum</i> <i>Plasmodium knowlesi</i> <i>Porphyra purpurea</i>
35	<i>Toxoplasma gondii</i> <i>Treponema pallidum</i> <i>Trichomonas tenax</i> <i>Trichomonas vaginalis</i> <i>Trypanosoma brucei</i>
40	<i>Trypanosoma brucei</i> subsp. <i>brucei</i> <i>Trypanosoma congolense</i> <i>Trypanosoma cruzi</i>

Table 5. Antimicrobial agents resistance genes selected for diagnostic purposes.

	Gene	Antimicrobial agent	Bacteria ¹	ACCESSION NO.	SEQ ID NO.
5	<i>aac(3)-Ib</i> ²	Aminoglycosides	<i>Enterobacteriaceae</i> <i>Pseudomonads</i>	L06157	
	<i>aac(3)-IIb</i> ²	Aminoglycosides	<i>Enterobacteriaceae</i> , <i>Pseudomonads</i>	M97172	
	<i>aac(3)-IVa</i> ²	Aminoglycosides	<i>Enterobacteriaceae</i>	X01385	
10	<i>aac(3)-VIa</i> ²	Aminoglycosides	<i>Enterobacteriaceae</i> , <i>Pseudomonads</i>	M88012	
	<i>aac(2')-Ia</i> ²	Aminoglycosides	<i>Enterobacteriaceae</i> , <i>Pseudomonads</i>	X04555	
	<i>aac(6')-aph(2'')</i> ²	Aminoglycosides	<i>Enterococcus</i> sp., <i>Staphylococcus</i> sp.		83-86 ³
15	<i>aac(6')-Ia</i> ²	Aminoglycosides	<i>Enterobacteriaceae</i> , <i>Pseudomonads</i>	M18967	
	<i>aac(6')-Ic</i> ²	Aminoglycosides	<i>Enterobacteriaceae</i> , <i>Pseudomonads</i>	M94066	
20	<i>aac(6')-IIa</i> ²	Aminoglycosides	<i>Pseudomonads</i>		112 ⁴
	<i>aadB</i> [<i>ant(2'')-Ia</i> ²]	Aminoglycosides	<i>Enterobacteriaceae</i>		53-54 ³
	<i>aacC1</i> [<i>aac(3)-Ia</i> ²]	Aminoglycosides	<i>Pseudomonads</i>		55-56 ³
	<i>aacC2</i> [<i>aac(3)-IIa</i> ²]	Aminoglycosides	<i>Pseudomonads</i>		57-58 ³
	<i>aacC3</i> [<i>aac(3)-III</i> ²]	Aminoglycosides	<i>Pseudomonads</i>		59-60 ³
25	<i>aacA4</i> [<i>aac(6')-Ib</i> ²]	Aminoglycosides	<i>Pseudomonads</i>		65-66 ³
	<i>ant(3'')-Ia</i> ²	Aminoglycosides	<i>Enterobacteriaceae</i> , <i>Enterococcus</i> sp., <i>Staphylococcus</i> sp.	X02340 M10241	
	<i>ant(4')-Ia</i> ²	Aminoglycosides	<i>Staphylococcus</i> sp.	V01282	
30	<i>aph(3')-Ia</i> ²	Aminoglycosides	<i>Enterobacteriaceae</i> , <i>Pseudomonads</i>	J01839	
	<i>aph(3')-IIa</i> ²	Aminoglycosides	<i>Enterobacteriaceae</i> , <i>Pseudomonads</i>	V00618	
	<i>aph(3')-IIIa</i> ²	Aminoglycosides	<i>Enterococcus</i> sp., <i>Staphylococcus</i> sp.	V01547	
35	<i>aph(3')-VIa</i> ²	Aminoglycosides	<i>Enterobacteriaceae</i> , <i>Pseudomonads</i>	X07753	
	<i>rpsL</i> ²	Streptomycin	<i>M. tuberculosis</i> , <i>M. avium</i> complex	X80120 U14749 X70995 L08011	
40					
	<i>bla_{OXA}</i> ^{5,6}	β -lactams	<i>Enterobacteriaceae</i> , <i>Pseudomonads</i>	Y10693 AJ238349 AJ009819 X06046 X03037 X07260 U13880 X75562 AF034958 J03427 Z22590 U59183 L38523 U63835 AF043100 AF060206 U85514 AF043381 AF024602 AF064820	110 ⁴
45					
50					
55					
60					
	<i>bla_{ROB}</i> ⁵	β -lactams	<i>Haemophilus</i> sp., <i>Pasteurella</i> sp.		45-48 ³
65					

Table 5. Antimicrobial agents resistance genes selected for diagnostic purposes (continued).

Gene	Antimicrobial agent	Bacteria ¹	ACCESSION NO.	SEQ ID NO.
5 <i>bla_{SHV}</i> ^{5,6}	β -lactams	<i>Enterobacteriaceae</i> , <i>Pseudomonas aeruginosa</i>	AF124984	41-44 ³
			AF148850	
			M59181	
			X98099	
			M33655	
10			AF148851	
			X53433	
			L47119	
			AF074954	
			X53817	
15			AF096930	
			X55640	
			Y11069	
			U20270	
			U92041	
20			S82452	
			X98101	
			X98105	
			AF164577	
			AJ011428	
25			AF116855	
			AB023477	
			AF293345	
			AF227204	
			AF208796	
30			AF132290	37-40 ³
			AF012911	
			U48775	
			AF093512	
			AF052748	
35			X64523	
			Y13612	
			X57972	
			AF157413	
			U31280	
40			U36911	
			U48775	
			V00613	
			X97254	
			AJ012256	
45			X04515	
			AF126482	
			U09188	
			M88143	
			Y14574	
50			AF188200	
			AJ251946	
			Y17581	
			Y17582	
			Y17583	
55			M88143	
			U37195	
			Y17584	
			X64523	
			U95363	
60			Y10279	
			Y10280	
			Y10281	
			AF027199	
			AF104441	
65			AF104442	
			AF062386	
			X57972	
			AF047171	
			AF188199	
70			AF157553	
			AF190694	
			AF190695	
			AF190693	
			AF190692	
75				

Table 5. Antimicrobial agents resistance genes selected for diagnostic purposes (continued).

Gene	Antimicrobial agent	Bacteria ¹	ACCESSION NO.	SEQ ID NO.
5	<i>bla</i> _{CARB} ⁵	<i>Pseudomonas</i> sp., <i>Enterobacteriaceae</i>	J05162	
			S46063	
			M69058	
			U14749	
			D86225	
10			D13210	
			Z18955	
			AF071555	
			AF153200	
			AF030945	
15	<i>bla</i> _{CTX-M-1} ⁵	<i>Enterobacteriaceae</i>	X92506	
20	<i>bla</i> _{CTX-M-2} ⁵	<i>Enterobacteriaceae</i>	X92507	
25	<i>bla</i> _{CMY-2} ⁷	<i>Enterobacteriaceae</i>	X91840	
			AJ007826	
			AJ011293	
			AJ011291	
			Y17716	
30	<i>bla</i> _{IMP} ⁵	<i>Enterobacteriaceae</i> , <i>Pseudomonas aeruginosa</i>	Y16783	
			Y16781	
			Y15130	
			U77414	
			S83226	
35	<i>bla</i> _{PER-1} ⁵	<i>Enterobacteriaceae</i> , <i>Pseudomonadaceae</i>	Y15412	
			X78117	
			AJ223604	
			S71932	
			D50438	
40	<i>bla</i> _{PER-2} ⁷	<i>Enterobacteriaceae</i>	D29636	
			X98393	
			AB010417	
			D78375	
			Z21957	
	<i>bla</i> _Z ¹²	<i>Enterococcus</i> sp., <i>Staphylococcus</i> sp.		111 ⁴
	<i>mecA</i> ¹²	<i>Staphylococcus</i> sp.		97-98 ³

Table 5. Antimicrobial agents resistance genes selected for diagnostic purposes (continued).

Gene	Antimicrobial agent	Bacteria ¹	ACCESSION NO.	SEQ ID NO.
5 <i>pbp1a</i> ¹³	β -lactams	<i>Streptococcus pneumoniae</i>	M90527	1004-1018, 1648,2056-2064, 2273-2276
			X67872	
			AB006868	
			AB006874	
			X67873	
			AB006878	
			AB006875	
			AB006877	
			AB006879	
			AF046237	
			AF046235	
			AF026431	
			AF046232	
			AF046233	
			AF046236	
			X67871	
			Z49095	
			AF046234	
			AB006873	
			X67866	
X67868				
AB006870				
AB006869				
AB006872				
X67870				
AB006871				
X67867				
X67869				
AB006876				
AF046230				
AF046238				
Z49094				
40 <i>pbp2b</i> ¹³	β -lactams	<i>Streptococcus pneumoniae</i>	X16022	1019-1033
			M25516	
			M25518	
			M25515	
			U20071	
			U20084	
			U20082	
			U20067	
			U20079	
			Z22185	
			U20072	
			U20083	
			U20081	
			M25522	
			U20075	
			U20070	
			U20077	
			U20068	
			Z22184	
			U20069	
U20078				
M25521				
M25525				
M25519				
Z21981				
M25523				
M25526				
U20076				
U20074				
M25520				
M25517				
M25524				
Z22230				
U20073				
U20080				

Table 5. Antimicrobial agents resistance genes selected for diagnostic purposes (continued).

Gene	Antimicrobial agent	Bacteria ¹	ACCESSION NO.	SEQ ID NO.
5 <i>pbp2x</i> ¹³	β -lactams	<i>Streptococcus pneumoniae</i>	X16367 X65135 AB011204 AB011209 AB011199 AB011200 AB011201 AB011202 AB011198 AB011208 AB011205 AB015852 AB011210 AB015849 AB015850 AB015851 AB015847 AB015846 AB011207 AB015848 Z49096	1034-1048
10				
15				
20				
25				
<i>int</i>	-lactams, trimethoprim	<i>Enterobacteriaceae</i> ,		99-102 ³
30 <i>sul</i>	aminoglycosides, antiseptic, chloramphenicol	<i>Pseudomonads</i>		103-106 ³
<i>ermA</i> ¹⁴	Macrolides, lincosamides, streptogramin B	<i>Staphylococcus</i> sp.		113 ⁴
35 <i>ermB</i> ¹⁴	Macrolides, lincosamides, streptogramin B	<i>Enterobacteriaceae</i> , <i>Staphylococcus</i> sp. <i>Enterococcus</i> sp. <i>Streptococcus</i> sp.		114 ⁴
40 <i>ermC</i> ¹⁴	Macrolides, lincosamides, streptogramin B	<i>Enterobacteriaceae</i> , <i>Staphylococcus</i> sp.		115 ⁴
45 <i>ereA</i> ¹²	Macrolides	<i>Enterobacteriaceae</i> , <i>Staphylococcus</i> sp.	M11277 E01199 AF099140 A15097 X03988	
<i>ereB</i> ¹²	Macrolides	<i>Enterobacteriaceae</i> <i>Staphylococcus</i> sp.		
50 <i>msrA</i> ¹²	Macrolides	<i>Staphylococcus</i> sp.		77-80 ³
<i>mefA</i> , <i>mefE</i> ⁸	Macrolides	<i>Streptococcus</i> sp.	U70055 U83667 D16251 U34344 U36578 J03947 M14039 A15070 E01245 AF110130 AJ238249	
55 <i>mphA</i> ⁸	Macrolides	<i>Enterobacteriaceae</i> , <i>Staphylococcus</i> sp.		
<i>linA/linA'</i> ⁹	Lincosamides	<i>Staphylococcus</i> sp.		
60 <i>linB</i> ¹⁰	Lincosamides	<i>Enterococcus faecium</i>		
<i>vga</i> ¹⁵	Streptogramin	<i>Staphylococcus</i> sp.	M90056 U82085 M36022 M20219 AF015628	89-90 ³
65 <i>vgb</i> ¹⁵	Streptogramin	<i>Staphylococcus</i> sp.		

Table 5. Antimicrobial agents resistance genes selected for diagnostic purposes (continued).

	Gene	Antimicrobial agent	Bacteria ¹	ACCESSION NO.	SEQ ID NO.
5	<i>vat</i> ¹⁵ <i>vatB</i> ¹⁵	Streptogramin Streptogramin	<i>Staphylococcus</i> sp. <i>Staphylococcus</i> sp.	L07778 U19459 L38809	87-88 ³
10	<i>sata</i> ¹⁵ <i>mupA</i> ¹²	Streptogramin Mupirocin	<i>Enterococcus faecium</i> <i>Staphylococcus aureus</i>	L12033 X75439 X59478 X59477	81-82 ³
15	<i>gyrA</i> ¹⁶	Quinolones	Gram-positive and gram-negative bacteria	X95718 X06744 X57174 X16817 X71437 AF065152 AF060881 D32252	1255, 1607-1608, 1764-1776, 2013-2014, 2277-2280
20	<i>parC/grlA</i> ¹⁶	Quinolones	Gram-positive and gram-negative bacteria	AB005036 AF056287 X95717 AF129764 AB017811 AF065152	1777-1785
25	<i>parE/grlB</i> ¹⁶	Quinolones	Gram-positive bacteria	X95717 AF065153 AF058920	
30	<i>norA</i> ¹⁶	Quinolones	<i>Staphylococcus</i> sp.	D90119 M80252 M97169 U23763 X65646 M55620 X15100 A24651 M28717 A00568 A00569 X74948 Y00723 A24362 A00569 M93113 M62822 M58516 V01277 X02166 M77169 X53796 J01841 X07848	
35	<i>mexR (nalB)</i> ¹⁶ <i>nfxB</i> ¹⁶ <i>cat</i> ¹²	Quinolones Quinolones Chloramphenicol	<i>Pseudomonas aeruginosa</i> <i>Pseudomonas aeruginosa</i> Gram-positive and gram-negative bacteria		
40					
45					
50					
55	<i>ppf</i> lo-like <i>embB</i> ¹⁷ <i>pncA</i> ¹⁷	Chloramphenicol Ethambutol Pyrazinamide	<i>Mycobacterium tuberculosis</i> <i>Mycobacterium tuberculosis</i>	AF071555 U68480 U59967	
60	<i>rpoB</i> ¹⁷	Rifampin	<i>Mycobacterium tuberculosis</i>	AF055891 AF055892 S71246 L27989 AF055893 AF106077 U02492	
65	<i>inhA</i> ¹⁷	Isoniazid	<i>Mycobacterium tuberculosis</i>		

Table 5. Antimicrobial agents resistance genes selected for diagnostic purposes (continued).

	Gene	Antimicrobial agent	Bacteria ¹	ACCESSION NO.	SEQ ID NO.
5	<i>vanA</i> ¹²	Vancomycin	<i>Enterococcus</i> sp.		67-70 ³
	<i>vanB</i> ¹²	Vancomycin	<i>Enterococcus</i> sp.		1049-1057
	<i>vanC1</i> ¹²	Vancomycin	<i>Enterococcus gallinarum</i>		116 ⁴
10	<i>vanC2</i> ¹²	Vancomycin	<i>Enterococcus casseliflavus</i>		117 ⁴
					1058-1059
					1060-1063
				U94521	
				U94522	
				U94523	
15				U94524	
				U94525	
				L29638	
	<i>vanC3</i> ¹²	Vancomycin	<i>Enterococcus flavescens</i>		1064-1066
				L29639	
20	<i>vanD</i> ¹⁸	Vancomycin	<i>Enterococcus faecium</i>	U72706	
	<i>vanE</i> ¹²	Vancomycin	<i>Enterococcus faecium</i>	AF130997	
	<i>tetB</i> ¹⁹	Tetracycline	Gram-negative bacteria	AF136925	
				J01830	
25				AF162223	
				AP000342	
				S83213	
				U81141	
				V00611	
30	<i>tetM</i> ¹⁹	Tetracycline	Gram-negative and Gram-positive bacteria	X52632	
				AF116348	
				U50983	
				X92947	
				M211136	
35				U08812	
	<i>sul II</i> ²⁰	Sulfonamides	Gram-negative bacteria	X04388	
				M36657	
				AF017389	
				AF017391	
40	<i>dhfrIa</i> ²⁰	Trimethoprim	Gram-negative bacteria	AJ238350	
				X17477	
				K00052	
				U09476	
				X00926	
45	<i>dhfrIb</i> ²⁰	Trimethoprim	Gram-negative bacteria	Z50805	
	<i>dhfrV</i> ²⁰	Trimethoprim	Gram-negative bacteria	Z50804	
	<i>dhfrVI</i> ²⁰	Trimethoprim	Gram-negative bacteria	X12868	
	<i>dhfrVII</i> ²⁰	Trimethoprim	Gram-negative bacteria	Z86002	
				U31119	
50				AF139109	
	<i>dhfrVIII</i> ²⁰	Trimethoprim	Gram-negative bacteria	X58425	
				U10186	
				U09273	
	<i>dhfrIX</i> ²⁰	Trimethoprim	Gram-negative bacteria	X57730	
55	<i>dhfrXII</i> ²⁰	Trimethoprim	Gram-negative bacteria	Z21672	
				AF175203	
				AF180731	
				M84522	
	<i>dhfrXIII</i> ²⁰	Trimethoprim	Gram-negative bacteria	Z50802	
60	<i>dhfrXV</i> ²⁰	Trimethoprim	Gram-negative bacteria	Z83331	
	<i>dhfrXVII</i> ²⁰	Trimethoprim	Gram-negative bacteria	AF170088	
				AF180469	
				AF169041	

Table 5. Antimicrobial agents resistance genes selected for diagnostic purposes (continued).

Gene	Antimicrobial agent	Bacteria ¹	ACCESSION NO.	SEQ ID NO.
5 <i>dfra</i> ²⁰	Trimethoprim	<i>Staphylococcus</i> sp.	AF045472 U40259 AF051916 X13290 Y07536 Z16422 Z48233	
10				
15				
		1 Bacteria having high incidence for the specified antibiotic resistance gene. The presence of the antibiotic resistance genes in other bacteria is not excluded.		
		2 Shaw, K. J., P. N. Rather, R. S. Hare, and G. H. Miller. 1993. Molecular genetics of aminoglycoside resistance genes and familial relationships of the aminoglycoside-modifying enzymes. Microbiol. Rev. 57:138-163.		
20		3 Antibiotic resistance genes from our assigned US patent no. 6,001,564 for which we have selected PCR primer pairs.		
		4 These SEQ ID NOs. refer to a previous patent (publication WO98/20157).		
		5 Bush, K., G.A. Jacoby and A. Medeiros. 1995. A functional classification scheme for β -lactamase and its correlation with molecular structure. Antimicrob. Agents. Chemother. 39:1211-1233.		
25		6 Nucleotide mutations in <i>bla</i> _{SHV} , <i>bla</i> _{TEM} , and <i>bla</i> _{OXA} , are associated with extended-spectrum β -lactamase or inhibitor-resistant β -lactamase.		
		7 Bauerfeind, A., Y. Chong, and K. Lee. 1998. Plasmid-encoded AmpC beta-lactamases: how far have we gone 10 ears after discovery? Yonsei Med. J. 39:520-525.		
30		8 Sutcliffe, J., T. Grebe, A. Tait-Kamradt, and L. Wondrack. 1996. Detection of erythromycin-resistant determinants by PCR. Antimicrob. Agent Chemother. 40:2562-2566.		
		9 Leclerc, R., A., Brisson-Noël, J. Duval, and P. Courvalin. 1991. Phenotypic expression and genetic heterogeneity of lincosamide inactivation in <i>Staphylococcus</i> sp. Antimicrob. Agents. Chemother. 31:1887-1891.		
35		10 Bozdogan, B., L. Berrezouga, M.-S. Kuo, D. A. Yurek, K. A. Farley, B. J. Stockman, and R. Leclercq. 1999. A new gene, <i>linB</i> , conferring resistance to lincosamides by nucleotidylation in <i>Enterococcus faecium</i> HM1025. Antimicrob. Agents. Chemother. 43:925-929.		
		11 Cockerill III, F.R. 1999. Genetic methods for assessing antimicrobial resistance. Antimicrob. Agents. Chemother. 43:199-212.		
40		12 Tenover, F. C., T. Popovic, and O. Olsvik. 1996. Genetic methods for detecting antibacterial resistance genes. pp. 1368-1378. In Murray, P. R., E. J. Baron, M. A. Pfaller, F. C. Tenover, R. H. Tenover (eds). Manual of clinical microbiology. 6th ed., ASM Press, Washington, D.C. USA		
		13 Dowson, C. G., T. J. Tracey, and B. G. Spratt. 1994. Origin and molecular epidemiology of penicillin-binding-protein-mediated resistance to β -lactam antibiotics. Trends Molec. Microbiol. 2: 361-366.		
45		14 Jensen, L. B., N. Frimodt-Moller, F. M. Aarestrup. 1999. Presence of <i>erm</i> gene classes in Gram-positive bacteria of animal and human origin in Denmark. FEMS Microbiol. 170:151-158.		
		15 Thal, L. A., and M. J. Zervos. 1999. Occurrence and epidemiology of resistance to virginimycin and streptogramins. J. Antimicrob. Chemother. 43:171-176.		
50		16 Martinez J. L., A. Alonso, J. M. Gomez-Gomez, and F. Baquero. 1998. Quinolone resistance by mutations in chromosomal gyrase genes. Just the tip of the iceberg? J. Antimicrob. Chemother. 42:683-688		
		17 Cockerill III, F.R. 1999. Genetic methods for assessing antimicrobial resistance. Antimicrob. Agents. Chemother. 43:199-212.		
55		18 Casadewall, B. and P. Courvalin. 1999 Characterization of the <i>vanD</i> glycopeptide resistance gene cluster from <i>Enterococcus faecium</i> BM 4339. J. Bacteriol. 181:3644-3648.		
		19 Roberts, M.C. 1999. Genetic mobility and distribution of tetracycline resistance determinants. Ciba Found. Symp. 207:206-222.		
60		20 Huovinen, P., L. Sundström, G. Swedberg, and O. Sköld. 1995. Trimethoprim and sulfonamide resistance. Antimicrob. Agent Chemother. 39:279-289.		

Table 6. List of bacterial toxins selected for diagnostic purposes.

	Organism	Toxin	Accession number
5	<i>Actinobacillus actinomycetemcomitans</i>	Cytolethal distending toxin (<i>cdtA</i> , <i>cdtB</i> , <i>cdtC</i>)	AF006830
	<i>Actinomyces pyogenes</i>	Leukotoxin (<i>ltxA</i>)	M27399
	<i>Aeromonas hydrophila</i>	Hemolysin (pyolysin)	U84782
10		Aerolysin (<i>aerA</i>)	M16495
		Haemolysin (<i>hlyA</i>)	U81555
15	<i>Bacillus anthracis</i>	Cytotoxic enterotoxin (<i>alt</i>)	L77573
	<i>Bacillus cereus</i>	Anthrax toxin (<i>cya</i>)	M23179
		Enterotoxin (<i>bceT</i>)	D17312
			AF192766, AF192767
		Enterotoxigenic hemolysin BL	AJ237785
20	<i>Bacillus mycoides</i>	Non-haemolytic enterotoxins A,B and C (<i>nhe</i>)	Y19005
	<i>Bacillus pseudomycoides</i>	Hemolytic enterotoxin HBL	AJ243150 to AJ243153
	<i>Bacteroides fragilis</i>	Hemolytic enterotoxin HBL	AJ243154 to AJ243156
		Enterotoxin (<i>bftP</i>)	U67735
25		Matrix metalloprotease/enterotoxin (fragilysin)	S75941, AF038459
		Metalloprotease toxin-2	U90931
			AF081785
30	<i>Bordetella bronchiseptica</i>	Metalloprotease toxin-3	AF056297
		Adenylate cyclase hemolysin (<i>cyaA</i>)	Z37112, U22953
		Dermonecrotic toxin (<i>dnt</i>)	U59687
35	<i>Bordetella pertussis</i>	Pertussis toxin (S1 subunit, <i>tox</i>)	AB020025
			AJ006151
			AJ006153
			AJ006155
			AJ006157
			AJ006159
40			AJ007363
			M14378, M16494
			AJ007364
			M13223
			X16347
45		Adenyl cyclase (<i>cya</i>)	18323
	<i>Campylobacter jejuni</i>	Dermonecrotic toxin (<i>dnt</i>)	U10527
50	<i>Citrobacter freundii</i>	Cytolethal distending toxin (<i>cdtA</i> , <i>cdtB</i> , <i>cdtC</i>)	U51121
	<i>Clostridium botulinum</i>	Shiga-like toxin (<i>slt-IIcA</i>)	X67514, S53206
		Botulism toxin (BoNT) (A,B,E and F serotypes are neurotoxic for humans; the other serotypes have not been considered)	X52066, X52088
			X73423
			M30196
55			X70814
			X70819
			X71343
			Z11934
			X70817
60			M81186
			X70818
			X70815
			X62089
			X62683
			S76749
65			X81714
			X70816

Table 6. List of bacterial toxins selected for diagnostic purposes (continued).

Organism	Toxin	Accession number
5 <i>Clostridium botulinum</i> (continued)		X70820 X70281 L35496 M92906
10 <i>Clostridium difficile</i>	A toxin (enterotoxin) (<i>tcdA</i>) (<i>cdtA</i>)	AB012304 AF053400 Y12616
15 <i>Clostridium perfringens</i>	B toxin (cytotoxin) (<i>toxB</i>) (<i>cdtB</i>)	X51797 X17194 M30307 Z23277 X53138
20 <i>Clostridium perfringens</i>	Alpha (phospholipase C) (<i>cpa</i>)	L43545 L43546 L43547 L43548 X13608 X17300 D10248
25 <i>Clostridium perfringens</i>	Beta (dermonecrotic protein) (<i>cpb</i>)	L13198 X83275 L77965
30 <i>Clostridium perfringens</i>	Enterotoxin (<i>cpe</i>)	AJ000766 M98037 X81849 X71844 Y16009
35 <i>Clostridium perfringens</i>	Enterotoxin pseudogene (not expressed)	AF037328 AF037329 AF037330
40 <i>Clostridium perfringens</i>	Epsilon toxin (<i>etxD</i>)	M80837 M95206 X60694
45 <i>Clostridium perfringens</i>	Iota (Ia and Ib)	X73562
50 <i>Clostridium perfringens</i>	Lambda (metalloprotease)	D45904
55 <i>Clostridium sordellii</i>	Theta (perfringolysin O)	M36704
<i>Clostridium tetani</i>	Cytotoxin L	X82638
<i>Corynebacterium diphtheriae</i>	Tetanos toxin	X06214 X04436 X00703
<i>Corynebacterium pseudotuberculosis</i>	Diphtheriae toxin	
<i>Corynebacterium pseudotuberculosis</i>	Phospholipase C	A21336
55 <i>Eikenella corrodens</i>	lysine decarboxylase (<i>cadA</i>)	U89166
<i>Enterobacter cloacae</i>	Shiga-like toxin II	Z50754, U33502
<i>Enterococcus faecalis</i>	Cytolysin B (<i>cylB</i>)	M38052
<i>Escherichia coli</i> (EHEC)	Hemolysin toxin (<i>hlyA</i> and <i>ehxA</i>)	AF043471 X94129 X79839 X86087 AB011549 AF074613
60 <i>Escherichia coli</i> (EHEC)		

Table 6. List of bacterial toxins selected for diagnostic purposes (continued).

Organism	Toxin	Accession number
5 <i>Escherichia coli</i> (EHEC)	Shiga-like (Vero cytotoxin) (<i>stx</i>)	X81418, M36727 M14107, E03962 M10133, E03959 M12863, X07865 X81417, Y10775 X81416, Z50754 X81415, X67515 Z36900, AF043627 L11078, M19473 L04539, M17358 L11079, M19437 X65949, M24352 M21534, X07903 M29153, Z36899 Z37725 Z36901 X61283 AB017524 U72191 X61283 M17874 M17873 J01605 AB011677
10		
15		
20		
25 <i>Escherichia coli</i> (ETEC)	Enterotoxin (heat-labile) (<i>eltB</i>)	L11241 M58746 M29255 V00612 J01831 U03293 U04208 U89305
30	Enterotoxin (heat-stable) (<i>astA</i>) (<i>estA1</i>)	U42629
35 <i>Escherichia coli</i> (other)	Cytolethal-distending toxin (<i>cdt</i>) (3 genes)	U47048 AF056581 U53215 U07145 U80067 U80068 AF077938 AF077939 AF077940 AF077941 AF057703 X15127 M24199 X60035 U25452 U25443 U25446 U25449 X57775, Z28388 X51512 X52478 M30186 X14956 AF060869
40	Cytotoxic necrotizing factor 1 (<i>cnf1</i>)	
45 <i>Haemophilus ducreyi</i> <i>Helicobacter pylori</i>	Microcin 24 (<i>mtfS</i>) Autotransporter enterotoxin (<i>Per</i>) (cytotoxin) Cytolethal distending toxin (<i>cdtA</i> , <i>cdtB</i> , <i>cdtC</i>) Vacuolating toxin (<i>vacA</i>)	
50 <i>Legionella pneumophila</i> <i>Listeria monocytogenes</i>	Structural toxin protein (<i>rtxA</i>) Listeriolysin O (<i>lisA</i> , <i>hlyA</i>)	
55		
60 <i>Pasteurella multocida</i>	Mitogenic toxin (dermonecrotic toxin)	
<i>Proteus mirabilis</i> <i>Pseudomonas aeruginosa</i> <i>Salmonella typhimurium</i>	Hemolysin (<i>hpmA</i>) Cytotoxin (Enterotoxin A) Calmodulin-sensitive adenylate cyclase toxin (<i>cya</i>)	
65	Cytolysin (salmolysin) (<i>stxA</i>) Enterotoxin (<i>stn</i>)	U03842 L16014

Table 6. List of bacterial toxins selected for diagnostic purposes (continued).

	Organism	Toxin	Accession number
5	<i>Serratia marcescens</i>	Hemolysin (<i>shlA</i>)	M22618
	<i>Shigella dysenteriae</i> type 1	Shiga toxin (<i>stxA</i> and <i>stxB</i>)	X07903, M32511
			M19437
			M24352, M21947
10	<i>Shigella flexneri</i>	ShET2 enterotoxin (<i>senA</i>)	Z54211
			Z47381
15	<i>Shigella sonnei</i> <i>Sphingomonas paucimobilis</i> <i>Staphylococcus aureus</i>	Enterotoxin 1 (<i>set1A</i> and <i>set1B</i>)	U35656
		Hemolysin E (<i>hlyE</i> , <i>clyA</i> , <i>sheA</i>)	AF200955
		Shiga toxin (<i>stxA</i> and <i>stxB</i>)	AJ132761
		Beta-hemolysin (<i>hlyA</i>)	L01270
		Gamma-hemolysin (<i>hlg2</i>)	D42143 L01055
20		Enterotoxin	U93688
		Enterotoxin A (<i>sea</i>)	L22565, L22566 M18970
25		Enterotoxin B	M11118
		Enterotoxin C1 (<i>entC1</i>)	X05815
30		Enterotoxin C2 (<i>entC2</i>)	P34071
		Enterotoxin C3 (<i>entC3</i>)	X51661
		Enterotoxin D (<i>sed</i>)	M94872
35		Enterotoxin E	M21319
		Enterotoxin G (<i>seg</i>)	AF064773
40		Enterotoxin H (<i>seh</i>)	U11702
		Enterotoxin I (<i>sei</i>)	AF064774
		Enterotoxin J	AF053140
45		Exfoliative toxin A (ETA, Epidermolytic toxin A)	M17347 M17357 L25372, M20371
		Exfoliative toxin B (ETB)	M17348, M13775
50		Leukocidin R (F and S component, <i>lukF</i> and <i>lukS</i> ; Hemolysin B and C)	X64389, S53213 X72700 L01055
55		Toxic shock syndrome toxin 1 (TSST-1, alpha toxin, alpha hemolysin)	X01645 M90536 J02615 U93688
60	<i>Staphylococcus epidermidis</i>	Delta toxin (<i>hld</i>)	AF068634
	<i>Staphylococcus intermedius</i>	Enterotoxin 1	U91526
65		Leukocidin R (F and S component, <i>lukF</i> and <i>lukS</i> ; synergohymenotropic toxin)	X79188
		Pneumolysin	X52474

Table 6. List of bacterial toxins selected for diagnostic purposes (continued).

	Organism	Toxin	Accession number
5	<i>Streptococcus pyogenes</i>	<i>Streptococcus</i> pyrogenic exotoxin A (<i>speA</i>)	X61553 to X61573 X03929 U40453, M19350
		Pyrogenic exotoxin B (<i>speB</i>) M86905, M35110	U63134
10	<i>Vibrio cholerae</i>	Cholerae toxin (<i>ctxA</i> and <i>ctxB</i> subunits)	X00171 X76390 X58786 X58785, S55782 D30052 D30053 K02679 AF175708
15			
20		Accessory cholera enterotoxin (<i>ace</i>)	Z22569, AF175708
		Heat-stable enterotoxin (<i>sto</i>)	X74108, M85198 M97591, L03220
		<i>Zonula occludens</i> toxin (<i>zot</i>)	M83563, AF175708
25	<i>Vibrio parahaemolyticus</i>	Thermostable direct hemolysin (<i>tdh</i>)	S67841
	<i>Vibrio vulnificus</i>	Cytolysin (<i>vvhA</i>)	M34670
	<i>Yersinia enterocolitica</i>	Heat-stable enterotoxin (<i>yst</i>)	U09235, X65999
30		Heat-stable enterotoxin type B (<i>ystB</i>)	D88145
		Heat-stable enterotoxin type C (<i>ystC</i>)	D63578
	<i>Yersinia kristensenii</i>	Enterotoxin	X69218
	<i>Yersinia pestis</i>	Toxin	X92727
35			

Table 7. Origin of the nucleic acids and/or sequences in the sequence listing.

SEQ ID NO.		Archaeal, bacterial, fungal or parasitical species	SourceGene*	
5	1	<i>Acinetobacter baumannii</i>	This patent	tuf
	2	<i>Actinomyces meyeri</i>	This patent	tuf
	3	<i>Aerococcus viridans</i>	This patent	tuf
	4	<i>Achromobacter xylosoxidans</i> subsp. <i>denitrificans</i>	This patent	tuf
	5	<i>Anaerorhabdus furcosus</i>	This patent	tuf
10	6	<i>Bacillus anthracis</i>	This patent	tuf
	7	<i>Bacillus cereus</i>	This patent	tuf
	8	<i>Bacteroides distasonis</i>	This patent	tuf
	9	<i>Enterococcus casseliflavus</i>	This patent	tuf
15	10	<i>Staphylococcus saprophyticus</i>	This patent	tuf
	11	<i>Bacteroides ovatus</i>	This patent	tuf
	12	<i>Bartonella henselae</i>	This patent	tuf
	13	<i>Bifidobacterium adolescentis</i>	This patent	tuf
20	14	<i>Bifidobacterium dentium</i>	This patent	tuf
	15	<i>Brucella abortus</i>	This patent	tuf
	16	<i>Burkholderia cepacia</i>	This patent	tuf
	17	<i>Cedecea davisae</i>	This patent	tuf
25	18	<i>Cedecea neteri</i>	This patent	tuf
	19	<i>Cedecea lapagei</i>	This patent	tuf
	20	<i>Chlamydia pneumoniae</i>	This patent	tuf
	21	<i>Chlamydia psittaci</i>	This patent	tuf
30	22	<i>Chlamydia trachomatis</i>	This patent	tuf
	23	<i>Chryseobacterium meningosepticum</i>	This patent	tuf
	24	<i>Citrobacter amalonaticus</i>	This patent	tuf
	25	<i>Citrobacter braakii</i>	This patent	tuf
35	26	<i>Citrobacter koseri</i>	This patent	tuf
	27	<i>Citrobacter farneri</i>	This patent	tuf
	28	<i>Citrobacter freundii</i>	This patent	tuf
	29	<i>Citrobacter sedlakii</i>	This patent	tuf
40	30	<i>Citrobacter werkmanii</i>	This patent	tuf
	31	<i>Citrobacter youngae</i>	This patent	tuf
	32	<i>Clostridium perfringens</i>	This patent	tuf
	33	<i>Comamonas acidovorans</i>	This patent	tuf
45	34	<i>Corynebacterium bovis</i>	This patent	tuf
	35	<i>Corynebacterium cervicis</i>	This patent	tuf
	36	<i>Corynebacterium flavescens</i>	This patent	tuf
	37	<i>Corynebacterium kutscheri</i>	This patent	tuf
50	38	<i>Corynebacterium minutissimum</i>	This patent	tuf
	39	<i>Corynebacterium mycetoides</i>	This patent	tuf
	40	<i>Corynebacterium pseudogenitalium</i>	This patent	tuf
	41	<i>Corynebacterium renale</i>	This patent	tuf
55	42	<i>Corynebacterium ulcerans</i>	This patent	tuf
	43	<i>Corynebacterium urealyticum</i>	This patent	tuf
	44	<i>Corynebacterium xerosis</i>	This patent	tuf
	45	<i>Coxiella burnetii</i>	This patent	tuf
60	46	<i>Edwardsiella hoshinae</i>	This patent	tuf
	47	<i>Edwardsiella tarda</i>	This patent	tuf
	48	<i>Eikenella corrodens</i>	This patent	tuf
	49	<i>Enterobacter aerogenes</i>	This patent	tuf
65	50	<i>Enterobacter agglomerans</i>	This patent	tuf
	51	<i>Enterobacter amnigenus</i>	This patent	tuf
	52	<i>Enterobacter asburiae</i>	This patent	tuf
	53	<i>Enterobacter cancerogenus</i>	This patent	tuf
	54	<i>Enterobacter cloacae</i>	This patent	tuf
	55	<i>Enterobacter gergoviae</i>	This patent	tuf
	56	<i>Enterobacter hormaechei</i>	This patent	tuf
	57	<i>Enterobacter sakazakii</i>	This patent	tuf
	58	<i>Enterococcus casseliflavus</i>	This patent	tuf
	59	<i>Enterococcus cecorum</i>	This patent	tuf
	60	<i>Enterococcus dispar</i>	This patent	tuf
	61	<i>Enterococcus durans</i>	This patent	tuf

Table 7. Origin of the nucleic acids and/or sequences in the sequence listing (continued).

	SEQ ID NO.	Archaeal, bacterial, fungal or parasitical species	Source	Gene*
5	62	<i>Enterococcus faecalis</i>	This patent	<i>tuf</i>
	63	<i>Enterococcus faecalis</i>	This patent	<i>tuf</i>
	64	<i>Enterococcus faecium</i>	This patent	<i>tuf</i>
	65	<i>Enterococcus flavescens</i>	This patent	<i>tuf</i>
	66	<i>Enterococcus gallinarum</i>	This patent	<i>tuf</i>
10	67	<i>Enterococcus hirae</i>	This patent	<i>tuf</i>
	68	<i>Enterococcus mundtii</i>	This patent	<i>tuf</i>
	69	<i>Enterococcus pseudoavium</i>	This patent	<i>tuf</i>
	70	<i>Enterococcus raffinosus</i>	This patent	<i>tuf</i>
	71	<i>Enterococcus saccharolyticus</i>	This patent	<i>tuf</i>
15	72	<i>Enterococcus solitarius</i>	This patent	<i>tuf</i>
	73	<i>Enterococcus casseliflavus</i>	This patent	<i>tuf</i> (C)
	74	<i>Staphylococcus saprophyticus</i>	This patent	unknown
	75	<i>Enterococcus flavescens</i>	This patent	<i>tuf</i> (C)
	76	<i>Enterococcus gallinarum</i>	This patent	<i>tuf</i> (C)
20	77	<i>Ehrlichia canis</i>	This patent	<i>tuf</i>
	78	<i>Escherichia coli</i>	This patent	<i>tuf</i>
	79	<i>Escherichia fergusonii</i>	This patent	<i>tuf</i>
	80	<i>Escherichia hermannii</i>	This patent	<i>tuf</i>
	81	<i>Escherichia vulneris</i>	This patent	<i>tuf</i>
25	82	<i>Eubacterium lentum</i>	This patent	<i>tuf</i>
	83	<i>Eubacterium nodatum</i>	This patent	<i>tuf</i>
	84	<i>Ewingella americana</i>	This patent	<i>tuf</i>
	85	<i>Francisella tularensis</i>	This patent	<i>tuf</i>
	86	<i>Fusobacterium nucleatum</i> subsp. <i>polymorphum</i>	This patent	<i>tuf</i>
30	87	<i>Gemella haemolysans</i>	This patent	<i>tuf</i>
	88	<i>Gemella morbillorum</i>	This patent	<i>tuf</i>
	89	<i>Haemophilus actinomycetemcomitans</i>	This patent	<i>tuf</i>
	90	<i>Haemophilus aphrophilus</i>	This patent	<i>tuf</i>
	91	<i>Haemophilus ducreyi</i>	This patent	<i>tuf</i>
35	92	<i>Haemophilus haemolyticus</i>	This patent	<i>tuf</i>
	93	<i>Haemophilus parahaemolyticus</i>	This patent	<i>tuf</i>
	94	<i>Haemophilus parainfluenzae</i>	This patent	<i>tuf</i>
	95	<i>Haemophilus paraphrophilus</i>	This patent	<i>tuf</i>
	96	<i>Haemophilus segnis</i>	This patent	<i>tuf</i>
40	97	<i>Hafnia alvei</i>	This patent	<i>tuf</i>
	98	<i>Kingella kingae</i>	This patent	<i>tuf</i>
	99	<i>Klebsiella ornithinolytica</i>	This patent	<i>tuf</i>
	100	<i>Klebsiella oxytoca</i>	This patent	<i>tuf</i>
	101	<i>Klebsiella planticola</i>	This patent	<i>tuf</i>
45	102	<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	This patent	<i>tuf</i>
	103	<i>Klebsiella pneumoniae pneumoniae</i>	This patent	<i>tuf</i>
	104	<i>Klebsiella pneumoniae</i> subsp. <i>rhinoscleromatis</i>	This patent	<i>tuf</i>
	105	<i>Kluyvera ascorbata</i>	This patent	<i>tuf</i>
	106	<i>Kluyvera cryocrescens</i>	This patent	<i>tuf</i>
50	107	<i>Kluyvera georgiana</i>	This patent	<i>tuf</i>
	108	<i>Lactobacillus casei</i> subsp. <i>casei</i>	This patent	<i>tuf</i>
	109	<i>Lactococcus lactis</i> subsp. <i>lactis</i>	This patent	<i>tuf</i>
	110	<i>Leclercia adecarboxylata</i>	This patent	<i>tuf</i>
	111	<i>Legionella micdadei</i>	This patent	<i>tuf</i>
55	112	<i>Legionella pneumophila</i> subsp. <i>pneumophila</i>	This patent	<i>tuf</i>
	113	<i>Leminorella grimontii</i>	This patent	<i>tuf</i>
	114	<i>Leminorella richardii</i>	This patent	<i>tuf</i>
	115	<i>Leptospira interrogans</i>	This patent	<i>tuf</i>
	116	<i>Megamonas hypermegale</i>	This patent	<i>tuf</i>
60	117	<i>Mitsuokella multacidus</i>	This patent	<i>tuf</i>
	118	<i>Mobiluncus curtisii</i> subsp. <i>holmesii</i>	This patent	<i>tuf</i>
	119	<i>Moellerella wisconsensis</i>	This patent	<i>tuf</i>
	120	<i>Moraxella catarrhalis</i>	This patent	<i>tuf</i>
	121	<i>Morganella morganii</i> subsp. <i>morganii</i>	This patent	<i>tuf</i>
65	122	<i>Mycobacterium tuberculosis</i>	This patent	<i>tuf</i>

Table 7. Origin of the nucleic acids and/or sequences in the sequence listing (continued).

	SEQ ID NO.	Archaeal, bacterial, fungal or parasitical species	Source	Gene*
5	123	<i>Neisseria cinerea</i>	This patent	<i>tuf</i>
	124	<i>Neisseria elongata</i> subsp. <i>elongata</i>	This patent	<i>tuf</i>
	125	<i>Neisseria flavescens</i>	This patent	<i>tuf</i>
	126	<i>Neisseria gonorrhoeae</i>	This patent	<i>tuf</i>
	127	<i>Neisseria lactamica</i>	This patent	<i>tuf</i>
10	128	<i>Neisseria meningitidis</i>	This patent	<i>tuf</i>
	129	<i>Neisseria mucosa</i>	This patent	<i>tuf</i>
	130	<i>Neisseria sicca</i>	This patent	<i>tuf</i>
15	131	<i>Neisseria subflava</i>	This patent	<i>tuf</i>
	132	<i>Neisseria weaveri</i>	This patent	<i>tuf</i>
	133	<i>Ochrobactrum anthropi</i>	This patent	<i>tuf</i>
	134	<i>Pantoea agglomerans</i>	This patent	<i>tuf</i>
	135	<i>Pantoea dispersa</i>	This patent	<i>tuf</i>
20	136	<i>Pasteurella multocida</i>	This patent	<i>tuf</i>
	137	<i>Peptostreptococcus anaerobius</i>	This patent	<i>tuf</i>
	138	<i>Peptostreptococcus asaccharolyticus</i>	This patent	<i>tuf</i>
	139	<i>Peptostreptococcus prevotii</i>	This patent	<i>tuf</i>
	140	<i>Porphyromonas asaccharolytica</i>	This patent	<i>tuf</i>
25	141	<i>Porphyromonas gingivalis</i>	This patent	<i>tuf</i>
	142	<i>Pragia fontium</i>	This patent	<i>tuf</i>
	143	<i>Prevotella melaninogenica</i>	This patent	<i>tuf</i>
	144	<i>Prevotella oralis</i>	This patent	<i>tuf</i>
	145	<i>Propionibacterium acnes</i>	This patent	<i>tuf</i>
30	146	<i>Proteus mirabilis</i>	This patent	<i>tuf</i>
	147	<i>Proteus penneri</i>	This patent	<i>tuf</i>
	148	<i>Proteus vulgaris</i>	This patent	<i>tuf</i>
	149	<i>Providencia alcalifaciens</i>	This patent	<i>tuf</i>
	150	<i>Providencia rettgeri</i>	This patent	<i>tuf</i>
35	151	<i>Providencia rustigianii</i>	This patent	<i>tuf</i>
	152	<i>Providencia stuartii</i>	This patent	<i>tuf</i>
	153	<i>Pseudomonas aeruginosa</i>	This patent	<i>tuf</i>
	154	<i>Pseudomonas fluorescens</i>	This patent	<i>tuf</i>
	155	<i>Pseudomonas stutzeri</i>	This patent	<i>tuf</i>
40	156	<i>Psychrobacter phenylpyruvicum</i>	This patent	<i>tuf</i>
	157	<i>Rahnella aquatilis</i>	This patent	<i>tuf</i>
	158	<i>Salmonella choleraesuis</i> subsp. <i>arizonae</i>	This patent	<i>tuf</i>
	159	<i>Salmonella choleraesuis</i> subsp. <i>choleraesuis</i> serotype Choleraesuis	This patent	<i>tuf</i>
	160	<i>Salmonella choleraesuis</i> subsp. <i>diarizonae</i>	This patent	<i>tuf</i>
45	161	<i>Salmonella choleraesuis</i> subsp. <i>choleraesuis</i> serotype Heidelberg	This patent	<i>tuf</i>
	162	<i>Salmonella choleraesuis</i> subsp. <i>houtenae</i>	This patent	<i>tuf</i>
	163	<i>Salmonella choleraesuis</i> subsp. <i>indica</i>	This patent	<i>tuf</i>
	164	<i>Salmonella choleraesuis</i> subsp. <i>salamae</i>	This patent	<i>tuf</i>
	165	<i>Salmonella choleraesuis</i> subsp. <i>choleraesuis</i> serotype Typhi	This patent	<i>tuf</i>
50	166	<i>Serratia fonticola</i>	This patent	<i>tuf</i>
	167	<i>Serratia liquefaciens</i>	This patent	<i>tuf</i>
	168	<i>Serratia marcescens</i>	This patent	<i>tuf</i>
	169	<i>Serratia odorifera</i>	This patent	<i>tuf</i>
	170	<i>Serratia plymuthica</i>	This patent	<i>tuf</i>
55	171	<i>Serratia rubidaea</i>	This patent	<i>tuf</i>
	172	<i>Shigella boydii</i>	This patent	<i>tuf</i>
	173	<i>Shigella dysenteriae</i>	This patent	<i>tuf</i>
	174	<i>Shigella flexneri</i>	This patent	<i>tuf</i>
	175	<i>Shigella sonnei</i>	This patent	<i>tuf</i>
60	176	<i>Staphylococcus aureus</i>	This patent	<i>tuf</i>
	177	<i>Staphylococcus aureus</i>	This patent	<i>tuf</i>
	178	<i>Staphylococcus aureus</i>	This patent	<i>tuf</i>
	179	<i>Staphylococcus aureus</i>	This patent	<i>tuf</i>
	180	<i>Staphylococcus aureus</i> subsp. <i>aureus</i>	This patent	<i>tuf</i>
65	181	<i>Staphylococcus auricularis</i>	This patent	<i>tuf</i>
	182	<i>Staphylococcus capitis</i> subsp. <i>capitis</i>	This patent	<i>tuf</i>

Table 7. Origin of the nucleic acids and/or sequences in the sequence listing (continued).

	SEQ ID NO.	Archaeal, bacterial, fungal or parasitical species	Source	Gene*
5	183	<i>Macrococcus caseolyticus</i>	This patent	<i>tuf</i>
	184	<i>Staphylococcus cohnii</i> subsp. <i>cohnii</i>	This patent	<i>tuf</i>
	185	<i>Staphylococcus epidermidis</i>	This patent	<i>tuf</i>
	186	<i>Staphylococcus haemolyticus</i>	This patent	<i>tuf</i>
	187	<i>Staphylococcus warneri</i>	This patent	<i>tuf</i>
10	188	<i>Staphylococcus haemolyticus</i>	This patent	<i>tuf</i>
	189	<i>Staphylococcus haemolyticus</i>	This patent	<i>tuf</i>
	190	<i>Staphylococcus haemolyticus</i>	This patent	<i>tuf</i>
	191	<i>Staphylococcus hominis</i> subsp. <i>hominis</i>	This patent	<i>tuf</i>
	192	<i>Staphylococcus warneri</i>	This patent	<i>tuf</i>
15	193	<i>Staphylococcus hominis</i>	This patent	<i>tuf</i>
	194	<i>Staphylococcus hominis</i>	This patent	<i>tuf</i>
	195	<i>Staphylococcus hominis</i>	This patent	<i>tuf</i>
	196	<i>Staphylococcus hominis</i>	This patent	<i>tuf</i>
	197	<i>Staphylococcus lugdunensis</i>	This patent	<i>tuf</i>
20	198	<i>Staphylococcus saprophyticus</i>	This patent	<i>tuf</i>
	199	<i>Staphylococcus saprophyticus</i>	This patent	<i>tuf</i>
	200	<i>Staphylococcus saprophyticus</i>	This patent	<i>tuf</i>
	201	<i>Staphylococcus sciuri</i> subsp. <i>sciuri</i>	This patent	<i>tuf</i>
	202	<i>Staphylococcus warneri</i>	This patent	<i>tuf</i>
25	203	<i>Staphylococcus warneri</i>	This patent	<i>tuf</i>
	204	<i>Bifidobacterium longum</i>	This patent	<i>tuf</i>
	205	<i>Stenotrophomonas maltophilia</i>	This patent	<i>tuf</i>
	206	<i>Streptococcus acidominimus</i>	This patent	<i>tuf</i>
	207	<i>Streptococcus agalactiae</i>	This patent	<i>tuf</i>
30	208	<i>Streptococcus agalactiae</i>	This patent	<i>tuf</i>
	209	<i>Streptococcus agalactiae</i>	This patent	<i>tuf</i>
	210	<i>Streptococcus agalactiae</i>	This patent	<i>tuf</i>
	211	<i>Streptococcus anginosus</i>	This patent	<i>tuf</i>
	212	<i>Streptococcus bovis</i>	This patent	<i>tuf</i>
35	213	<i>Streptococcus anginosus</i>	This patent	<i>tuf</i>
	214	<i>Streptococcus cricetus</i>	This patent	<i>tuf</i>
	215	<i>Streptococcus cristatus</i>	This patent	<i>tuf</i>
	216	<i>Streptococcus downei</i>	This patent	<i>tuf</i>
	217	<i>Streptococcus dysgalactiae</i>	This patent	<i>tuf</i>
40	218	<i>Streptococcus equi</i> subsp. <i>equi</i>	This patent	<i>tuf</i>
	219	<i>Streptococcus ferus</i>	This patent	<i>tuf</i>
	220	<i>Streptococcus gordonii</i>	This patent	<i>tuf</i>
	221	<i>Streptococcus anginosus</i>	This patent	<i>tuf</i>
	222	<i>Streptococcus macacae</i>	This patent	<i>tuf</i>
45	223	<i>Streptococcus gordonii</i>	This patent	<i>tuf</i>
	224	<i>Streptococcus mutans</i>	This patent	<i>tuf</i>
	225	<i>Streptococcus parasanguinis</i>	This patent	<i>tuf</i>
	226	<i>Streptococcus rattii</i>	This patent	<i>tuf</i>
	227	<i>Streptococcus sanguinis</i>	This patent	<i>tuf</i>
50	228	<i>Streptococcus sobrinus</i>	This patent	<i>tuf</i>
	229	<i>Streptococcus suis</i>	This patent	<i>tuf</i>
	230	<i>Streptococcus uberis</i>	This patent	<i>tuf</i>
	231	<i>Streptococcus vestibularis</i>	This patent	<i>tuf</i>
	232	<i>Tatumella ptyseos</i>	This patent	<i>tuf</i>
55	233	<i>Trabulsiella guamensis</i>	This patent	<i>tuf</i>
	234	<i>Veillonella parvula</i>	This patent	<i>tuf</i>
	235	<i>Yersinia enterocolitica</i>	This patent	<i>tuf</i>
	236	<i>Yersinia frederiksenii</i>	This patent	<i>tuf</i>
	237	<i>Yersinia intermedia</i>	This patent	<i>tuf</i>
60	238	<i>Yersinia pestis</i>	This patent	<i>tuf</i>
	239	<i>Yersinia pseudotuberculosis</i>	This patent	<i>tuf</i>
	240	<i>Yersinia rohdei</i>	This patent	<i>tuf</i>
	241	<i>Yokenella regensburgei</i>	This patent	<i>tuf</i>
	242	<i>Achromobacter xylosoxidans</i> subsp. <i>denitrificans</i>	This patent	<i>atpD</i>
65	243	<i>Acinetobacter baumannii</i>	This patent	<i>atpD</i>
	244	<i>Acinetobacter twoffii</i>	This patent	<i>atpD</i>

Table 7. Origin of the nucleic acids and/or sequences in the sequence listing (continued).

	SEQ ID NO.	Archaeal, bacterial, fungal or parasitical species	Source	Gene*
5	245	<i>Staphylococcus saprophyticus</i>	This patent	<i>atpD</i>
	246	<i>Alcaligenes faecalis</i> subsp. <i>faecalis</i>	This patent	<i>atpD</i>
	247	<i>Bacillus anthracis</i>	This patent	<i>atpD</i>
	248	<i>Bacillus cereus</i>	This patent	<i>atpD</i>
	249	<i>Bacteroides distasonis</i>	This patent	<i>atpD</i>
10	250	<i>Bacteroides ovatus</i>	This patent	<i>atpD</i>
	251	<i>Leclercia adecarboxylata</i>	This patent	<i>atpD</i>
	252	<i>Stenotrophomonas maltophilia</i>	This patent	<i>atpD</i>
15	253	<i>Bartonella henselae</i>	This patent	<i>atpD</i>
	254	<i>Bifidobacterium adolescentis</i>	This patent	<i>atpD</i>
	255	<i>Brucella abortus</i>	This patent	<i>atpD</i>
	256	<i>Cedecea davisae</i>	This patent	<i>atpD</i>
	257	<i>Cedecea lapagei</i>	This patent	<i>atpD</i>
20	258	<i>Cedecea neteri</i>	This patent	<i>atpD</i>
	259	<i>Chryseobacterium meningosepticum</i>	This patent	<i>atpD</i>
	260	<i>Citrobacter amalonaticus</i>	This patent	<i>atpD</i>
	261	<i>Citrobacter braakii</i>	This patent	<i>atpD</i>
	262	<i>Citrobacter koseri</i>	This patent	<i>atpD</i>
25	263	<i>Citrobacter farmeri</i>	This patent	<i>atpD</i>
	264	<i>Citrobacter freundii</i>	This patent	<i>atpD</i>
	265	<i>Citrobacter koseri</i>	This patent	<i>atpD</i>
	266	<i>Citrobacter sedlakii</i>	This patent	<i>atpD</i>
	267	<i>Citrobacter werkmanii</i>	This patent	<i>atpD</i>
30	268	<i>Citrobacter youngae</i>	This patent	<i>atpD</i>
	269	<i>Clostridium innocuum</i>	This patent	<i>atpD</i>
	270	<i>Clostridium perfringens</i>	This patent	<i>atpD</i>
	272	<i>Corynebacterium diphtheriae</i>	This patent	<i>atpD</i>
	273	<i>Corynebacterium pseudodiphtheriticum</i>	This patent	<i>atpD</i>
35	274	<i>Corynebacterium ulcerans</i>	This patent	<i>atpD</i>
	275	<i>Corynebacterium urealyticum</i>	This patent	<i>atpD</i>
	276	<i>Coxiella burnetii</i>	This patent	<i>atpD</i>
	277	<i>Edwardsiella hoshinae</i>	This patent	<i>atpD</i>
	278	<i>Edwardsiella tarda</i>	This patent	<i>atpD</i>
40	279	<i>Eikenella corrodens</i>	This patent	<i>atpD</i>
	280	<i>Enterobacter agglomerans</i>	This patent	<i>atpD</i>
	281	<i>Enterobacter amnigenus</i>	This patent	<i>atpD</i>
	282	<i>Enterobacter asburiae</i>	This patent	<i>atpD</i>
	283	<i>Enterobacter cancerogenus</i>	This patent	<i>atpD</i>
45	284	<i>Enterobacter cloacae</i>	This patent	<i>atpD</i>
	285	<i>Enterobacter gergoviae</i>	This patent	<i>atpD</i>
	286	<i>Enterobacter hormaechei</i>	This patent	<i>atpD</i>
	287	<i>Enterobacter sakazakii</i>	This patent	<i>atpD</i>
	288	<i>Enterococcus avium</i>	This patent	<i>atpD</i>
50	289	<i>Enterococcus casseliflavus</i>	This patent	<i>atpD</i>
	290	<i>Enterococcus durans</i>	This patent	<i>atpD</i>
	291	<i>Enterococcus faecalis</i>	This patent	<i>atpD</i>
	292	<i>Enterococcus faecium</i>	This patent	<i>atpD</i>
	293	<i>Enterococcus gallinarum</i>	This patent	<i>atpD</i>
55	294	<i>Enterococcus saccharolyticus</i>	This patent	<i>atpD</i>
	295	<i>Escherichia fergusonii</i>	This patent	<i>atpD</i>
	296	<i>Escherichia hermannii</i>	This patent	<i>atpD</i>
	297	<i>Escherichia vulneris</i>	This patent	<i>atpD</i>
	298	<i>Eubacterium lentum</i>	This patent	<i>atpD</i>
60	299	<i>Ewingella americana</i>	This patent	<i>atpD</i>
	300	<i>Francisella tularensis</i>	This patent	<i>atpD</i>
	301	<i>Fusobacterium gonidiaformans</i>	This patent	<i>atpD</i>
	302	<i>Fusobacterium necrophorum</i> subsp. <i>necrophorum</i>	This patent	<i>atpD</i>
	303	<i>Fusobacterium nucleatum</i> subsp. <i>polymorphum</i>	This patent	<i>atpD</i>
65	304	<i>Gardnerella vaginalis</i>	This patent	<i>atpD</i>
	305	<i>Gemella haemolysans</i>	This patent	<i>atpD</i>
	306	<i>Gemella morbillorum</i>	This patent	<i>atpD</i>

Table 7. Origin of the nucleic acids and/ r sequences in the sequence listing (continued).

	SEQ ID NO.	Archaeal, bacterial, fungal or parasitcal species	Source	Gene*
5	307	<i>Haemophilus ducreyi</i>	This patent	<i>atpD</i>
	308	<i>Haemophilus haemolyticus</i>	This patent	<i>atpD</i>
	309	<i>Haemophilus parahaemolyticus</i>	This patent	<i>atpD</i>
	310	<i>Haemophilus parainfluenzae</i>	This patent	<i>atpD</i>
	311	<i>Hafnia alvei</i>	This patent	<i>atpD</i>
10	312	<i>Kingella kingae</i>	This patent	<i>atpD</i>
	313	<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	This patent	<i>atpD</i>
	314	<i>Klebsiella ornithinolytica</i>	This patent	<i>atpD</i>
	315	<i>Klebsiella oxytoca</i>	This patent	<i>atpD</i>
	316	<i>Klebsiella planticola</i>	This patent	<i>atpD</i>
15	317	<i>Klebsiella pneumoniae</i> subsp. <i>pneumoniae</i>	This patent	<i>atpD</i>
	318	<i>Kluyvera ascorbata</i>	This patent	<i>atpD</i>
	319	<i>Kluyvera cryocrescens</i>	This patent	<i>atpD</i>
	320	<i>Kluyvera georgiana</i>	This patent	<i>atpD</i>
	321	<i>Lactobacillus acidophilus</i>	This patent	<i>atpD</i>
20	322	<i>Legionella pneumophila</i> subsp. <i>pneumophila</i>	This patent	<i>atpD</i>
	323	<i>Leminorella grimontii</i>	This patent	<i>atpD</i>
	324	<i>Listeria monocytogenes</i>	This patent	<i>atpD</i>
	325	<i>Micrococcus lylae</i>	This patent	<i>atpD</i>
	326	<i>Moellerella wisconsensis</i>	This patent	<i>atpD</i>
25	327	<i>Moraxella catarrhalis</i>	This patent	<i>atpD</i>
	328	<i>Moraxella osloensis</i>	This patent	<i>atpD</i>
	329	<i>Morganella morganii</i> subsp. <i>morganii</i>	This patent	<i>atpD</i>
	330	<i>Pantoea agglomerans</i>	This patent	<i>atpD</i>
	331	<i>Pantoea dispersa</i>	This patent	<i>atpD</i>
30	332	<i>Pasteurella multocida</i>	This patent	<i>atpD</i>
	333	<i>Pragia fontium</i>	This patent	<i>atpD</i>
	334	<i>Proteus mirabilis</i>	This patent	<i>atpD</i>
	335	<i>Proteus vulgaris</i>	This patent	<i>atpD</i>
	336	<i>Providencia alcalifaciens</i>	This patent	<i>atpD</i>
35	337	<i>Providencia rettgeri</i>	This patent	<i>atpD</i>
	338	<i>Providencia rustigianii</i>	This patent	<i>atpD</i>
	339	<i>Providencia stuartii</i>	This patent	<i>atpD</i>
	340	<i>Psychrobacter phenylpyruvicum</i>	This patent	<i>atpD</i>
	341	<i>Rahnella aquatilis</i>	This patent	<i>atpD</i>
40	342	<i>Salmonella choleraesuis</i> subsp. <i>arizonae</i>	This patent	<i>atpD</i>
	343	<i>Salmonella choleraesuis</i> subsp. <i>choleraesuis</i> serotype Choleraesuis	This patent	<i>atpD</i>
	344	<i>Salmonella choleraesuis</i> subsp. <i>diarizonae</i>	This patent	<i>atpD</i>
	345	<i>Salmonella choleraesuis</i> subsp. <i>houtenae</i>	This patent	<i>atpD</i>
45	346	<i>Salmonella choleraesuis</i> subsp. <i>indica</i>	This patent	<i>atpD</i>
	347	<i>Salmonella choleraesuis</i> subsp. <i>choleraesuis</i> serotype Paratyphi A	This patent	<i>atpD</i>
	348	<i>Salmonella choleraesuis</i> subsp. <i>choleraesuis</i> serotype Paratyphi B	This patent	<i>atpD</i>
50	349	<i>Salmonella choleraesuis</i> subsp. <i>salamae</i>	This patent	<i>atpD</i>
	350	<i>Salmonella choleraesuis</i> subsp. <i>choleraesuis</i> serotype Typhi	This patent	<i>atpD</i>
	351	<i>Salmonella choleraesuis</i> subsp. <i>choleraesuis</i> serotype Typhimurium	This patent	<i>atpD</i>
	352	<i>Salmonella choleraesuis</i> subsp. <i>choleraesuis</i> serotype Virchow	This patent	<i>atpD</i>
55	353	<i>Serratia ficaria</i>	This patent	<i>atpD</i>
	354	<i>Serratia fonticola</i>	This patent	<i>atpD</i>
	355	<i>Serratia grimesii</i>	This patent	<i>atpD</i>
	356	<i>Serratia liquefaciens</i>	This patent	<i>atpD</i>
60	357	<i>Serratia marcescens</i>	This patent	<i>atpD</i>
	358	<i>Serratia odorifera</i>	This patent	<i>atpD</i>
	359	<i>Serratia plymuthica</i>	This patent	<i>atpD</i>
	360	<i>Serratia rubidaea</i>	This patent	<i>atpD</i>
	361	<i>Pseudomonas putida</i>	This patent	<i>atpD</i>
65	362	<i>Shigella boydii</i>	This patent	<i>atpD</i>
	363	<i>Shigella dysenteriae</i>	This patent	<i>atpD</i>

Table 7. Origin of the nucleic acids and/or sequences in the sequence listing (continued).

SEQ ID NO.	Archaeal, bacterial, fungal or parasitical species	SourceGene*
5	364 <i>Shigella flexneri</i>	This patent
	365 <i>Shigella sonnei</i>	This patent
	366 <i>Staphylococcus aureus</i>	This patent
	367 <i>Staphylococcus auricularis</i>	This patent
	368 <i>Staphylococcus capitis</i> subsp. <i>capitis</i>	This patent
10	369 <i>Staphylococcus cohnii</i> subsp. <i>cohnii</i>	This patent
	370 <i>Staphylococcus epidermidis</i>	This patent
	371 <i>Staphylococcus haemolyticus</i>	This patent
	372 <i>Staphylococcus hominis</i> subsp. <i>hominis</i>	This patent
	373 <i>Staphylococcus hominis</i>	This patent
15	374 <i>Staphylococcus lugdunensis</i>	This patent
	375 <i>Staphylococcus saprophyticus</i>	This patent
	376 <i>Staphylococcus simulans</i>	This patent
	377 <i>Staphylococcus warneri</i>	This patent
	378 <i>Streptococcus acidominimus</i>	This patent
20	379 <i>Streptococcus agalactiae</i>	This patent
	380 <i>Streptococcus agalactiae</i>	This patent
	381 <i>Streptococcus agalactiae</i>	This patent
	382 <i>Streptococcus agalactiae</i>	This patent
	383 <i>Streptococcus agalactiae</i>	This patent
25	384 <i>Streptococcus dysgalactiae</i>	This patent
	385 <i>Streptococcus equi</i> subsp. <i>equi</i>	This patent
	386 <i>Streptococcus anginosus</i>	This patent
	387 <i>Streptococcus salivarius</i>	This patent
	388 <i>Streptococcus suis</i>	This patent
30	389 <i>Streptococcus uberis</i>	This patent
	390 <i>Tatumella pyoseos</i>	This patent
	391 <i>Trabulsiella guamensis</i>	This patent
	392 <i>Yersinia bercovieri</i>	This patent
	393 <i>Yersinia enterocolitica</i>	This patent
35	394 <i>Yersinia frederiksenii</i>	This patent
	395 <i>Yersinia intermedia</i>	This patent
	396 <i>Yersinia pseudotuberculosis</i>	This patent
	397 <i>Yersinia rohdei</i>	This patent
	398 <i>Yokenella regensburgei</i>	This patent
40	399 <i>Yarrowia lipolytica</i>	This patent
	400 <i>Absidia corymbifera</i>	This patent
	401 <i>Alternaria alternata</i>	This patent
	402 <i>Aspergillus flavus</i>	This patent
	403 <i>Aspergillus fumigatus</i>	This patent
45	404 <i>Aspergillus fumigatus</i>	This patent
	405 <i>Aspergillus niger</i>	This patent
	406 <i>Blastoschizomyces capitatus</i>	This patent
	407 <i>Candida albicans</i>	This patent
	408 <i>Candida albicans</i>	This patent
50	409 <i>Candida albicans</i>	This patent
	410 <i>Candida albicans</i>	This patent
	411 <i>Candida albicans</i>	This patent
	412 <i>Candida dubliniensis</i>	This patent
	413 <i>Candida catenulata</i>	This patent
55	414 <i>Candida dubliniensis</i>	This patent
	415 <i>Candida dubliniensis</i>	This patent
	416 <i>Candida famata</i>	This patent
	417 <i>Candida glabrata</i>	WO98/20157
	418 <i>Candida guilliermondii</i>	This patent
60	419 <i>Candida haemulonii</i>	This patent
	420 <i>Candida inconspicua</i>	This patent
	421 <i>Candida kefyr</i>	This patent
	422 <i>Candida krusei</i>	WO98/20157
	423 <i>Candida lambica</i>	This patent
65	424 <i>Candida lusitanae</i>	This patent
	425 <i>Candida norvegensis</i>	This patent

Table 7. Origin of the nucleic acids and/or sequences in the sequence listing (continued).

	SEQ ID NO.	Archaeal, bacterial, fungal or parasitological species	Source	Gene*
5	426	<i>Candida parapsilosis</i>	WO98/20157	<i>tuf</i> (EF-1)
	427	<i>Candida rugosa</i>	This patent	<i>tuf</i> (EF-1)
	428	<i>Candida sphaerica</i>	This patent	<i>tuf</i> (EF-1)
	429	<i>Candida tropicalis</i>	WO98/20157	<i>tuf</i> (EF-1)
	430	<i>Candida utilis</i>	This patent	<i>tuf</i> (EF-1)
10	431	<i>Candida viswanathii</i>	This patent	<i>tuf</i> (EF-1)
	432	<i>Candida zeylanoides</i>	This patent	<i>tuf</i> (EF-1)
	433	<i>Coccidioides immitis</i>	This patent	<i>tuf</i> (EF-1)
15	434	<i>Cryptococcus albidus</i>	This patent	<i>tuf</i> (EF-1)
	435	<i>Exophiala jeanselmei</i>	This patent	<i>tuf</i> (EF-1)
	436	<i>Fusarium oxysporum</i>	This patent	<i>tuf</i> (EF-1)
	437	<i>Geotrichum</i> sp.	This patent	<i>tuf</i> (EF-1)
	438	<i>Histoplasma capsulatum</i>	This patent	<i>tuf</i> (EF-1)
20	439	<i>Issatchenkia orientalis</i> Kudrjanzev	This patent	<i>tuf</i> (EF-1)
	440	<i>Malassezia furfur</i>	This patent	<i>tuf</i> (EF-1)
	441	<i>Malassezia pachydermatis</i>	This patent	<i>tuf</i> (EF-1)
	442	<i>Malbranchea filamentosa</i>	This patent	<i>tuf</i> (EF-1)
	443	<i>Metschnikowia pulcherrima</i>	This patent	<i>tuf</i> (EF-1)
25	444	<i>Paecilomyces lilacinus</i>	This patent	<i>tuf</i> (EF-1)
	445	<i>Paracoccidioides brasiliensis</i>	This patent	<i>tuf</i> (EF-1)
	446	<i>Penicillium marneffei</i>	This patent	<i>tuf</i> (EF-1)
	447	<i>Pichia anomala</i>	This patent	<i>tuf</i> (EF-1)
	448	<i>Pichia anomala</i>	This patent	<i>tuf</i> (EF-1)
30	449	<i>Pseudallescheria boydii</i>	This patent	<i>tuf</i> (EF-1)
	450	<i>Rhizopus oryzae</i>	This patent	<i>tuf</i> (EF-1)
	451	<i>Rhodotorula minuta</i>	This patent	<i>tuf</i> (EF-1)
	452	<i>Sporobolomyces salmonicolor</i>	This patent	<i>tuf</i> (EF-1)
	453	<i>Sporothrix schenckii</i>	This patent	<i>tuf</i> (EF-1)
35	454	<i>Stephanoascus ciferrii</i>	This patent	<i>tuf</i> (EF-1)
	455	<i>Trichophyton mentagrophytes</i>	This patent	<i>tuf</i> (EF-1)
	456	<i>Trichosporon cutaneum</i>	This patent	<i>tuf</i> (EF-1)
	457	<i>Wangiella dermatitidis</i>	This patent	<i>tuf</i> (EF-1)
	458	<i>Aspergillus fumigatus</i>	This patent	<i>atpD</i>
40	459	<i>Blastoschizomyces capitatus</i>	This patent	<i>atpD</i>
	460	<i>Candida albicans</i>	This patent	<i>atpD</i>
	461	<i>Candida dubliniensis</i>	This patent	<i>atpD</i>
	462	<i>Candida famata</i>	This patent	<i>atpD</i>
	463	<i>Candida glabrata</i>	This patent	<i>atpD</i>
45	464	<i>Candida guilliermondii</i>	This patent	<i>atpD</i>
	465	<i>Candida haemulonii</i>	This patent	<i>atpD</i>
	466	<i>Candida inconspicua</i>	This patent	<i>atpD</i>
	467	<i>Candida kefyr</i>	This patent	<i>atpD</i>
	468	<i>Candida krusei</i>	This patent	<i>atpD</i>
50	469	<i>Candida lambica</i>	This patent	<i>atpD</i>
	470	<i>Candida lusitanae</i>	This patent	<i>atpD</i>
	471	<i>Candida norvegensis</i>	This patent	<i>atpD</i>
	472	<i>Candida parapsilosis</i>	This patent	<i>atpD</i>
	473	<i>Candida rugosa</i>	This patent	<i>atpD</i>
55	474	<i>Candida sphaerica</i>	This patent	<i>atpD</i>
	475	<i>Candida tropicalis</i>	This patent	<i>atpD</i>
	476	<i>Candida utilis</i>	This patent	<i>atpD</i>
	477	<i>Candida viswanathii</i>	This patent	<i>atpD</i>
	478	<i>Candida zeylanoides</i>	This patent	<i>atpD</i>
60	479	<i>Coccidioides immitis</i>	This patent	<i>atpD</i>
	480	<i>Cryptococcus albidus</i>	This patent	<i>atpD</i>
	481	<i>Fusarium oxysporum</i>	This patent	<i>atpD</i>
	482	<i>Geotrichum</i> sp.	This patent	<i>atpD</i>
	483	<i>Histoplasma capsulatum</i>	This patent	<i>atpD</i>
65	484	<i>Malassezia furfur</i>	This patent	<i>atpD</i>
	485	<i>Malassezia pachydermatis</i>	This patent	<i>atpD</i>
	486	<i>Metschnikowia pulcherrima</i>	This patent	<i>atpD</i>
	487	<i>Penicillium marneffei</i>	This patent	<i>atpD</i>

Table 7. Origin of the nucleic acids and/or sequences in the sequence listing (continued).

	SEQ ID NO.	Archaeal, bacterial, fungal or parasitical species	Source	Gene*
5	488	<i>Pichia anomala</i>	This patent	<i>atpD</i>
	489	<i>Pichia anomala</i>	This patent	<i>atpD</i>
	490	<i>Rhodotorula minuta</i>	This patent	<i>atpD</i>
	491	<i>Rhodotorula mucilaginosa</i>	This patent	<i>atpD</i>
	492	<i>Sporobolomyces salmonicolor</i>	This patent	<i>atpD</i>
10	493	<i>Sporothrix schenckii</i>	This patent	<i>atpD</i>
	494	<i>Stephanoascus ciferrii</i>	This patent	<i>atpD</i>
	495	<i>Trichophyton mentagrophytes</i>	This patent	<i>atpD</i>
	496	<i>Wangiella dermatitidis</i>	This patent	<i>atpD</i>
15	497	<i>Yarrowia lipolytica</i>	This patent	<i>atpD</i>
	498	<i>Aspergillus fumigatus</i>	This patent	<i>tuf</i> (M)
	499	<i>Blastoschizomyces capitatus</i>	This patent	<i>tuf</i> (M)
	500	<i>Candida rugosa</i>	This patent	<i>tuf</i> (M)
20	501	<i>Coccidioides immitis</i>	This patent	<i>tuf</i> (M)
	502	<i>Fusarium oxysporum</i>	This patent	<i>tuf</i> (M)
	503	<i>Histoplasma capsulatum</i>	This patent	<i>tuf</i> (M)
	504	<i>Paracoccidioides brasiliensis</i>	This patent	<i>tuf</i> (M)
25	505	<i>Penicillium marneffei</i>	This patent	<i>tuf</i> (M)
	506	<i>Pichia anomala</i>	This patent	<i>tuf</i> (M)
	507	<i>Trichophyton mentagrophytes</i>	This patent	<i>tuf</i> (M)
	508	<i>Yarrowia lipolytica</i>	This patent	<i>tuf</i> (M)
30	509	<i>Babesia bigemina</i>	This patent	<i>tuf</i> (EF-1)
	510	<i>Babesia bovis</i>	This patent	<i>tuf</i> (EF-1)
	511	<i>Crithidia fasciculata</i>	This patent	<i>tuf</i> (EF-1)
	512	<i>Entamoeba histolytica</i>	This patent	<i>tuf</i> (EF-1)
35	513	<i>Giardia lamblia</i>	This patent	<i>tuf</i> (EF-1)
	514	<i>Leishmania tropica</i>	This patent	<i>tuf</i> (EF-1)
	515	<i>Leishmania aethiopica</i>	This patent	<i>tuf</i> (EF-1)
	516	<i>Leishmania tropica</i>	This patent	<i>tuf</i> (EF-1)
40	517	<i>Leishmania donovani</i>	This patent	<i>tuf</i> (EF-1)
	518	<i>Leishmania infantum</i>	This patent	<i>tuf</i> (EF-1)
	519	<i>Leishmania enriettii</i>	This patent	<i>tuf</i> (EF-1)
	520	<i>Leishmania gerbilli</i>	This patent	<i>tuf</i> (EF-1)
45	521	<i>Leishmania hertigi</i>	This patent	<i>tuf</i> (EF-1)
	522	<i>Leishmania major</i>	This patent	<i>tuf</i> (EF-1)
	523	<i>Leishmania amazonensis</i>	This patent	<i>tuf</i> (EF-1)
	524	<i>Leishmania mexicana</i>	This patent	<i>tuf</i> (EF-1)
50	525	<i>Leishmania tarentolae</i>	This patent	<i>tuf</i> (EF-1)
	526	<i>Leishmania tropica</i>	This patent	<i>tuf</i> (EF-1)
	527	<i>Neospora caninum</i>	This patent	<i>tuf</i> (EF-1)
	528	<i>Trichomonas vaginalis</i>	This patent	<i>tuf</i> (EF-1)
55	529	<i>Trypanosoma brucei</i> subsp. <i>brucei</i>	This patent	<i>tuf</i> (EF-1)
	530	<i>Crithidia fasciculata</i>	This patent	<i>atpD</i>
	531	<i>Leishmania tropica</i>	This patent	<i>atpD</i>
	532	<i>Leishmania aethiopica</i>	This patent	<i>atpD</i>
60	533	<i>Leishmania donovani</i>	This patent	<i>atpD</i>
	534	<i>Leishmania infantum</i>	This patent	<i>atpD</i>
	535	<i>Leishmania gerbilli</i>	This patent	<i>atpD</i>
	536	<i>Leishmania hertigi</i>	This patent	<i>atpD</i>
65	537	<i>Leishmania major</i>	This patent	<i>atpD</i>
	538	<i>Leishmania amazonensis</i>	This patent	<i>atpD</i>
	607	<i>Enterococcus faecalis</i>	WO98/20157	<i>tuf</i>
	608	<i>Enterococcus faecium</i>	WO98/20157	<i>tuf</i>
65	609	<i>Enterococcus gallinarum</i>	WO98/20157	<i>tuf</i>
	610	<i>Haemophilus influenzae</i>	WO98/20157	<i>tuf</i>
	611	<i>Staphylococcus epidermidis</i>	WO98/20157	<i>tuf</i>
	612	<i>Salmonella choleraesuis</i> subsp. <i>choleraesuis</i>	This patent	<i>tuf</i>
65	613	serotype Paratyphi A <i>Serratia ficaria</i>	This patent	<i>tuf</i>
	614	<i>Enterococcus malodoratus</i>	This patent	<i>tuf</i> (C)
	615	<i>Enterococcus durans</i>	This patent	<i>tuf</i> (C)
	616	<i>Enterococcus pseudoavium</i>	This patent	<i>tuf</i> (C)

Table 7. Origin of the nucleic acids and/or sequences in the sequence listing (continued).

SEQ ID NO.	Archaeal, bacterial, fungal or parasitical species	Source	Gene*
5	617 <i>Enterococcus dispar</i>	This patent	<i>tuf</i> (C)
	618 <i>Enterococcus avium</i>	This patent	<i>tuf</i> (C)
	619 <i>Saccharomyces cerevisiae</i>	Database	<i>tuf</i> (M)
	621 <i>Enterococcus faecium</i>	This patent	<i>tuf</i> (C)
	622 <i>Saccharomyces cerevisiae</i>	This patent	<i>tuf</i> (EF-1)
10	623 <i>Cryptococcus neoformans</i>	This patent	<i>tuf</i> (EF-1)
	624 <i>Candida albicans</i>	WO98/20157	<i>tuf</i> (EF-1)
	662 <i>Corynebacterium diphtheriae</i>	WO98/20157	<i>tuf</i>
	663 <i>Candida catenulata</i>	This patent	<i>atpD</i>
	665 <i>Saccharomyces cerevisiae</i>	Database	<i>tuf</i> (EF-1)
15	666 <i>Saccharomyces cerevisiae</i>	Database	<i>atpD</i>
	667 <i>Trypanosoma cruzi</i>	This patent	<i>atpD</i>
	668 <i>Corynebacterium glutamicum</i>	Database	<i>tuf</i>
	669 <i>Escherichia coli</i>	Database	<i>atpD</i>
	670 <i>Helicobacter pylori</i>	Database	<i>atpD</i>
20	671 <i>Clostridium acetobutylicum</i>	Database	<i>atpD</i>
	672 <i>Cytophaga lytica</i>	Database	<i>atpD</i>
	673 <i>Ehrlichia risticii</i>	This patent	<i>atpD</i>
	674 <i>Vibrio cholerae</i>	This patent	<i>atpD</i>
	675 <i>Vibrio cholerae</i>	This patent	<i>tuf</i>
25	676 <i>Leishmania enriettii</i>	This patent	<i>atpD</i>
	677 <i>Babesia microti</i>	This patent	<i>tuf</i> (EF-1)
	678 <i>Cryptococcus neoformans</i>	This patent	<i>atpD</i>
	679 <i>Cryptococcus neoformans</i>	This patent	<i>atpD</i>
	680 <i>Cunninghamella bertholletiae</i>	This patent	<i>atpD</i>
30	684 <i>Candida tropicalis</i>	Database	<i>atpD</i> (V)
	685 <i>Enterococcus hirae</i>	Database	<i>atpD</i> (V)
	686 <i>Chlamydia pneumoniae</i>	Database	<i>atpD</i> (V)
	687 <i>Halobacterium salinarum</i>	Database	<i>atpD</i> (V)
	688 <i>Homo sapiens</i>	Database	<i>atpD</i> (V)
35	689 <i>Plasmodium falciparum</i>	Database	<i>atpD</i> (V)
	690 <i>Saccharomyces cerevisiae</i>	Database	<i>atpD</i> (V)
	691 <i>Schizosaccharomyces pombe</i>	Database	<i>atpD</i> (V)
	692 <i>Trypanosoma congolense</i>	Database	<i>atpD</i> (V)
	693 <i>Thermus thermophilus</i>	Database	<i>atpD</i> (V)
40	698 <i>Escherichia coli</i>	WO98/20157	<i>tuf</i>
	709 <i>Borrelia burgdorferi</i>	Database	<i>atpD</i> (V)
	710 <i>Treponema pallidum</i>	Database	<i>atpD</i> (V)
	711 <i>Chlamydia trachomatis</i>	Genome project	<i>atpD</i> (V)
	712 <i>Enterococcus faecalis</i>	Genome project	<i>atpD</i> (V)
45	713 <i>Methanosarcina barkeri</i>	Database	<i>atpD</i> (V)
	714 <i>Methanococcus jannaschii</i>	Database	<i>atpD</i> (V)
	715 <i>Porphyromonas gingivalis</i>	Genome project	<i>atpD</i> (V)
	716 <i>Streptococcus pneumoniae</i>	Genome project	<i>atpD</i> (V)
	717 <i>Burkholderia mallei</i>	This patent	<i>tuf</i>
50	718 <i>Burkholderia pseudomallei</i>	This patent	<i>tuf</i>
	719 <i>Clostridium beijerinckii</i>	This patent	<i>tuf</i>
	720 <i>Clostridium innocuum</i>	This patent	<i>tuf</i>
	721 <i>Clostridium novyi</i>	This patent	<i>tuf</i>
	722 <i>Clostridium septicum</i>	This patent	<i>tuf</i>
55	723 <i>Clostridium tertium</i>	This patent	<i>tuf</i>
	724 <i>Clostridium tetani</i>	This patent	<i>tuf</i>
	725 <i>Enterococcus malodoratus</i>	This patent	<i>tuf</i>
	726 <i>Enterococcus sulfureus</i>	This patent	<i>tuf</i>
	727 <i>Lactococcus garvieae</i>	This patent	<i>tuf</i>
60	728 <i>Mycoplasma pirum</i>	This patent	<i>tuf</i>
	729 <i>Mycoplasma salivarium</i>	This patent	<i>tuf</i>
	730 <i>Neisseria polysaccharea</i>	This patent	<i>tuf</i>
	731 <i>Salmonella choleraesuis</i> subsp. <i>choleraesuis</i>	This patent	<i>tuf</i>
	serotype Enteritidis		
65			

Table 7. Origin of the nucleic acids and/ r sequences in the sequence listing (continued).

	SEQ ID NO.	Archaeal, bacterial, fungal or parasitical species	Source	Gene*
5	732	<i>Salmonella choleraesuis</i> subsp. <i>choleraesuis</i> serotype Gallinarum	This patent	<i>tuf</i>
	733	<i>Salmonella choleraesuis</i> subsp. <i>choleraesuis</i> serotype Paratyphi B	This patent	<i>tuf</i>
	734	<i>Salmonella choleraesuis</i> subsp. <i>choleraesuis</i> serotype Virchow	This patent	<i>tuf</i>
10	735	<i>Serratia grimesii</i>	This patent	<i>tuf</i>
	736	<i>Clostridium difficile</i>	This patent	<i>tuf</i>
	737	<i>Burkholderia pseudomallei</i>	This patent	<i>atpD</i>
	738	<i>Clostridium bifermentans</i>	This patent	<i>atpD</i>
15	739	<i>Clostridium beijerinckii</i>	This patent	<i>atpD</i>
	740	<i>Clostridium difficile</i>	This patent	<i>atpD</i>
	741	<i>Clostridium ramosum</i>	This patent	<i>atpD</i>
	742	<i>Clostridium septicum</i>	This patent	<i>atpD</i>
20	743	<i>Clostridium tertium</i>	This patent	<i>atpD</i>
	744	<i>Comamonas acidovorans</i>	This patent	<i>atpD</i>
	745	<i>Klebsiella pneumoniae</i> subsp. <i>rhinoscleromatis</i>	This patent	<i>atpD</i>
	746	<i>Neisseria canis</i>	This patent	<i>atpD</i>
25	747	<i>Neisseria cinerea</i>	This patent	<i>atpD</i>
	748	<i>Neisseria cuniculi</i>	This patent	<i>atpD</i>
	749	<i>Neisseria elongata</i> subsp. <i>elongata</i>	This patent	<i>atpD</i>
	750	<i>Neisseria flavescens</i>	This patent	<i>atpD</i>
30	751	<i>Neisseria gonorrhoeae</i>	This patent	<i>atpD</i>
	752	<i>Neisseria gonorrhoeae</i>	This patent	<i>atpD</i>
	753	<i>Neisseria lactamica</i>	This patent	<i>atpD</i>
	754	<i>Neisseria meningitidis</i>	This patent	<i>atpD</i>
35	755	<i>Neisseria mucosa</i>	This patent	<i>atpD</i>
	756	<i>Neisseria subflava</i>	This patent	<i>atpD</i>
	757	<i>Neisseria weaveri</i>	This patent	<i>atpD</i>
	758	<i>Neisseria animalis</i>	This patent	<i>atpD</i>
40	759	<i>Proteus penneri</i>	This patent	<i>atpD</i>
	760	<i>Salmonella choleraesuis</i> subsp. <i>choleraesuis</i> serotype Enteritidis	This patent	<i>atpD</i>
	761	<i>Yersinia pestis</i>	This patent	<i>atpD</i>
	762	<i>Burkholderia mallei</i>	This patent	<i>atpD</i>
45	763	<i>Clostridium sordellii</i>	This patent	<i>atpD</i>
	764	<i>Clostridium novyi</i>	This patent	<i>atpD</i>
	765	<i>Clostridium botulinum</i>	This patent	<i>atpD</i>
	766	<i>Clostridium histolyticum</i>	This patent	<i>atpD</i>
50	767	<i>Peptostreptococcus prevotii</i>	This patent	<i>atpD</i>
	768	<i>Absidia corymbifera</i>	This patent	<i>atpD</i>
	769	<i>Alternaria alternata</i>	This patent	<i>atpD</i>
	770	<i>Aspergillus flavus</i>	This patent	<i>atpD</i>
55	771	<i>Mucor circinelloides</i>	This patent	<i>atpD</i>
	772	<i>Piedraia hortai</i>	This patent	<i>atpD</i>
	773	<i>Pseudallescheria boydii</i>	This patent	<i>atpD</i>
	774	<i>Rhizopus oryzae</i>	This patent	<i>atpD</i>
60	775	<i>Scopulariopsis koningii</i>	This patent	<i>atpD</i>
	776	<i>Trichophyton mentagrophytes</i>	This patent	<i>atpD</i>
	777	<i>Trichophyton tonsurans</i>	This patent	<i>atpD</i>
	778	<i>Trichosporon cutaneum</i>	This patent	<i>atpD</i>
65	779	<i>Cladophialophora carrionii</i>	This patent	<i>tuf</i> (EF-1)
	780	<i>Cunninghamella bertholletiae</i>	This patent	<i>tuf</i> (EF-1)
	781	<i>Curvularia lunata</i>	This patent	<i>tuf</i> (EF-1)
	782	<i>Fonsecaea pedrosoi</i>	This patent	<i>tuf</i> (EF-1)
65	783	<i>Microsporium audouinii</i>	This patent	<i>tuf</i> (EF-1)
	784	<i>Mucor circinelloides</i>	This patent	<i>tuf</i> (EF-1)
	785	<i>Phialophora verrucosa</i>	This patent	<i>tuf</i> (EF-1)
	786	<i>Saksenaea vasiformis</i>	This patent	<i>tuf</i> (EF-1)
65	787	<i>Syncephalastrum racemosum</i>	This patent	<i>tuf</i> (EF-1)
	788	<i>Trichophyton tonsurans</i>	This patent	<i>tuf</i> (EF-1)
	789	<i>Trichophyton mentagrophytes</i>	This patent	<i>tuf</i> (EF-1)

Table 7. Origin of the nucleic acids and/or sequences in the sequence listing (continued).

	SEQ ID NO.	Archaeal, bacterial, fungal or parasitological species	Source	Gene*
5	790	<i>Bipolaris hawaiiensis</i>	This patent	<i>tuf</i> (EF-1)
	791	<i>Aspergillus fumigatus</i>	This patent	<i>tuf</i> (M)
	792	<i>Trichophyton mentagrophytes</i>	This patent	<i>tuf</i> (M)
	827	<i>Clostridium novyi</i>	This patent	<i>atpD</i> (V)
10	828	<i>Clostridium difficile</i>	This patent	<i>atpD</i> (V)
	829	<i>Clostridium septicum</i>	This patent	<i>atpD</i> (V)
	830	<i>Clostridium botulinum</i>	This patent	<i>atpD</i> (V)
	831	<i>Clostridium perfringens</i>	This patent	<i>atpD</i> (V)
15	832	<i>Clostridium tetani</i>	This patent	<i>atpD</i> (V)
	833	<i>Streptococcus pyogenes</i>	Database	<i>atpD</i> (V)
	834	<i>Babesia bovis</i>	This patent	<i>atpD</i> (V)
	835	<i>Cryptosporidium parvum</i>	This patent	<i>atpD</i> (V)
20	836	<i>Leishmania infantum</i>	This patent	<i>atpD</i> (V)
	837	<i>Leishmania major</i>	This patent	<i>atpD</i> (V)
	838	<i>Leishmania tarentolae</i>	This patent	<i>atpD</i> (V)
	839	<i>Trypanosoma brucei</i>	This patent	<i>atpD</i> (V)
25	840	<i>Trypanosoma cruzi</i>	This patent	<i>tuf</i> (EF-1)
	841	<i>Trypanosoma cruzi</i>	This patent	<i>tuf</i> (EF-1)
	842	<i>Trypanosoma cruzi</i>	This patent	<i>tuf</i> (EF-1)
	843	<i>Babesia bovis</i>	This patent	<i>tuf</i> (M)
30	844	<i>Leishmania aethiopica</i>	This patent	<i>tuf</i> (M)
	845	<i>Leishmania amazonensis</i>	This patent	<i>tuf</i> (M)
	846	<i>Leishmania donovani</i>	This patent	<i>tuf</i> (M)
	847	<i>Leishmania infantum</i>	This patent	<i>tuf</i> (M)
35	848	<i>Leishmania enriettii</i>	This patent	<i>tuf</i> (M)
	849	<i>Leishmania gerbilli</i>	This patent	<i>tuf</i> (M)
	850	<i>Leishmania major</i>	This patent	<i>tuf</i> (M)
	851	<i>Leishmania mexicana</i>	This patent	<i>tuf</i> (M)
40	852	<i>Leishmania tarentolae</i>	This patent	<i>tuf</i> (M)
	853	<i>Trypanosoma cruzi</i>	This patent	<i>tuf</i> (M)
	854	<i>Trypanosoma cruzi</i>	This patent	<i>tuf</i> (M)
	855	<i>Trypanosoma cruzi</i>	This patent	<i>tuf</i> (M)
45	856	<i>Babesia bigemina</i>	This patent	<i>atpD</i>
	857	<i>Babesia bovis</i>	This patent	<i>atpD</i>
	858	<i>Babesia microti</i>	This patent	<i>atpD</i>
	859	<i>Leishmania guyanensis</i>	This patent	<i>atpD</i>
50	860	<i>Leishmania mexicana</i>	This patent	<i>atpD</i>
	861	<i>Leishmania tropica</i>	This patent	<i>atpD</i>
	862	<i>Leishmania tropica</i>	This patent	<i>atpD</i>
	863	<i>Bordetella pertussis</i>	Database	<i>tuf</i>
55	864	<i>Trypanosoma brucei brucei</i>	Database	<i>tuf</i> (EF-1)
	865	<i>Cryptosporidium parvum</i>	This patent	<i>tuf</i> (EF-1)
	866	<i>Staphylococcus saprophyticus</i>	This patent	<i>atpD</i>
	867	<i>Zoogloea ramigera</i>	This patent	<i>atpD</i>
60	868	<i>Staphylococcus saprophyticus</i>	This patent	<i>tuf</i>
	869	<i>Enterococcus casseliflavus</i>	This patent	<i>tuf</i>
	870	<i>Enterococcus casseliflavus</i>	This patent	<i>tuf</i>
	871	<i>Enterococcus flavescens</i>	This patent	<i>tuf</i>
65	872	<i>Enterococcus gallinarum</i>	This patent	<i>tuf</i>
	873	<i>Enterococcus gallinarum</i>	This patent	<i>tuf</i>
	874	<i>Staphylococcus haemolyticus</i>	This patent	<i>tuf</i>
	875	<i>Staphylococcus epidermidis</i>	This patent	<i>tuf</i>
70	876	<i>Staphylococcus epidermidis</i>	This patent	<i>tuf</i>
	877	<i>Staphylococcus epidermidis</i>	This patent	<i>tuf</i>
	878	<i>Staphylococcus epidermidis</i>	This patent	<i>tuf</i>
	879	<i>Enterococcus gallinarum</i>	This patent	<i>tuf</i>
75	880	<i>Pseudomonas aeruginosa</i>	This patent	<i>tuf</i>
	881	<i>Enterococcus casseliflavus</i>	This patent	<i>tuf</i>
	882	<i>Enterococcus casseliflavus</i>	This patent	<i>tuf</i>
	883	<i>Enterococcus faecalis</i>	This patent	<i>tuf</i>
80	884	<i>Enterococcus faecalis</i>	This patent	<i>tuf</i>
	885	<i>Enterococcus faecium</i>	This patent	<i>tuf</i>

Table 7. Origin of the nucleic acids and/or sequences in the sequence listing (continued).

SEQ ID NO.	Archaeal, bacterial, fungal or parasitical species	Source	Gene*
5	886 <i>Enterococcus faecium</i>	This patent	<i>tuf</i>
	887 <i>Zoogloea ramigera</i>	This patent	<i>tuf</i>
	888 <i>Enterococcus faecalis</i>	This patent	<i>tuf</i>
	889 <i>Aspergillus fumigatus</i>	This patent	<i>atpD</i>
10	890 <i>Penicillium marneffeii</i>	This patent	<i>atpD</i>
	891 <i>Paecilomyces lilacinus</i>	This patent	<i>atpD</i>
	892 <i>Penicillium marneffeii</i>	This patent	<i>atpD</i>
	893 <i>Sporothrix schenckii</i>	This patent	<i>atpD</i>
15	894 <i>Malbranchea filamentosa</i>	This patent	<i>atpD</i>
	895 <i>Paecilomyces lilacinus</i>	This patent	<i>atpD</i>
	896 <i>Aspergillus niger</i>	This patent	<i>atpD</i>
	897 <i>Aspergillus fumigatus</i>	This patent	<i>tuf</i> (EF-1)
20	898 <i>Penicillium marneffeii</i>	This patent	<i>tuf</i> (EF-1)
	899 <i>Piedraia hortai</i>	This patent	<i>tuf</i> (EF-1)
	900 <i>Paecilomyces lilacinus</i>	This patent	<i>tuf</i> (EF-1)
	901 <i>Paracoccidioides brasiliensis</i>	This patent	<i>tuf</i> (EF-1)
25	902 <i>Sporothrix schenckii</i>	This patent	<i>tuf</i> (EF-1)
	903 <i>Penicillium marneffeii</i>	This patent	<i>tuf</i> (EF-1)
	904 <i>Curvularia lunata</i>	This patent	<i>tuf</i> (M)
	905 <i>Aspergillus niger</i>	This patent	<i>tuf</i> (M)
30	906 <i>Bipolaris hawaiiensis</i>	This patent	<i>tuf</i> (M)
	907 <i>Aspergillus flavus</i>	This patent	<i>tuf</i> (M)
	908 <i>Alternaria alternata</i>	This patent	<i>tuf</i> (M)
	909 <i>Penicillium marneffeii</i>	This patent	<i>tuf</i> (M)
35	910 <i>Penicillium marneffeii</i>	This patent	<i>tuf</i> (M)
	918 <i>Escherichia coli</i>	Database	<i>recA</i>
	929 <i>Bacteroides fragilis</i>	This patent	<i>atpD</i> (V)
	930 <i>Bacteroides distasonis</i>	This patent	<i>atpD</i> (V)
40	931 <i>Porphyromonas asaccharolytica</i>	This patent	<i>atpD</i> (V)
	932 <i>Listeria monocytogenes</i>	This patent	<i>tuf</i>
	939 <i>Saccharomyces cerevisiae</i>	Database	<i>recA</i> (Rad51)
	940 <i>Saccharomyces cerevisiae</i>	Database	<i>recA</i> (Dmc1)
45	941 <i>Cryptococcus humicola</i>	This patent	<i>atpD</i>
	942 <i>Escherichia coli</i>	This patent	<i>atpD</i>
	943 <i>Escherichia coli</i>	This patent	<i>atpD</i>
	944 <i>Escherichia coli</i>	This patent	<i>atpD</i>
50	945 <i>Escherichia coli</i>	This patent	<i>atpD</i>
	946 <i>Neisseria polysaccharea</i>	This patent	<i>atpD</i>
	947 <i>Neisseria sicca</i>	This patent	<i>atpD</i>
	948 <i>Streptococcus mitis</i>	This patent	<i>atpD</i>
55	949 <i>Streptococcus mitis</i>	This patent	<i>atpD</i>
	950 <i>Streptococcus mitis</i>	This patent	<i>atpD</i>
	951 <i>Streptococcus oralis</i>	This patent	<i>atpD</i>
	952 <i>Streptococcus pneumoniae</i>	This patent	<i>atpD</i>
60	953 <i>Streptococcus pneumoniae</i>	This patent	<i>atpD</i>
	954 <i>Streptococcus pneumoniae</i>	This patent	<i>atpD</i>
	955 <i>Streptococcus pneumoniae</i>	This patent	<i>atpD</i>
	956 <i>Babesia microti</i>	This patent	<i>atpD</i> (V)
65	957 <i>Entamoeba histolytica</i>	This patent	<i>atpD</i> (V)
	958 <i>Fusobacterium nucleatum</i> subsp. <i>polymorphum</i>	This patent	<i>atpD</i> (V)
	959 <i>Leishmania aethiopica</i>	This patent	<i>atpD</i> (V)
	960 <i>Leishmania tropica</i>	This patent	<i>atpD</i> (V)
65	961 <i>Leishmania guyanensis</i>	This patent	<i>atpD</i> (V)
	962 <i>Leishmania donovani</i>	This patent	<i>atpD</i> (V)
	963 <i>Leishmania hertigi</i>	This patent	<i>atpD</i> (V)
	964 <i>Leishmania mexicana</i>	This patent	<i>atpD</i> (V)
65	965 <i>Leishmania tropica</i>	This patent	<i>atpD</i> (V)
	966 <i>Peptostreptococcus anaerobius</i>	This patent	<i>atpD</i> (V)
	967 <i>Bordetella pertussis</i>	This patent	<i>tuf</i>
	968 <i>Bordetella pertussis</i>	This patent	<i>tuf</i>
65	969 <i>Enterococcus columbae</i>	This patent	<i>tuf</i>

Table 7. Origin of the nucleic acids and/or sequences in the sequence listing (continued).

	SEQ ID NO.	Archaeal, bacterial, fungal or parasitcal species	Source	Gene*
5	970	<i>Enterococcus flavescens</i>	This patent	<i>tuf</i>
	971	<i>Streptococcus pneumoniae</i>	This patent	<i>tuf</i>
	972	<i>Escherichia coli</i>	This patent	<i>tuf</i>
	973	<i>Escherichia coli</i>	This patent	<i>tuf</i>
	974	<i>Escherichia coli</i>	This patent	<i>tuf</i>
10	975	<i>Escherichia coli</i>	This patent	<i>tuf</i>
	976	<i>Mycobacterium avium</i>	This patent	<i>tuf</i>
	977	<i>Streptococcus pneumoniae</i>	This patent	<i>tuf</i>
15	978	<i>Mycobacterium gordonae</i>	This patent	<i>tuf</i>
	979	<i>Streptococcus pneumoniae</i>	This patent	<i>tuf</i>
	980	<i>Mycobacterium tuberculosis</i>	This patent	<i>tuf</i>
	981	<i>Staphylococcus warneri</i>	This patent	<i>tuf</i>
	982	<i>Streptococcus mitis</i>	This patent	<i>tuf</i>
20	983	<i>Streptococcus mitis</i>	This patent	<i>tuf</i>
	984	<i>Streptococcus mitis</i>	This patent	<i>tuf</i>
	985	<i>Streptococcus oralis</i>	This patent	<i>tuf</i>
	986	<i>Streptococcus pneumoniae</i>	This patent	<i>tuf</i>
	987	<i>Enterococcus hirae</i>	This patent	<i>tuf</i> (C)
25	988	<i>Enterococcus mundtii</i>	This patent	<i>tuf</i> (C)
	989	<i>Enterococcus raffinosus</i>	This patent	<i>tuf</i> (C)
	990	<i>Bacillus anthracis</i>	This patent	<i>recA</i>
	991	<i>Prevotella melaninogenica</i>	This patent	<i>recA</i>
	992	<i>Enterococcus casseliflavus</i>	This patent	<i>tuf</i>
30	993	<i>Streptococcus pyogenes</i>	Database	<i>speA</i>
	1002	<i>Streptococcus pyogenes</i>	WO98/20157	<i>tuf</i>
	1003	<i>Bacillus cereus</i>	This patent	<i>recA</i>
	1004	<i>Streptococcus pneumoniae</i>	This patent	<i>pbp1a</i>
	1005	<i>Streptococcus pneumoniae</i>	This patent	<i>pbp1a</i>
35	1006	<i>Streptococcus pneumoniae</i>	This patent	<i>pbp1a</i>
	1007	<i>Streptococcus pneumoniae</i>	This patent	<i>pbp1a</i>
	1008	<i>Streptococcus pneumoniae</i>	This patent	<i>pbp1a</i>
	1009	<i>Streptococcus pneumoniae</i>	This patent	<i>pbp1a</i>
	1010	<i>Streptococcus pneumoniae</i>	This patent	<i>pbp1a</i>
40	1011	<i>Streptococcus pneumoniae</i>	This patent	<i>pbp1a</i>
	1012	<i>Streptococcus pneumoniae</i>	This patent	<i>pbp1a</i>
	1013	<i>Streptococcus pneumoniae</i>	This patent	<i>pbp1a</i>
	1014	<i>Streptococcus pneumoniae</i>	This patent	<i>pbp1a</i>
	1015	<i>Streptococcus pneumoniae</i>	This patent	<i>pbp1a</i>
45	1016	<i>Streptococcus pneumoniae</i>	This patent	<i>pbp1a</i>
	1017	<i>Streptococcus pneumoniae</i>	This patent	<i>pbp1a</i>
	1018	<i>Streptococcus pneumoniae</i>	This patent	<i>pbp1a</i>
	1019	<i>Streptococcus pneumoniae</i>	This patent	<i>pbp2b</i>
	1020	<i>Streptococcus pneumoniae</i>	This patent	<i>pbp2b</i>
50	1021	<i>Streptococcus pneumoniae</i>	This patent	<i>pbp2b</i>
	1022	<i>Streptococcus pneumoniae</i>	This patent	<i>pbp2b</i>
	1023	<i>Streptococcus pneumoniae</i>	This patent	<i>pbp2b</i>
	1024	<i>Streptococcus pneumoniae</i>	This patent	<i>pbp2b</i>
	1025	<i>Streptococcus pneumoniae</i>	This patent	<i>pbp2b</i>
55	1026	<i>Streptococcus pneumoniae</i>	This patent	<i>pbp2b</i>
	1027	<i>Streptococcus pneumoniae</i>	This patent	<i>pbp2b</i>
	1028	<i>Streptococcus pneumoniae</i>	This patent	<i>pbp2b</i>
	1029	<i>Streptococcus pneumoniae</i>	This patent	<i>pbp2b</i>
	1030	<i>Streptococcus pneumoniae</i>	This patent	<i>pbp2b</i>
60	1031	<i>Streptococcus pneumoniae</i>	This patent	<i>pbp2b</i>
	1032	<i>Streptococcus pneumoniae</i>	This patent	<i>pbp2b</i>
	1033	<i>Streptococcus pneumoniae</i>	This patent	<i>pbp2b</i>
	1034	<i>Streptococcus pneumoniae</i>	This patent	<i>pbp2x</i>
	1035	<i>Streptococcus pneumoniae</i>	This patent	<i>pbp2x</i>
65	1036	<i>Streptococcus pneumoniae</i>	This patent	<i>pbp2x</i>
	1037	<i>Streptococcus pneumoniae</i>	This patent	<i>pbp2x</i>

Table 7. Origin of the nucleic acids and/or sequences in the sequence listing (continued).

	SEQ ID NO.	Archaeal, bacterial, fungal or parasitical species	Source	Gene*
5	1038	<i>Streptococcus pneumoniae</i>	This patent	<i>pbp2x</i>
	1039	<i>Streptococcus pneumoniae</i>	This patent	<i>pbp2x</i>
	1040	<i>Streptococcus pneumoniae</i>	This patent	<i>pbp2x</i>
	1041	<i>Streptococcus pneumoniae</i>	This patent	<i>pbp2x</i>
	1042	<i>Streptococcus pneumoniae</i>	This patent	<i>pbp2x</i>
10	1043	<i>Streptococcus pneumoniae</i>	This patent	<i>pbp2x</i>
	1044	<i>Streptococcus pneumoniae</i>	This patent	<i>pbp2x</i>
	1045	<i>Streptococcus pneumoniae</i>	This patent	<i>pbp2x</i>
	1046	<i>Streptococcus pneumoniae</i>	This patent	<i>pbp2x</i>
	1047	<i>Streptococcus pneumoniae</i>	This patent	<i>pbp2x</i>
15	1048	<i>Streptococcus pneumoniae</i>	This patent	<i>pbp2x</i>
	1049	<i>Enterococcus faecium</i>	This patent	<i>vanA</i>
	1050	<i>Enterococcus gallinarum</i>	This patent	<i>vanA</i>
	1051	<i>Enterococcus faecium</i>	This patent	<i>vanA</i>
	1052	<i>Enterococcus faecium</i>	This patent	<i>vanA</i>
20	1053	<i>Enterococcus faecium</i>	This patent	<i>vanA</i>
	1054	<i>Enterococcus faecalis</i>	This patent	<i>vanA</i>
	1055	<i>Enterococcus gallinarum</i>	This patent	<i>vanA</i>
	1056	<i>Enterococcus faecium</i>	This patent	<i>vanA</i>
	1057	<i>Enterococcus flavescens</i>	This patent	<i>vanA</i>
25	1058	<i>Enterococcus gallinarum</i>	This patent	<i>vanC1</i>
	1059	<i>Enterococcus gallinarum</i>	This patent	<i>vanC1</i>
	1060	<i>Enterococcus casseliflavus</i>	This patent	<i>vanC2</i>
	1061	<i>Enterococcus casseliflavus</i>	This patent	<i>vanC2</i>
	1062	<i>Enterococcus casseliflavus</i>	This patent	<i>vanC2</i>
30	1063	<i>Enterococcus casseliflavus</i>	This patent	<i>vanC2</i>
	1064	<i>Enterococcus flavescens</i>	This patent	<i>vanC3</i>
	1065	<i>Enterococcus flavescens</i>	This patent	<i>vanC3</i>
	1066	<i>Enterococcus flavescens</i>	This patent	<i>vanC3</i>
	1067	<i>Enterococcus faecium</i>	This patent	<i>vanXY</i>
35	1068	<i>Enterococcus faecium</i>	This patent	<i>vanXY</i>
	1069	<i>Enterococcus faecium</i>	This patent	<i>vanXY</i>
	1070	<i>Enterococcus faecalis</i>	This patent	<i>vanXY</i>
	1071	<i>Enterococcus gallinarum</i>	This patent	<i>vanXY</i>
	1072	<i>Enterococcus faecium</i>	This patent	<i>vanXY</i>
40	1073	<i>Enterococcus flavescens</i>	This patent	<i>vanXY</i>
	1074	<i>Enterococcus faecium</i>	This patent	<i>vanXY</i>
	1075	<i>Enterococcus gallinarum</i>	This patent	<i>vanXY</i>
	1076	<i>Escherichia coli</i>	Database	<i>stx₁</i>
	1077	<i>Escherichia coli</i>	Database	<i>stx₂</i>
45	1093	<i>Staphylococcus saprophyticus</i>	This patent	unknown
	1117	<i>Enterococcus faecium</i>	Database	<i>vanB</i>
	1138	<i>Enterococcus gallinarum</i>	Database	<i>vanC1</i>
	1139	<i>Enterococcus faecium</i>	Database	<i>vanA</i>
	1140	<i>Enterococcus casseliflavus</i>	Database	<i>vanC2</i>
50	1141	<i>Enterococcus faecium</i>	Database	<i>vanHAXY</i>
	1169	<i>Streptococcus pneumoniae</i>	Database	<i>pbp1a</i>
	1172	<i>Streptococcus pneumoniae</i>	Database	<i>pbp2b</i>
	1173	<i>Streptococcus pneumoniae</i>	Database	<i>pbp2x</i>
	1178	<i>Staphylococcus aureus</i>	Database	<i>mecA</i>
55	1183	<i>Streptococcus pneumoniae</i>	Database	<i>hexA</i>
	1184	<i>Streptococcus pneumoniae</i>	This patent	<i>hexA</i>
	1185	<i>Streptococcus pneumoniae</i>	This patent	<i>hexA</i>
	1186	<i>Streptococcus pneumoniae</i>	This patent	<i>hexA</i>
	1187	<i>Streptococcus pneumoniae</i>	This patent	<i>hexA</i>
60				

Table 7. Origin of the nucleic acids and/or sequences in the sequence listing (continued).

SEQ ID NO.	Archaeal, bacterial, fungal or parasitical species	Source	Gene*
5	1188 <i>Streptococcus oralis</i>	This patent	<i>hexA</i>
	1189 <i>Streptococcus mitis</i>	This patent	<i>hexA</i>
	1190 <i>Streptococcus mitis</i>	This patent	<i>hexA</i>
	1191 <i>Streptococcus mitis</i>	This patent	<i>hexA</i>
	1198 <i>Staphylococcus saprophyticus</i>	This patent	unknown
10	1215 <i>Streptococcus pyogenes</i>	Database	<i>pcp</i>
	1230 <i>Escherichia coli</i>	Database	<i>tuf</i> (EF-G)
	1242 <i>Enterococcus faecium</i>	Database	<i>ddl</i>
	1243 <i>Enterococcus faecalis</i>	Database	<i>mtiF</i> , <i>mtiD</i>
	1244 <i>Staphylococcus aureus</i> subsp. <i>aureus</i>	This patent	unknown
15	1245 <i>Bacillus anthracis</i>	This patent	<i>atpD</i>
	1246 <i>Bacillus mycoides</i>	This patent	<i>atpD</i>
	1247 <i>Bacillus thuringiensis</i>	This patent	<i>atpD</i>
	1248 <i>Bacillus thuringiensis</i>	This patent	<i>atpD</i>
	1249 <i>Bacillus thuringiensis</i>	This patent	<i>atpD</i>
20	1250 <i>Bacillus weihenstephanensis</i>	This patent	<i>atpD</i>
	1251 <i>Bacillus thuringiensis</i>	This patent	<i>atpD</i>
	1252 <i>Bacillus thuringiensis</i>	This patent	<i>atpD</i>
	1253 <i>Bacillus cereus</i>	This patent	<i>atpD</i>
	1254 <i>Bacillus cereus</i>	This patent	<i>atpD</i>
25	1255 <i>Staphylococcus aureus</i>	This patent	<i>gyrA</i>
	1256 <i>Bacillus weihenstephanensis</i>	This patent	<i>atpD</i>
	1257 <i>Bacillus anthracis</i>	This patent	<i>atpD</i>
	1258 <i>Bacillus thuringiensis</i>	This patent	<i>atpD</i>
	1259 <i>Bacillus cereus</i>	This patent	<i>atpD</i>
30	1260 <i>Bacillus cereus</i>	This patent	<i>atpD</i>
	1261 <i>Bacillus thuringiensis</i>	This patent	<i>atpD</i>
	1262 <i>Bacillus thuringiensis</i>	This patent	<i>atpD</i>
	1263 <i>Bacillus thuringiensis</i>	This patent	<i>atpD</i>
	1264 <i>Bacillus thuringiensis</i>	This patent	<i>atpD</i>
35	1265 <i>Bacillus anthracis</i>	This patent	<i>atpD</i>
	1266 <i>Paracoccidioides brasiliensis</i>	This patent	<i>tuf</i> (EF-1)
	1267 <i>Blastomyces dermatitidis</i>	This patent	<i>tuf</i> (EF-1)
	1268 <i>Histoplasma capsulatum</i>	This patent	<i>tuf</i> (EF-1)
	1269 <i>Trichophyton rubrum</i>	This patent	<i>tuf</i> (EF-1)
40	1270 <i>Microsporium canis</i>	This patent	<i>tuf</i> (EF-1)
	1271 <i>Aspergillus versicolor</i>	This patent	<i>tuf</i> (EF-1)
	1272 <i>Exophiala moniliae</i>	This patent	<i>tuf</i> (EF-1)
	1273 <i>Hortaea wemeckii</i>	This patent	<i>tuf</i> (EF-1)
	1274 <i>Fusarium solani</i>	This patent	<i>tuf</i> (EF-1)
45	1275 <i>Aureobasidium pullulans</i>	This patent	<i>tuf</i> (EF-1)
	1276 <i>Blastomyces dermatitidis</i>	This patent	<i>tuf</i> (EF-1)
	1277 <i>Exophiala dermatitidis</i>	This patent	<i>tuf</i> (EF-1)
	1278 <i>Fusarium moniliforme</i>	This patent	<i>tuf</i> (EF-1)
	1279 <i>Aspergillus terreus</i>	This patent	<i>tuf</i> (EF-1)
50	1280 <i>Aspergillus fumigatus</i>	This patent	<i>tuf</i> (EF-1)
	1281 <i>Cryptococcus laurentii</i>	This patent	<i>tuf</i> (EF-1)
	1282 <i>Emmonsia parva</i>	This patent	<i>tuf</i> (EF-1)
	1283 <i>Fusarium solani</i>	This patent	<i>tuf</i> (EF-1)
	1284 <i>Sporothrix schenckii</i>	This patent	<i>tuf</i> (EF-1)
55	1285 <i>Aspergillus nidulans</i>	This patent	<i>tuf</i> (EF-1)
	1286 <i>Cladophialophora carionii</i>	This patent	<i>tuf</i> (EF-1)
	1287 <i>Exserohilum rostratum</i>	This patent	<i>tuf</i> (EF-1)
	1288 <i>Bacillus thuringiensis</i>	This patent	<i>recA</i>
	1289 <i>Bacillus thuringiensis</i>	This patent	<i>recA</i>
60	1299 <i>Staphylococcus aureus</i>	Database	<i>gyrA</i>
	1300 <i>Escherichia coli</i>	Database	<i>gyrA</i>
	1307 <i>Staphylococcus aureus</i>	Database	<i>gyrB</i>
	1320 <i>Escherichia coli</i>	Database	<i>parC</i> (<i>grA</i>)
	1321 <i>Staphylococcus aureus</i>	Database	<i>parC</i> (<i>grA</i>)
65	1328 <i>Staphylococcus aureus</i>	Database	<i>parE</i> (<i>grB</i>)

Table 7. Origin of the nucleic acids and/or sequences in the sequence listing (continued).

SEQ ID NO.	Archaeal, bacterial, fungal or parasitical species	Source	Gene*
5	1348 unidentified bacterium	Database	aac2Ia
	1351 <i>Pseudomonas aeruginosa</i>	Database	aac3Ib
	1356 <i>Serratia marcescens</i>	Database	aac3I/b
	1361 <i>Escherichia coli</i>	Database	aac3IVa
	1366 <i>Enterobacter cloacae</i>	Database	aac3VIa
10	1371 <i>Citrobacter koseri</i>	Database	aac6Ia
	1376 <i>Serratia marcescens</i>	Database	aac6Ic
	1381 <i>Escherichia coli</i>	Database	ant3Ia
	1386 <i>Staphylococcus aureus</i>	Database	ant4Ia
	1391 <i>Escherichia coli</i>	Database	aph3Ia
15	1396 <i>Escherichia coli</i>	Database	aph3IIa
	1401 <i>Enterococcus faecalis</i>	Database	aph3IIIa
	1406 <i>Acinetobacter baumannii</i>	Database	aph3VIa
	1411 <i>Pseudomonas aeruginosa</i>	Database	blaCARB
	1416 <i>Klebsiella pneumoniae</i>	Database	blaCMY-2
20	1423 <i>Escherichia coli</i>	Database	blaCTX-M-1
	1428 <i>Salmonella choleraesuis</i> subsp. <i>choleraesuis</i> serotype Typhimurium	Database	blaCTX-M-2
	1433 <i>Pseudomonas aeruginosa</i>	Database	blaIMP
	1438 <i>Escherichia coli</i>	Database	blaOXA2
25	1439 <i>Pseudomonas aeruginosa</i>	Database	blaOXA10
	1442 <i>Pseudomonas aeruginosa</i>	Database	blaPER1
	1445 <i>Salmonella choleraesuis</i> subsp. <i>choleraesuis</i> serotype Typhimurium	Database	blaPER2
	1452 <i>Staphylococcus epidermidis</i>	Database	dfrA
30	1461 <i>Escherichia coli</i>	Database	dhfrIa
	1470 <i>Escherichia coli</i>	Database	dhfrIb
	1475 <i>Escherichia coli</i>	Database	dhfrV
	1480 <i>Proteus mirabilis</i>	Database	dhfrVI
	1489 <i>Escherichia coli</i>	Database	dhfrVII
35	1494 <i>Escherichia coli</i>	Database	dhfrVIII
	1499 <i>Escherichia coli</i>	Database	dhfrIX
	1504 <i>Escherichia coli</i>	Database	dhfrXII
	1507 <i>Escherichia coli</i>	Database	dhfrXIII
	1512 <i>Escherichia coli</i>	Database	dhfrXV
40	1517 <i>Escherichia coli</i>	Database	dhfrXVII
	1518 <i>Acinetobacter lwoffii</i>	This patent	fusA
	1519 <i>Acinetobacter lwoffii</i>	This patent	fusA-tuf spacer
	1520 <i>Acinetobacter lwoffii</i>	This patent	tuf
	1521 <i>Haemophilus influenzae</i>	This patent	fusA
45	1522 <i>Haemophilus influenzae</i>	This patent	fusA-tuf spacer
	1523 <i>Haemophilus influenzae</i>	This patent	tuf
	1524 <i>Proteus mirabilis</i>	This patent	fusA
	1525 <i>Proteus mirabilis</i>	This patent	fusA-tuf spacer
	1526 <i>Proteus mirabilis</i>	This patent	tuf
50	1527 <i>Campylobacter curvus</i>	This patent	atpD
	1530 <i>Escherichia coli</i>	Database	ereA
	1535 <i>Escherichia coli</i>	Database	ereB
	1540 <i>Staphylococcus haemolyticus</i>	Database	linA
	1545 <i>Enterococcus faecium</i>	Database	linB
55	1548 <i>Streptococcus pyogenes</i>	Database	mefA
	1551 <i>Streptococcus pneumoniae</i>	Database	mefE
	1560 <i>Escherichia coli</i>	Database	mphA
	1561 <i>Candida albicans</i>	This patent	tuf (EF-1)
	1562 <i>Candida dubliniensis</i>	This patent	tuf (EF-1)
60	1563 <i>Candida famata</i>	This patent	tuf (EF-1)
	1564 <i>Candida glabrata</i>	This patent	tuf (EF-1)
	1565 <i>Candida guilliermondii</i>	This patent	tuf (EF-1)
	1566 <i>Candida haemulonii</i>	This patent	tuf (EF-1)
	1567 <i>Candida kefyr</i>	This patent	tuf (EF-1)
65	1568 <i>Candida lusitanae</i>	This patent	tuf (EF-1)

Table 7. Origin of the nucleic acids and/or sequences in the sequence listing (continued).

SEQ ID NO.	Archaeal, bacterial, fungal or parasitical species	Source	Gene*
5	1569 <i>Candida sphaerica</i>	This patent	<i>tuf</i> (EF-1)
	1570 <i>Candida tropicalis</i>	This patent	<i>tuf</i> (EF-1)
	1571 <i>Candida viswanathii</i>	This patent	<i>tuf</i> (EF-1)
	1572 <i>Alcaligenes faecalis</i> subsp. <i>faecalis</i>	This patent	<i>tuf</i>
	1573 <i>Prevotella buccalis</i>	This patent	<i>tuf</i>
10	1574 <i>Succinivibrio dextrinosolvens</i>	This patent	<i>tuf</i>
	1575 <i>Tetragenococcus halophilus</i>	This patent	<i>tuf</i>
	1576 <i>Campylobacter jejuni</i> subsp. <i>jejuni</i>	This patent	<i>atpD</i>
	1577 <i>Campylobacter rectus</i>	This patent	<i>atpD</i>
	1578 <i>Enterococcus casseliflavus</i>	This patent	<i>fusA</i>
15	1579 <i>Enterococcus gallinarum</i>	This patent	<i>fusA</i>
	1580 <i>Streptococcus mitis</i>	This patent	<i>fusA</i>
	1585 <i>Enterococcus faecium</i>	Database	<i>satG</i>
	1590 Cloning vector pFW16	Database	<i>tetM</i>
	1594 <i>Enterococcus faecium</i>	Database	<i>vanD</i>
20	1599 <i>Enterococcus faecalis</i>	Database	<i>vanE</i>
	1600 <i>Campylobacter jejuni</i> subsp. <i>doylei</i>	This patent	<i>atpD</i>
	1601 <i>Enterococcus sulfureus</i>	This patent	<i>atpD</i>
	1602 <i>Enterococcus solitarius</i>	This patent	<i>atpD</i>
	1603 <i>Campylobacter sputorum</i> subsp. <i>sputorum</i>	This patent	<i>atpD</i>
25	1604 <i>Enterococcus pseudoavium</i>	This patent	<i>atpD</i>
	1607 <i>Klebsiella omithinolytica</i>	This patent	<i>gyrA</i>
	1608 <i>Klebsiella oxytoca</i>	This patent	<i>gyrA</i>
	1613 <i>Staphylococcus aureus</i>	Database	<i>vatB</i>
	1618 <i>Staphylococcus cohnii</i>	Database	<i>vatC</i>
30	1623 <i>Staphylococcus aureus</i>	Database	<i>vga</i>
	1628 <i>Staphylococcus aureus</i>	Database	<i>vgaB</i>
	1633 <i>Staphylococcus aureus</i>	Database	<i>vga</i>
	1638 <i>Aspergillus fumigatus</i>	This patent	<i>atpD</i>
	1639 <i>Aspergillus fumigatus</i>	This patent	<i>atpD</i>
35	1640 <i>Bacillus mycoides</i>	This patent	<i>atpD</i>
	1641 <i>Bacillus mycoides</i>	This patent	<i>atpD</i>
	1642 <i>Bacillus mycoides</i>	This patent	<i>atpD</i>
	1643 <i>Bacillus pseudomycooides</i>	This patent	<i>atpD</i>
	1644 <i>Bacillus pseudomycooides</i>	This patent	<i>atpD</i>
40	1645 <i>Budvicia aquatica</i>	This patent	<i>atpD</i>
	1646 <i>Buttiauxella agrestis</i>	This patent	<i>atpD</i>
	1647 <i>Candida norvegica</i>	This patent	<i>atpD</i>
	1648 <i>Streptococcus pneumoniae</i>	This patent	<i>pbp1a</i>
	1649 <i>Campylobacter lari</i>	This patent	<i>atpD</i>
45	1650 <i>Coccidioides immitis</i>	This patent	<i>atpD</i>
	1651 <i>Ermonesia parva</i>	This patent	<i>atpD</i>
	1652 <i>Erwinia amylovora</i>	This patent	<i>atpD</i>
	1653 <i>Fonsecaea pedrosoi</i>	This patent	<i>atpD</i>
	1654 <i>Fusarium moniliforme</i>	This patent	<i>atpD</i>
50	1655 <i>Klebsiella oxytoca</i>	This patent	<i>atpD</i>
	1656 <i>Microsporium audouinii</i>	This patent	<i>atpD</i>
	1657 <i>Obesumbacterium proteus</i>	This patent	<i>atpD</i>
	1658 <i>Paracoccidioides brasiliensis</i>	This patent	<i>atpD</i>
	1659 <i>Plesiomonas shigelloides</i>	This patent	<i>atpD</i>
55	1660 <i>Shewanella putrefaciens</i>	This patent	<i>atpD</i>
	1662 <i>Campylobacter curvus</i>	This patent	<i>tuf</i>
	1663 <i>Campylobacter rectus</i>	This patent	<i>tuf</i>
	1664 <i>Fonsecaea pedrosoi</i>	This patent	<i>tuf</i>
	1666 <i>Microsporium audouinii</i>	This patent	<i>tuf</i>
60	1667 <i>Piedraia hortai</i>	This patent	<i>tuf</i>
	1668 <i>Escherichia coli</i>	Database	<i>tuf</i>
	1669 <i>Saksenaea vasiformis</i>	This patent	<i>tuf</i>
	1670 <i>Trichophyton tonsurans</i>	This patent	<i>tuf</i>
	1671 <i>Enterobacter aerogenes</i>	This patent	<i>atpD</i>
65	1672 <i>Bordetella pertussis</i>	Database	<i>atpD</i>
	1673 <i>Arcanobacterium haemolyticum</i>	This patent	<i>tuf</i>

Table 7. Origin of the nucleic acids and/or sequences in the sequence listing (continued).

SEQ ID NO.	Archaeal, bacterial, fungal or parasitical species	Source	Gene*
5	1674 <i>Butyrivibrio fibrisolvens</i>	This patent	tuf
	1675 <i>Campylobacter jejuni</i> subsp. <i>doylei</i>	This patent	tuf
	1676 <i>Campylobacter lari</i>	This patent	tuf
	1677 <i>Campylobacter sputorum</i> subsp. <i>sputorum</i>	This patent	tuf
	1678 <i>Campylobacter upsaliensis</i>	This patent	tuf
10	1679 <i>Globicatella sanguis</i>	This patent	tuf
	1680 <i>Lactobacillus acidophilus</i>	This patent	tuf
	1681 <i>Leuconostoc mesenteroides</i> subsp. <i>dextranicum</i>	This patent	tuf
	1682 <i>Prevotella buccalis</i>	This patent	tuf
	1683 <i>Ruminococcus bromii</i>	This patent	tuf
15	1684 <i>Paracoccidioides brasiliensis</i>	This patent	atpD
	1685 <i>Candida norvegica</i>	This patent	tuf (EF-1)
	1686 <i>Aspergillus nidulans</i>	This patent	tuf
	1687 <i>Aspergillus terreus</i>	This patent	tuf
	1688 <i>Candida norvegica</i>	This patent	tuf
20	1689 <i>Candida parapsilosis</i>	This patent	tuf
	1702 <i>Streptococcus gordonii</i>	WO98/20157	recA
	1703 <i>Streptococcus mutans</i>	WO98/20157	recA
	1704 <i>Streptococcus pneumoniae</i>	WO98/20157	recA
	1705 <i>Streptococcus pyogenes</i>	WO98/20157	recA
25	1706 <i>Streptococcus salivarius</i> subsp. <i>thermophilus</i>	WO98/20157	recA
	1707 <i>Escherichia coli</i>	WO98/20157	oxa
	1708 <i>Enterococcus faecalis</i>	WO98/20157	blaZ
	1709 <i>Pseudomonas aeruginosa</i>	WO98/20157	aac6'-IIa
	1710 <i>Staphylococcus aureus</i>	WO98/20157	ermA
30	1711 <i>Escherichia coli</i>	WO98/20157	ermB
	1712 <i>Staphylococcus aureus</i>	WO98/20157	ermC
	1713 <i>Enterococcus faecalis</i>	WO98/20157	vanB
	1714 <i>Campylobacter jejuni</i> subsp. <i>jejuni</i>	This patent	recA
	1715 <i>Abiotrophia adiacens</i>	WO98/20157	tuf
35	1716 <i>Abiotrophia defectiva</i>	WO98/20157	tuf
	1717 <i>Corynebacterium accolens</i>	WO98/20157	tuf
	1718 <i>Corynebacterium genitalium</i>	WO98/20157	tuf
	1719 <i>Corynebacterium jeikeium</i>	WO98/20157	tuf
	1720 <i>Corynebacterium pseudodiphtheriticum</i>	WO98/20157	tuf
40	1721 <i>Corynebacterium striatum</i>	WO98/20157	tuf
	1722 <i>Enterococcus avium</i>	WO98/20157	tuf
	1723 <i>Gardnerella vaginalis</i>	WO98/20157	tuf
	1724 <i>Listeria innocua</i>	WO98/20157	tuf
	1725 <i>Listeria ivanovii</i>	WO98/20157	tuf
45	1726 <i>Listeria monocytogenes</i>	WO98/20157	tuf
	1727 <i>Listeria seeligeri</i>	WO98/20157	tuf
	1728 <i>Staphylococcus aureus</i>	WO98/20157	tuf
	1729 <i>Staphylococcus saprophyticus</i>	WO98/20157	tuf
	1730 <i>Staphylococcus simulans</i>	WO98/20157	tuf
50	1731 <i>Streptococcus agalactiae</i>	WO98/20157	tuf
	1732 <i>Streptococcus pneumoniae</i>	WO98/20157	tuf
	1733 <i>Streptococcus salivarius</i>	WO98/20157	tuf
	1734 <i>Agrobacterium radiobacter</i>	WO98/20157	tuf
	1735 <i>Bacillus subtilis</i>	WO98/20157	tuf
55	1736 <i>Bacteroides fragilis</i>	WO98/20157	tuf
	1737 <i>Borrelia burgdorferi</i>	WO98/20157	tuf
	1738 <i>Brevibacterium linens</i>	WO98/20157	tuf
	1739 <i>Chlamydia trachomatis</i>	WO98/20157	tuf
	1740 <i>Fibrobacter succinogenes</i>	WO98/20157	tuf
60	1741 <i>Flavobacterium ferrugineum</i>	WO98/20157	tuf
	1742 <i>Helicobacter pylori</i>	WO98/20157	tuf
	1743 <i>Micrococcus luteus</i>	WO98/20157	tuf
	1744 <i>Mycobacterium tuberculosis</i>	WO98/20157	tuf
	1745 <i>Mycoplasma genitalium</i>	WO98/20157	tuf
65	1746 <i>Neisseria gonorrhoeae</i>	WO98/20157	tuf

Table 7. Origin of the nucleic acids and/or sequences in the sequence listing (continued).

SEQ ID NO.	Archaeal, bacterial, fungal or parasitical species	Source	Gene*
5	1747 <i>Rickettsia prowazekii</i>	WO98/20157	tuf
	1748 <i>Salmonella choleraesuis</i> subsp. <i>choleraesuis</i>	WO98/20157	tuf
	serotype Typhimurium		
	1749 <i>Shewanella putrefaciens</i>	WO98/20157	tuf
10	1750 <i>Stigmatella aurantiaca</i>	WO98/20157	tuf
	1751 <i>Thiomonas cuprina</i>	WO98/20157	tuf
	1752 <i>Treponema pallidum</i>	WO98/20157	tuf
	1753 <i>Ureaplasma urealyticum</i>	WO98/20157	tuf
15	1754 <i>Wolinella succinogenes</i>	WO98/20157	tuf
	1755 <i>Burkholderia cepacia</i>	WO98/20157	tuf
	1756 <i>Bacillus anthracis</i>	This patent	recA
	1757 <i>Bacillus anthracis</i>	This patent	recA
20	1758 <i>Bacillus cereus</i>	This patent	recA
	1759 <i>Bacillus cereus</i>	This patent	recA
	1760 <i>Bacillus mycoides</i>	This patent	recA
	1761 <i>Bacillus pseudomycoides</i>	This patent	recA
25	1762 <i>Bacillus thuringiensis</i>	This patent	recA
	1763 <i>Bacillus thuringiensis</i>	This patent	recA
	1764 <i>Klebsiella oxytoca</i>	This patent	gyrA
	1765 <i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	This patent	gyrA
30	1766 <i>Klebsiella planticola</i>	This patent	gyrA
	1767 <i>Klebsiella pneumoniae</i>	This patent	gyrA
	1768 <i>Klebsiella pneumoniae</i> subsp. <i>pneumoniae</i>	This patent	gyrA
	1769 <i>Klebsiella pneumoniae</i> subsp. <i>pneumoniae</i>	This patent	gyrA
35	1770 <i>Klebsiella pneumoniae</i> subsp. <i>rhinoscleromatis</i>	This patent	gyrA
	1771 <i>Klebsiella terrigena</i>	This patent	gyrA
	1772 <i>Legionella pneumophila</i> subsp. <i>pneumophila</i>	This patent	gyrA
	1773 <i>Proteus mirabilis</i>	This patent	gyrA
40	1774 <i>Providencia rettgeri</i>	This patent	gyrA
	1775 <i>Proteus vulgaris</i>	This patent	gyrA
	1776 <i>Yersinia enterocolitica</i>	This patent	gyrA
	1777 <i>Klebsiella oxytoca</i>	This patent	parC (grlA)
45	1778 <i>Klebsiella oxytoca</i>	This patent	parC (grlA)
	1779 <i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	This patent	parC (grlA)
	1780 <i>Klebsiella planticola</i>	This patent	parC (grlA)
	1781 <i>Klebsiella pneumoniae</i>	This patent	parC (grlA)
50	1782 <i>Klebsiella pneumoniae</i> subsp. <i>pneumoniae</i>	This patent	parC (grlA)
	1783 <i>Klebsiella pneumoniae</i> subsp. <i>pneumoniae</i>	This patent	parC (grlA)
	1784 <i>Klebsiella pneumoniae</i> subsp. <i>rhinoscleromatis</i>	This patent	parC (grlA)
	1785 <i>Klebsiella terrigena</i>	This patent	parC (grlA)
55	1786 <i>Bacillus cereus</i>	This patent	fusA
	1787 <i>Bacillus cereus</i>	This patent	fusA
	1788 <i>Bacillus anthracis</i>	This patent	fusA
	1789 <i>Bacillus cereus</i>	This patent	fusA
60	1790 <i>Bacillus anthracis</i>	This patent	fusA
	1791 <i>Bacillus pseudomycoides</i>	This patent	fusA
	1792 <i>Bacillus cereus</i>	This patent	fusA
	1793 <i>Bacillus anthracis</i>	This patent	fusA
65	1794 <i>Bacillus cereus</i>	This patent	fusA
	1795 <i>Bacillus weihenstephanensis</i>	This patent	fusA
	1796 <i>Bacillus mycoides</i>	This patent	fusA
	1797 <i>Bacillus thuringiensis</i>	This patent	fusA
65	1798 <i>Bacillus weihenstephanensis</i>	This patent	fusA-tuf spacer
	1799 <i>Bacillus thuringiensis</i>	This patent	fusA-tuf spacer
	1800 <i>Bacillus anthracis</i>	This patent	fusA-tuf spacer
	1801 <i>Bacillus pseudomycoides</i>	This patent	fusA-tuf spacer
65	1802 <i>Bacillus anthracis</i>	This patent	fusA-tuf spacer
	1803 <i>Bacillus cereus</i>	This patent	fusA-tuf spacer
	1804 <i>Bacillus cereus</i>	This patent	fusA-tuf spacer
	1805 <i>Bacillus mycoides</i>	This patent	fusA-tuf spacer
65	1806 <i>Bacillus cereus</i>	This patent	fusA-tuf spacer

Table 7. Origin of the nucleic acids and/or sequences in the sequence listing (continued).

SEQ ID NO.	Archaeal, bacterial, fungal or parasitical species	Source	Gene*
5	1807 <i>Bacillus cereus</i>	This patent	<i>fusA-tuf</i> spacer
	1808 <i>Bacillus cereus</i>	This patent	<i>fusA-tuf</i> spacer
	1809 <i>Bacillus anthracis</i>	This patent	<i>fusA-tuf</i> spacer
	1810 <i>Bacillus mycoides</i>	This patent	<i>tuf</i>
	1811 <i>Bacillus thuringiensis</i>	This patent	<i>tuf</i>
10	1812 <i>Bacillus cereus</i>	This patent	<i>tuf</i>
	1813 <i>Bacillus weihenstephanensis</i>	This patent	<i>tuf</i>
	1814 <i>Bacillus anthracis</i>	This patent	<i>tuf</i>
	1815 <i>Bacillus cereus</i>	This patent	<i>tuf</i>
15	1816 <i>Bacillus cereus</i>	This patent	<i>tuf</i>
	1817 <i>Bacillus anthracis</i>	This patent	<i>tuf</i>
	1818 <i>Bacillus cereus</i>	This patent	<i>tuf</i>
	1819 <i>Bacillus anthracis</i>	This patent	<i>tuf</i>
20	1820 <i>Bacillus pseudomycoloides</i>	This patent	<i>tuf</i>
	1821 <i>Bacillus cereus</i>	This patent	<i>tuf</i>
	1822 <i>Streptococcus oralis</i>	This patent	<i>fusA</i>
	1823 <i>Budvicia aquatica</i>	This patent	<i>fusA</i>
25	1824 <i>Buttiauxella agrestis</i>	This patent	<i>fusA</i>
	1825 <i>Klebsiella oxytoca</i>	This patent	<i>fusA</i>
	1826 <i>Plesiomonas shigelloides</i>	This patent	<i>fusA</i>
	1827 <i>Shewanella putrefaciens</i>	This patent	<i>fusA</i>
30	1828 <i>Obesumbacterium proteus</i>	This patent	<i>fusA</i>
	1829 <i>Klebsiella oxytoca</i>	This patent	<i>fusA-tuf</i> spacer
	1830 <i>Budvicia aquatica</i>	This patent	<i>fusA-tuf</i> spacer
	1831 <i>Plesiomonas shigelloides</i>	This patent	<i>fusA-tuf</i> spacer
35	1832 <i>Obesumbacterium proteus</i>	This patent	<i>fusA-tuf</i> spacer
	1833 <i>Shewanella putrefaciens</i>	This patent	<i>fusA-tuf</i> spacer
	1834 <i>Buttiauxella agrestis</i>	This patent	<i>fusA-tuf</i> spacer
	1835 <i>Campylobacter coli</i>	This patent	<i>tuf</i>
40	1836 <i>Campylobacter fetus</i> subsp. <i>fetus</i>	This patent	<i>tuf</i>
	1837 <i>Campylobacter fetus</i> subsp. <i>venerealis</i>	This patent	<i>tuf</i>
	1838 <i>Buttiauxella agrestis</i>	This patent	<i>tuf</i>
	1839 <i>Klebsiella oxytoca</i>	This patent	<i>tuf</i>
45	1840 <i>Plesiomonas shigelloides</i>	This patent	<i>tuf</i>
	1841 <i>Shewanella putrefaciens</i>	This patent	<i>tuf</i>
	1842 <i>Obesumbacterium proteus</i>	This patent	<i>tuf</i>
	1843 <i>Budvicia aquatica</i>	This patent	<i>tuf</i>
50	1844 <i>Abiotrophia adiacens</i>	This patent	<i>atpD</i>
	1845 <i>Arcanobacterium haemolyticum</i>	This patent	<i>atpD</i>
	1846 <i>Basidiobolus ranarum</i>	This patent	<i>atpD</i>
	1847 <i>Blastomyces dermatitidis</i>	This patent	<i>atpD</i>
55	1848 <i>Blastomyces dermatitidis</i>	This patent	<i>atpD</i>
	1849 <i>Campylobacter coli</i>	This patent	<i>atpD</i>
	1850 <i>Campylobacter fetus</i> subsp. <i>fetus</i>	This patent	<i>atpD</i>
	1851 <i>Campylobacter fetus</i> subsp. <i>venerealis</i>	This patent	<i>atpD</i>
60	1852 <i>Campylobacter gracilis</i>	This patent	<i>atpD</i>
	1853 <i>Campylobacter jejuni</i> subsp. <i>jejuni</i>	This patent	<i>atpD</i>
	1854 <i>Enterococcus cecorum</i>	This patent	<i>atpD</i>
	1855 <i>Enterococcus columbae</i>	This patent	<i>atpD</i>
65	1856 <i>Enterococcus dispar</i>	This patent	<i>atpD</i>
	1857 <i>Enterococcus malodoratus</i>	This patent	<i>atpD</i>
	1858 <i>Enterococcus mundtii</i>	This patent	<i>atpD</i>
	1859 <i>Enterococcus raffinosus</i>	This patent	<i>atpD</i>
65	1860 <i>Globicatella sanguis</i>	This patent	<i>atpD</i>
	1861 <i>Lactococcus garvieae</i>	This patent	<i>atpD</i>
	1862 <i>Lactococcus lactis</i>	This patent	<i>atpD</i>
	1863 <i>Listeria ivanovii</i>	This patent	<i>atpD</i>
65	1864 <i>Succinivibrio dextrinosolvens</i>	This patent	<i>atpD</i>
	1865 <i>Tetragenococcus halophilus</i>	This patent	<i>atpD</i>
	1866 <i>Campylobacter fetus</i> subsp. <i>fetus</i>	This patent	<i>recA</i>
	1867 <i>Campylobacter fetus</i> subsp. <i>venerealis</i>	This patent	<i>recA</i>
	1868 <i>Campylobacter jejuni</i> subsp. <i>jejuni</i>	This patent	<i>recA</i>

Table 7. Origin of the nucleic acids and/or sequences in the sequence listing (continued).

SEQ ID NO.	Archaeal, bacterial, fungal or parasitical species	Source	Gene*
5	1869 <i>Enterococcus avium</i>	This patent	<i>recA</i>
	1870 <i>Enterococcus faecium</i>	This patent	<i>recA</i>
	1871 <i>Listeria monocytogenes</i>	This patent	<i>recA</i>
	1872 <i>Streptococcus mitis</i>	This patent	<i>recA</i>
	1873 <i>Streptococcus oralis</i>	This patent	<i>recA</i>
10	1874 <i>Aspergillus fumigatus</i>	This patent	<i>tuf</i> (M)
	1875 <i>Aspergillus versicolor</i>	This patent	<i>tuf</i> (M)
	1876 <i>Basidiobolus ranarum</i>	This patent	<i>tuf</i> (M)
	1877 <i>Campylobacter gracilis</i>	This patent	<i>tuf</i>
	1878 <i>Campylobacter jejuni</i> subsp. <i>jejuni</i>	This patent	<i>tuf</i>
15	1879 <i>Coccidioides immitis</i>	This patent	<i>tuf</i> (M)
	1880 <i>Erwinia amylovora</i>	This patent	<i>tuf</i>
	1881 <i>Salmonella choleraesuis</i> subsp. <i>choleraesuis</i> serotype Typhimurium	This patent	<i>tuf</i>
20	1899 <i>Klebsiella pneumoniae</i>	Database	<i>blaSHV</i>
	1900 <i>Klebsiella pneumoniae</i>	Database	<i>blaSHV</i>
	1901 <i>Escherichia coli</i>	Database	<i>blaSHV</i>
	1902 <i>Klebsiella pneumoniae</i>	Database	<i>blaSHV</i>
	1903 <i>Klebsiella pneumoniae</i>	Database	<i>blaSHV</i>
25	1904 <i>Escherichia coli</i>	Database	<i>blaSHV</i>
	1905 <i>Pseudomonas aeruginosa</i>	Database	<i>blaSHV</i>
	1927 <i>Neisseria meningitidis</i>	Database	<i>blaTEM</i>
	1928 <i>Escherichia coli</i>	Database	<i>blaTEM</i>
	1929 <i>Klebsiella oxytoca</i>	Database	<i>blaTEM</i>
30	1930 <i>Escherichia coli</i>	Database	<i>blaTEM</i>
	1931 <i>Escherichia coli</i>	Database	<i>blaTEM</i>
	1932 <i>Escherichia coli</i>	Database	<i>blaTEM</i>
	1933 <i>Escherichia coli</i>	Database	<i>blaTEM</i>
	1954 <i>Klebsiella pneumoniae</i> subsp. <i>pneumoniae</i>	Database	<i>gyrA</i>
35	1956 <i>Candida inconspicua</i>	This patent	<i>tuf</i> (M)
	1957 <i>Candida utilis</i>	This patent	<i>tuf</i> (M)
	1958 <i>Candida zeylanoides</i>	This patent	<i>tuf</i> (M)
	1959 <i>Candida catenulata</i>	This patent	<i>tuf</i> (M)
	1960 <i>Candida krusei</i>	This patent	<i>tuf</i> (M)
40	1965 Plasmid pGS05	Database	<i>sullI</i>
	1970 Transposon Tn10	Database	<i>tetB</i>
	1985 <i>Cryptococcus neoformans</i>	Database	<i>tuf</i> (EF-1)
	1986 <i>Cryptococcus neoformans</i>	Database	<i>tuf</i> (EF-1)
	1987 <i>Saccharomyces cerevisiae</i>	Database	<i>tuf</i> (EF-1)
45	1988 <i>Saccharomyces cerevisiae</i>	Database	<i>tuf</i> (EF-1)
	1989 <i>Eremothecium gossypii</i>	Database	<i>tuf</i> (EF-1)
	1990 <i>Eremothecium gossypii</i>	Database	<i>tuf</i> (EF-1)
	1991 <i>Aspergillus oryzae</i>	Database	<i>tuf</i> (EF-1)
	1992 <i>Aureobasidium pullulans</i>	Database	<i>tuf</i> (EF-1)
50	1993 <i>Histoplasma capsulatum</i>	Database	<i>tuf</i> (EF-1)
	1994 <i>Neurospora crassa</i>	Database	<i>tuf</i> (EF-1)
	1995 <i>Podospira anserina</i>	Database	<i>tuf</i> (EF-1)
	1996 <i>Podospira curvicolli</i>	Database	<i>tuf</i> (EF-1)
	1997 <i>Sordaria macrospora</i>	Database	<i>tuf</i> (EF-1)
55	1998 <i>Trichoderma reesei</i>	Database	<i>tuf</i> (EF-1)
	2004 <i>Candida albicans</i>	Database	<i>tuf</i> (M)
	2005 <i>Schizosaccharomyces pombe</i>	Database	<i>tuf</i> (M)
	2010 <i>Klebsiella pneumoniae</i>	Database	<i>blaTEM</i>
	2011 <i>Klebsiella pneumoniae</i>	Database	<i>blaTEM</i>
60	2013 <i>Kluyvera ascorbata</i>	This patent	<i>gyrA</i>
	2014 <i>Kluyvera georgiana</i>	This patent	<i>gyrA</i>
	2047 <i>Streptococcus pneumoniae</i>	Database	<i>pbp1A</i>
	2048 <i>Streptococcus pneumoniae</i>	Database	<i>pbp1A</i>
	2049 <i>Streptococcus pneumoniae</i>	Database	<i>pbp1A</i>

Table 7. Origin of the nucleic acids and/or sequences in the sequence listing (continued).

SEQ ID NO.	Archaeal, bacterial, fungal or parasitica species	Source	Gene*
5	2050 <i>Streptococcus pneumoniae</i>	Database	<i>pbp1A</i>
	2051 <i>Streptococcus pneumoniae</i>	Database	<i>pbp1A</i>
	2052 <i>Streptococcus pneumoniae</i>	Database	<i>pbp1A</i>
	2053 <i>Streptococcus pneumoniae</i>	Database	<i>pbp1A</i>
	2054 <i>Streptococcus pneumoniae</i>	Database	<i>gyrA</i>
10	2055 <i>Streptococcus pneumoniae</i>	Database	<i>parC</i>
	2056 <i>Streptococcus pneumoniae</i>	This patent	<i>pbp1A</i>
	2057 <i>Streptococcus pneumoniae</i>	This patent	<i>pbp1A</i>
	2058 <i>Streptococcus pneumoniae</i>	This patent	<i>pbp1A</i>
	2059 <i>Streptococcus pneumoniae</i>	This patent	<i>pbp1A</i>
15	2060 <i>Streptococcus pneumoniae</i>	This patent	<i>pbp1A</i>
	2061 <i>Streptococcus pneumoniae</i>	This patent	<i>pbp1A</i>
	2062 <i>Streptococcus pneumoniae</i>	This patent	<i>pbp1A</i>
	2063 <i>Streptococcus pneumoniae</i>	This patent	<i>pbp1A</i>
	2064 <i>Streptococcus pneumoniae</i>	This patent	<i>pbp1A</i>
20	2072 <i>Mycobacterium tuberculosis</i>	Database	<i>rpoB</i>
	2097 <i>Mycoplasma pneumoniae</i>	Database	<i>tuf</i>
	2101 <i>Mycobacterium tuberculosis</i>	Database	<i>inhA</i>
	2105 <i>Mycobacterium tuberculosis</i>	Database	<i>embB</i>
	2129 <i>Clostridium difficile</i>	Database	<i>cdtA</i>
25	2130 <i>Clostridium difficile</i>	Database	<i>cdtB</i>
	2137 <i>Pseudomonas putida</i>	Genome project	<i>tuf</i>
	2138 <i>Pseudomonas aeruginosa</i>	Genome project	<i>tuf</i>
	2139 <i>Campylobacter jejuni</i>	Database	<i>atpD</i>
	2140 <i>Streptococcus pneumoniae</i>	Database	<i>pbp1a</i>
30	2144 <i>Staphylococcus aureus</i>	Database	<i>mupA</i>
	2147 <i>Escherichia coli</i>	Database	<i>catI</i>
	2150 <i>Escherichia coli</i>	Database	<i>catII</i>
	2153 <i>Shigella flexneri</i>	Database	<i>catIII</i>
	2156 <i>Clostridium perfringens</i>	Database	<i>catP</i>
35	2159 <i>Staphylococcus aureus</i>	Database	<i>cat</i>
	2162 <i>Staphylococcus aureus</i>	Database	<i>cat</i>
	2165 <i>Salmonella typhimurium</i>	Database	<i>ppfla-like</i>
	2183 <i>Alcaligenes faecalis</i> subsp. <i>faecalis</i>	This patent	<i>tuf</i>
	2184 <i>Campylobacter coli</i>	This patent	<i>fusA</i>
40	2185 <i>Succinivibrio dextrinosolvens</i>	This patent	<i>tuf</i>
	2186 <i>Tetragenococcus halophilus</i>	This patent	<i>tuf</i>
	2187 <i>Campylobacter jejuni</i> subsp. <i>jejuni</i>	This patent	<i>fusA</i>
	2188 <i>Campylobacter jejuni</i> subsp. <i>jejuni</i>	This patent	<i>fusA</i>
	2189 <i>Leishmania guyanensis</i>	This patent	<i>atpD</i>
45	2190 <i>Trypanosoma brucei brucei</i>	This patent	<i>atpD</i>
	2191 <i>Aspergillus nidulans</i>	This patent	<i>atpD</i>
	2192 <i>Leishmania panamensis</i>	This patent	<i>atpD</i>
	2193 <i>Aspergillus nidulans</i>	This patent	<i>tuf (M)</i>
	2194 <i>Aureobasidium pullulans</i>	This patent	<i>tuf (M)</i>
50	2195 <i>Emmonsia parva</i>	This patent	<i>tuf (M)</i>
	2196 <i>Exserohilum rostratum</i>	This patent	<i>tuf (M)</i>
	2197 <i>Fusarium moniliforme</i>	This patent	<i>tuf (M)</i>
	2198 <i>Fusarium solani</i>	This patent	<i>tuf (M)</i>
	2199 <i>Histoplasma capsulatum</i>	This patent	<i>tuf (M)</i>
55	2200 <i>Kocuria kristinae</i>	This patent	<i>tuf</i>
	2201 <i>Vibrio mimicus</i>	This patent	<i>tuf</i>
	2202 <i>Citrobacter freundii</i>	This patent	<i>recA</i>
	2203 <i>Clostridium botulinum</i>	This patent	<i>recA</i>
	2204 <i>Francisella tularensis</i>	This patent	<i>recA</i>
60	2205 <i>Peptostreptococcus anaerobius</i>	This patent	<i>recA</i>
	2206 <i>Peptostreptococcus asaccharolyticus</i>	This patent	<i>recA</i>
	2207 <i>Providencia stuartii</i>	This patent	<i>recA</i>

Table 7. Origin of the nucleic acids and/or sequences in the sequence listing (continued).

SEQ ID NO.	Archaeal, bacterial, fungal or parasitical species	Source	Gene*
5	2208 <i>Salmonella choleraesuis</i> subsp. <i>choleraesuis</i> serotype Paratyphi A	This patent	<i>recA</i>
	2209 <i>Salmonella choleraesuis</i> subsp. <i>choleraesuis</i> serotype Typhimurium	This patent	<i>recA</i>
	2210 <i>Staphylococcus saprophyticus</i>	This patent	<i>recA</i>
10	2211 <i>Yersinia pseudotuberculosis</i>	This patent	<i>recA</i>
	2212 <i>Zoogloea ramigera</i>	This patent	<i>recA</i>
	2214 <i>Abiotrophia adiacens</i>	This patent	<i>fusA</i>
	2215 <i>Acinetobacter baumannii</i>	This patent	<i>fusA</i>
	2216 <i>Actinomyces meyeri</i>	This patent	<i>fusA</i>
15	2217 <i>Clostridium difficile</i>	This patent	<i>fusA</i>
	2218 <i>Corynebacterium diphtheriae</i>	This patent	<i>fusA</i>
	2219 <i>Enterobacter cloacae</i>	This patent	<i>fusA</i>
	2220 <i>Klebsiella pneumoniae</i> subsp. <i>pneumoniae</i>	This patent	<i>fusA</i>
	2221 <i>Listeria monocytogenes</i>	This patent	<i>fusA</i>
20	2222 <i>Mycobacterium avium</i>	This patent	<i>fusA</i>
	2223 <i>Mycobacterium gordonae</i>	This patent	<i>fusA</i>
	2224 <i>Mycobacterium kansasii</i>	This patent	<i>fusA</i>
	2225 <i>Mycobacterium terrae</i>	This patent	<i>fusA</i>
	2226 <i>Neisseria polysaccharea</i>	This patent	<i>fusA</i>
25	2227 <i>Staphylococcus epidermidis</i>	This patent	<i>fusA</i>
	2228 <i>Staphylococcus haemolyticus</i>	This patent	<i>fusA</i>
	2229 <i>Succinivibrio dextrinosolvens</i>	This patent	<i>fusA</i>
	2230 <i>Tetragenococcus halophilus</i>	This patent	<i>fusA</i>
	2231 <i>Veillonella parvula</i>	This patent	<i>fusA</i>
30	2232 <i>Yersinia pseudotuberculosis</i>	This patent	<i>fusA</i>
	2233 <i>Zoogloea ramigera</i>	This patent	<i>fusA</i>
	2234 <i>Aeromonas hydrophila</i>	This patent	<i>fusA</i>
	2235 <i>Abiotrophia adiacens</i>	This patent	<i>fusA-tuf</i> spacer
	2236 <i>Acinetobacter baumannii</i>	This patent	<i>fusA-tuf</i> spacer
35	2237 <i>Actinomyces meyeri</i>	This patent	<i>fusA-tuf</i> spacer
	2238 <i>Clostridium difficile</i>	This patent	<i>fusA-tuf</i> spacer
	2239 <i>Corynebacterium diphtheriae</i>	This patent	<i>fusA-tuf</i> spacer
	2240 <i>Enterobacter cloacae</i>	This patent	<i>fusA-tuf</i> spacer
	2241 <i>Klebsiella pneumoniae</i> subsp. <i>pneumoniae</i>	This patent	<i>fusA-tuf</i> spacer
40	2242 <i>Listeria monocytogenes</i>	This patent	<i>fusA-tuf</i> spacer
	2243 <i>Mycobacterium avium</i>	This patent	<i>fusA-tuf</i> spacer
	2244 <i>Mycobacterium gordonae</i>	This patent	<i>fusA-tuf</i> spacer
	2245 <i>Mycobacterium kansasii</i>	This patent	<i>fusA-tuf</i> spacer
	2246 <i>Mycobacterium terrae</i>	This patent	<i>fusA-tuf</i> spacer
45	2247 <i>Neisseria polysaccharea</i>	This patent	<i>fusA-tuf</i> spacer
	2248 <i>Staphylococcus epidermidis</i>	This patent	<i>fusA-tuf</i> spacer
	2249 <i>Staphylococcus haemolyticus</i>	This patent	<i>fusA-tuf</i> spacer
	2255 <i>Abiotrophia adiacens</i>	This patent	<i>tuf</i>
	2256 <i>Acinetobacter baumannii</i>	This patent	<i>tuf</i>
50	2257 <i>Actinomyces meyeri</i>	This patent	<i>tuf</i>
	2258 <i>Clostridium difficile</i>	This patent	<i>tuf</i>
	2259 <i>Corynebacterium diphtheriae</i>	This patent	<i>tuf</i>
	2260 <i>Enterobacter cloacae</i>	This patent	<i>tuf</i>
	2261 <i>Klebsiella pneumoniae</i> subsp. <i>pneumoniae</i>	This patent	<i>tuf</i>
55	2262 <i>Listeria monocytogenes</i>	This patent	<i>tuf</i>
	2263 <i>Mycobacterium avium</i>	This patent	<i>tuf</i>
	2264 <i>Mycobacterium gordonae</i>	This patent	<i>tuf</i>
	2265 <i>Mycobacterium kansasii</i>	This patent	<i>tuf</i>
	2266 <i>Mycobacterium terrae</i>	This patent	<i>tuf</i>
60	2267 <i>Neisseria polysaccharea</i>	This patent	<i>tuf</i>
	2268 <i>Staphylococcus epidermidis</i>	This patent	<i>tuf</i>
	2269 <i>Staphylococcus haemolyticus</i>	This patent	<i>tuf</i>
	2270 <i>Aeromonas hydrophila</i>	This patent	<i>tuf</i>
	2271 <i>Bilophila wadsworthia</i>	This patent	<i>tuf</i>
65	2272 <i>Brevundimonas diminuta</i>	This patent	<i>tuf</i>
	2273 <i>Streptococcus mitis</i>	This patent	<i>pbp1a</i>

Table 7. Origin of the nucleic acids and/or sequences in the sequence listing (continued).

SEQ ID NO.	Archaeal, bacterial, fungal or parasitical species	Source	Gene*
5	2274 <i>Streptococcus mitis</i>	This patent	<i>pbp1a</i>
	2275 <i>Streptococcus mitis</i>	This patent	<i>pbp1a</i>
	2276 <i>Streptococcus oralis</i>	This patent	<i>pbp1a</i>
	2277 <i>Escherichia coli</i>	This patent	<i>gyrA</i>
	2278 <i>Escherichia coli</i>	This patent	<i>gyrA</i>
10	2279 <i>Escherichia coli</i>	This patent	<i>gyrA</i>
	2280 <i>Escherichia coli</i>	This patent	<i>gyrA</i>
	2288 <i>Enterococcus faecium</i>	Database	<i>ddl</i>
	2293 <i>Enterococcus faecium</i>	Database	<i>vanA</i>
	2296 <i>Enterococcus faecalis</i>	Database	<i>vanB</i>
15			

* *tuf* indicates *tuf* sequences, *tuf* (C) indicates *tuf* sequences divergent from main (usually A and B) copies of the elongation factor-Tu, *tuf* (EF-1) indicates *tuf* sequences of the eukaryotic type (elongation factor 1 α), *tuf* (M) indicates *tuf* sequences from organellar (mostly mitochondrial) origin.

20

fusA indicates *fusA* sequences; *fusA-tuf* spacer indicates the intergenic region between *fusA* and *tuf*.

atpD indicates *atpD* sequences of the F-type, *atpD* (V) indicates *atpD* sequences of the V-type.

recA indicates *recA* sequences, *recA*(Rad51) indicates *rad51* sequences or homologs and *recA*(Dmc1) indicates *dmc1* sequences or homologs.

Table 8. Bacterial species used to test the specificity of the *Streptococcus agalactiae*-specific amplification primers derived from *tuf* sequences.

5	Strain	Reference number	Strain	Reference number
	<i>Streptococcus acidominimus</i>	ATCC 51726	<i>Bacteroides caccae</i>	ATCC 43185
	<i>Streptococcus agalactiae</i>	ATCC 12403	<i>Bacteroides vulgatus</i>	ATCC 8482
	<i>Streptococcus agalactiae</i>	ATCC 12973	<i>Bacteroides fragilis</i>	ATCC 25285
10	<i>Streptococcus agalactiae</i>	ATCC 13813	<i>Candida albicans</i>	ATCC 11006
	<i>Streptococcus agalactiae</i>	ATCC 27591	<i>Clostridium innocuum</i>	ATCC 14501
	<i>Streptococcus agalactiae</i>	CDCs 1073	<i>Clostridium ramosum</i>	ATCC 25582
	<i>Streptococcus anginosus</i>	ATCC 27335	<i>Lactobacillus casei</i> subsp. <i>casei</i>	ATCC 393
	<i>Streptococcus anginosus</i>	ATCC 33397	<i>Clostridium septicum</i>	ATCC 12464
15	<i>Streptococcus bovis</i>	ATCC 33317	<i>Corynebacterium cervicis</i>	NCTC 10604
	<i>Streptococcus anginosus</i>	ATCC 27823	<i>Corynebacterium genitalium</i>	ATCC 33031
	<i>Streptococcus cricetus</i>	ATCC 19642	<i>Corynebacterium urealyticum</i>	ATCC 43042
	<i>Streptococcus cristatus</i>	ATCC 51100	<i>Enterococcus faecalis</i>	ATCC 29212
	<i>Streptococcus downei</i>	ATCC 33748	<i>Enterococcus faecium</i>	ATCC 19434
20	<i>Streptococcus dysgalactiae</i>	ATCC 43078	<i>Eubacterium lentum</i>	ATCC 43055
	<i>Streptococcus equi</i> subsp. <i>equi</i>	ATCC 9528	<i>Eubacterium nodulum</i>	ATCC 33099
	<i>Streptococcus ferus</i>	ATCC 33477	<i>Gardnerella vaginalis</i>	ATCC 14018
	<i>Streptococcus gordonii</i>	ATCC 10558	<i>Lactobacillus acidophilus</i>	ATCC 4356
	<i>Streptococcus macacae</i>	ATCC 35911	<i>Lactobacillus crispatus</i>	ATCC 33820
25	<i>Streptococcus mitis</i>	ATCC 49456	<i>Lactobacillus gasseri</i>	ATCC 33323
	<i>Streptococcus mutans</i>	ATCC 25175	<i>Lactobacillus johnsonii</i>	ATCC 33200
	<i>Streptococcus oralis</i>	ATCC 35037	<i>Lactococcus lactis</i> subsp. <i>lactis</i>	ATCC 19435
	<i>Streptococcus parasanguinis</i>	ATCC 15912	<i>Lactococcus lactis</i> subsp. <i>lactis</i>	ATCC 11454
	<i>Streptococcus parauberis</i>	DSM 6631	<i>Listeria innocua</i>	ATCC 33090
30	<i>Streptococcus pneumoniae</i>	ATCC 27336	<i>Micrococcus luteus</i>	ATCC 9341
	<i>Streptococcus pyogenes</i>	ATCC 19615	<i>Escherichia coli</i>	ATCC 25922
	<i>Streptococcus rattii</i>	ATCC 19645	<i>Micrococcus lylae</i>	ATCC 27566
	<i>Streptococcus salivarius</i>	ATCC 7073	<i>Porphyromonas asaccharolytica</i>	ATCC 25260
	<i>Streptococcus sanguinis</i>	ATCC 10556	<i>Prevotella corporis</i>	ATCC 33547
35	<i>Streptococcus sobrinus</i>	ATCC 27352	<i>Prevotella melanogenica</i>	ATCC 25845
	<i>Streptococcus suis</i>	ATCC 43765	<i>Staphylococcus aureus</i>	ATCC 13301
	<i>Streptococcus uberis</i>	ATCC 19436	<i>Staphylococcus epidermidis</i>	ATCC 14990
	<i>Streptococcus vestibularis</i>	ATCC 49124	<i>Staphylococcus saprophyticus</i>	ATCC 15305
40				

Table 9. Bacterial species used to test the specificity of the *Streptococcus agalactiae*-specific amplification primers derived from *atpD* sequences.

5	Strain	Reference number	Strain	Reference number
	<i>Streptococcus acidominimus</i>	ATCC 51726	<i>Streptococcus gordonii</i>	ATCC 10558
	<i>Streptococcus agalactiae</i>	ATCC 12400	<i>Streptococcus macacae</i>	ATCC 35911
	<i>Streptococcus agalactiae</i>	ATCC 12403	<i>Streptococcus mitis</i>	ATCC 49456
10	<i>Streptococcus agalactiae</i>	ATCC 12973	<i>Streptococcus mutans</i>	ATCC 25175
	<i>Streptococcus agalactiae</i>	ATCC 13813	<i>Streptococcus oralis</i>	ATCC 35037
	<i>Streptococcus agalactiae</i>	ATCC 27591	<i>Streptococcus parasanguinis</i>	ATCC 15912
	<i>Streptococcus agalactiae</i>	CDCs-1073	<i>Streptococcus parauberis</i>	DSM 6631
	<i>Streptococcus anginosus</i>	ATCC 27335	<i>Streptococcus pneumoniae</i>	ATCC 27336
15	<i>Streptococcus anginosus</i>	ATCC 27823	<i>Streptococcus pyogenes</i>	ATCC 19615
	<i>Streptococcus bovis</i>	ATCC 33317	<i>Streptococcus rattii</i>	ATCC 19645
	<i>Streptococcus cricetus</i>	ATCC 19642	<i>Streptococcus salivarius</i>	ATCC 7073
	<i>Streptococcus cristatus</i>	ATCC 51100	<i>Streptococcus sanguinis</i>	ATCC 10556
	<i>Streptococcus downei</i>	ATCC 33748	<i>Streptococcus sobrinus</i>	ATCC 27352
20	<i>Streptococcus dysgalactiae</i>	ATCC 43078	<i>Streptococcus suis</i>	ATCC 43765
	<i>Streptococcus equi</i> subsp. <i>equi</i>	ATCC 9528	<i>Streptococcus uberis</i>	ATCC 19436
	<i>Streptococcus ferus</i>	ATCC 33477	<i>Streptococcus vestibularis</i>	ATCC 49124

Table 10. Bacterial species used to test the specificity of the *Enterococcus*-specific amplification primers derived from *tuf* sequences.

	Strain	Reference number	Strain	Reference number
5	Gram-positive species (n=74)			
	<i>Abiotrophia adiacens</i>	ATCC 49176	<i>Listeria innocua</i>	ATCC 33090
	<i>Abiotrophia defectiva</i>	ATCC 49175	<i>Listeria ivanovii</i>	ATCC 19119
	<i>Bacillus cereus</i>	ATCC 14579	<i>Listeria monocytogenes</i>	ATCC 15313
	<i>Bacillus subtilis</i>	ATCC 27370	<i>Listeria seeligeri</i>	ATCC 35967
10	<i>Bifidobacterium adolescentis</i>	ATCC 27534	<i>Micrococcus luteus</i>	ATCC 9341
	<i>Bifidobacterium breve</i>	ATCC 15700	<i>Pediococcus acidilacti</i>	ATCC 33314
	<i>Bifidobacterium dentium</i>	ATCC 27534	<i>Pediococcus pentosaceus</i>	ATCC 33316
	<i>Bifidobacterium longum</i>	ATCC 15707	<i>Peptococcus niger</i>	ATCC 27731
	<i>Clostridium perfringens</i>	ATCC 3124	<i>Peptostreptococcus anaerobius</i>	ATCC 27337
15	<i>Clostridium septicum</i>	ATCC 12464	<i>Peptostreptococcus indolicus</i>	ATCC 29247
	<i>Corynebacterium aquaticus</i>	ATCC 14665	<i>Peptostreptococcus micros</i>	ATCC 33270
	<i>Corynebacterium pseudodiphtheriticum</i>	ATCC 10700	<i>Propionibacterium acnes</i>	ATCC 6919
	<i>Enterococcus avium</i>	ATCC 14025	<i>Staphylococcus aureus</i>	ATCC 43300
20	<i>Enterococcus casseliflavus</i>	ATCC 25788	<i>Staphylococcus capitis</i>	ATCC 27840
	<i>Enterococcus cecorum</i>	ATCC 43199	<i>Staphylococcus epidermidis</i>	ATCC 14990
	<i>Enterococcus columbae</i>	ATCC 51263	<i>Staphylococcus haemolyticus</i>	ATCC 29970
	<i>Enterococcus dispar</i>	ATCC 51266	<i>Staphylococcus hominis</i>	ATCC 27844
	<i>Enterococcus durans</i>	ATCC 19432	<i>Staphylococcus lugdunensis</i>	ATCC 43809
25	<i>Enterococcus faecalis</i>	ATCC 29212	<i>Staphylococcus saprophyticus</i>	ATCC 15305
	<i>Enterococcus faecium</i>	ATCC 19434	<i>Staphylococcus simulans</i>	ATCC 27848
	<i>Enterococcus flavescens</i>	ATCC 49996	<i>Staphylococcus warneri</i>	ATCC 27836
	<i>Enterococcus gallinarum</i>	ATCC 49573	<i>Streptococcus agalactiae</i>	ATCC 13813
	<i>Enterococcus hirae</i>	ATCC 8044	<i>Streptococcus anginosus</i>	ATCC 33397
30	<i>Enterococcus malodoratus</i>	ATCC 43197	<i>Streptococcus bovis</i>	ATCC 33317
	<i>Enterococcus mundtii</i>	ATCC 43186	<i>Streptococcus constellatus</i>	ATCC 27823
	<i>Enterococcus pseudoavium</i>	ATCC 49372	<i>Streptococcus cristatus</i>	ATCC 51100
	<i>Enterococcus raffinosus</i>	ATCC 49427	<i>Streptococcus intermedius</i>	ATCC 27335
	<i>Enterococcus saccharolyticus</i>	ATCC 43076	<i>Streptococcus mitis</i>	ATCC 49456
35	<i>Enterococcus solitarius</i>	ATCC 49428	<i>Streptococcus mitis</i>	ATCC 3639
	<i>Enterococcus sulfureus</i>	ATCC 49903	<i>Streptococcus mutans</i>	ATCC 27175
	<i>Eubacterium lentum</i>	ATCC 49903	<i>Streptococcus parasanguinis</i>	ATCC 15912
	<i>Gemella haemolysans</i>	ATCC 10379	<i>Streptococcus pneumoniae</i>	ATCC 27736
	<i>Gemella morbillorum</i>	ATCC 27842	<i>Streptococcus pneumoniae</i>	ATCC 6303
40	<i>Lactobacillus acidophilus</i>	ATCC 4356	<i>Streptococcus pyogenes</i>	ATCC 19615
	<i>Leuconostoc mesenteroides</i>	ATCC 19225	<i>Streptococcus salivarius</i>	ATCC 7073
	<i>Listeria grayi</i>	ATCC 19120	<i>Streptococcus sanguinis</i>	ATCC 10556
	<i>Listeria grayi</i>	ATCC 19123	<i>Streptococcus suis</i>	ATCC 43765

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Table 10. Bacterial species used to test the specificity of the *Enterococcus*-specific amplification primers derived from *tuf* sequences (continued).

	Strain	Reference number	Strain	Reference number
5	Gram-negative species (n=39)			
	<i>Acidominococcus fermentans</i>	ATCC 2508	<i>Hafnia alvei</i>	ATCC 13337
	<i>Acinetobacter baumannii</i>	ATCC 19606	<i>Klebsiella oxytoca</i>	ATCC 13182
	<i>Alcaligenes faecalis</i>	ATCC 8750	<i>Meganomonas hypermegas</i>	ATCC 25560
	<i>Anaerobiospirillum</i>	ATCC 29305	<i>Mitsukoella multiacidus</i>	ATCC 27723
10	<i>succiniproducens</i>		<i>Moraxella catarrhalis</i>	ATCC 43628
	<i>Anaerorhabdus furcosus</i>	ATCC 25662	<i>Morganella morganii</i>	ATCC 25830
	<i>Bacteroides distasonis</i>	ATCC 8503	<i>Neisseria meningitidis</i>	ATCC 13077
	<i>Bacteroides thetaiotaomicron</i>	ATCC 29741	<i>Pasteurella aerogenes</i>	ATCC 27883
	<i>Bacteroides vulgatus</i>	ATCC 8482	<i>Proteus vulgaris</i>	ATCC 13315
15	<i>Bordetella pertussis</i>	LSPQ 3702	<i>Providencia alcalifaciens</i>	ATCC 9886
	<i>Bulkholderia cepacia</i>	LSPQ 2217	<i>Providencia rettgeri</i>	ATCC 9250
	<i>Butyrvibrio fibrinosolvens</i>	ATCC 19171	<i>Pseudomonas aeruginosa</i>	ATCC 27853
	<i>Cardiobacterium hominis</i>	ATCC 15826	<i>Salmonella typhimurium</i>	ATCC 14028
	<i>Citrobacter freundii</i>	ATCC 8090	<i>Serratia marcescens</i>	ATCC 13880
20	<i>Desulfovibrio vulgaris</i>	ATCC 29579	<i>Shigella flexneri</i>	ATCC 12022
	<i>Edwardsiella tarda</i>	ATCC 15947	<i>Shigella sonnei</i>	ATCC 29930
	<i>Enterobacter cloacae</i>	ATCC 13047	<i>Succinivibrio dextrinosolvens</i>	ATCC 19716
	<i>Escherichia coli</i>	ATCC 25922	<i>Tissierella praeacuta</i>	ATCC 25539
	<i>Fusobacterium russii</i>	ATCC 25533	<i>Veillonella parvula</i>	ATCC 10790
25	<i>Haemophilus influenzae</i>	ATCC 9007	<i>Yersinia enterocolitica</i>	ATCC 9610

Table 11. Microbial species for which *tuf* and/or *atpD* and/or *recA* sequences are available in public databases.

Species	Strain	Accession number	Coding gene*
<u>tuf sequences</u>			
Bacteria			
5	<i>Actinobacillus actinomycetemcomitans</i>	HK1651	Genome project ²
	<i>Actinobacillus actinomycetemcomitans</i>	HK1651	Genome project ²
	<i>Agrobacterium tumefaciens</i>	X99673	<i>tuf</i>
	<i>Agrobacterium tumefaciens</i>	X99673	<i>tuf</i> (EF-G)
	<i>Agrobacterium tumefaciens</i>	X99674	<i>tuf</i>
10	<i>Anacystis nidulans</i>	PCC 6301	X17442
	<i>Aquifex aeolicus</i>	VF5	AE000669
	<i>Aquifex aeolicus</i>	VF5	AE000669
	<i>Aquifex pyrophilus</i>		Genome project ²
	<i>Aquifex pyrophilus</i>		Y15787
15	<i>Bacillus anthracis</i>	Ames	Genome project ²
	<i>Bacillus anthracis</i>	Ames	Genome project ²
	<i>Bacillus halodurans</i>	C-125	AB017508
	<i>Bacillus halodurans</i>	C-125	AB017508
	<i>Bacillus stearothermophilus</i>	CCM 2184	AJ000260
20	<i>Bacillus subtilis</i>	168	D64127
	<i>Bacillus subtilis</i>	168	D64127
	<i>Bacillus subtilis</i>	DSM 10	Z99104
	<i>Bacillus subtilis</i>	DSM 10	Z99104
	<i>Bacteroides forsythus</i>	ATCC 43037	AB035466
25	<i>Bacteroides fragilis</i>	DSM 1151	- ¹
	<i>Bordetella bronchiseptica</i>	RB50	Genome project ²
	<i>Bordetella pertussis</i>	Tohama 1	Genome project ²
	<i>Bordetella pertussis</i>	Tohama 1	Genome project ²
	<i>Borrelia burgdorferi</i>	B31	U78193
30	<i>Borrelia burgdorferi</i>		AE001155
	<i>Brevibacterium linens</i>	DSM 20425	X76863
	<i>Buchnera aphidicola</i>	Ap	Y12307
	<i>Burkholderia pseudomallei</i>	K96243	Genome project ²
	<i>Campylobacter jejuni</i>	NCTC 11168	Y17167
35	<i>Campylobacter jejuni</i>	NCTC 11168	CJ11168X2
	<i>Chlamydia pneumoniae</i>	CWL029	AE001592
	<i>Chlamydia pneumoniae</i>	CWL029	AE001639
	<i>Chlamydia trachomatis</i>		M74221
	<i>Chlamydia trachomatis</i>	D/UW-3/CX	AE001317
40	<i>Chlamydia trachomatis</i>	D/UW-3/CX	AE001305
	<i>Chlamydia trachomatis</i>	F/IC-Cal-13	L22216
	<i>Chlorobium vibrioforme</i>	DSM 263	X77033
	<i>Chloroflexus aurantiacus</i>	DSM 636	X76865
	<i>Clostridium acetobutylicum</i>	ATCC 824	Genome project ²
45	<i>Clostridium difficile</i>	630	Genome project ²
	<i>Clostridium difficile</i>	630	Genome project ²
	<i>Corynebacterium diphtheriae</i>	NCTC 13129	Genome project ²
	<i>Corynebacterium diphtheriae</i>	NCTC 13129	Genome project ²
	<i>Corynebacterium glutamicum</i>	ASO 19	X77034
50	<i>Corynebacterium glutamicum</i>	MJ-233	E09634
	<i>Coxiella burnetii</i>	Nine Mile phase I	AF136604
	<i>Cytophaga lytica</i>	DSM 2039	X77035
	<i>Deinococcus radiodurans</i>	R1	AE001891
	<i>Deinococcus radiodurans</i>	R1	AE180092
55			

Table 11. Microbial species for which *tuf* and/or *atpD* and/or *recA* sequences are available in public databases (continued).

	Species	Strain	Accession number	Coding gene*
	<i>Deinococcus radiodurans</i>	R1	AE002041	<i>tuf</i>
	<i>Deinonema</i> sp.		- ¹	<i>tuf</i>
	<i>Eikenella corrodens</i>	ATCC 23834	Z12610	<i>tuf</i>
	<i>Eikenella corrodens</i>	ATCC 23834	Z12610	<i>tuf</i> (EF-G)
5	<i>Enterococcus faecalis</i>		Genome project ²	<i>tuf</i> (EF-G)
	<i>Escherichia coli</i>		J01690	<i>tuf</i>
	<i>Escherichia coli</i>		J01717	<i>tuf</i>
	<i>Escherichia coli</i>		X00415	<i>tuf</i> (EF-G)
	<i>Escherichia coli</i>		X57091	<i>tuf</i>
10	<i>Escherichia coli</i>	K-12 MG1655	U00006	<i>tuf</i>
	<i>Escherichia coli</i>	K-12 MG1655	U00096	<i>tuf</i>
	<i>Escherichia coli</i>	K-12 MG1655	AE000410	<i>tuf</i> (EF-G)
	<i>Fervidobacterium islandicum</i>	DSM 5733	Y15788	<i>tuf</i>
	<i>Fibrobacter succinogenes</i>	S85	X76866	<i>tuf</i>
15	<i>Flavobacterium ferrugineum</i>	DSM 13524	X76867	<i>tuf</i>
	<i>Flexistipes sinusarabici</i>		X59461	<i>tuf</i>
	<i>Gloeobacter violaceus</i>	PCC 7421	U09433	<i>tuf</i>
	<i>Gloeotheca</i> sp.	PCC 6501	U09434	<i>tuf</i>
	<i>Haemophilus actinomycetemcomitans</i>	HK1651	Genome project ²	<i>tuf</i>
20	<i>Haemophilus ducreyi</i>	35000	AF087414	<i>tuf</i> (EF-G)
	<i>Haemophilus influenzae</i>	Rd	U32739	<i>tuf</i>
	<i>Haemophilus influenzae</i>	Rd	U32746	<i>tuf</i>
	<i>Haemophilus influenzae</i>	Rd	U32739	<i>tuf</i> (EF-G)
	<i>Helicobacter pylori</i>	26695	AE000511	<i>tuf</i>
25	<i>Helicobacter pylori</i>	J99	AE001539	<i>tuf</i> (EF-G)
	<i>Helicobacter pylori</i>	J99	AE001541	<i>tuf</i>
	<i>Herpetosiphon aurantiacus</i>	Hpga1	X76868	<i>tuf</i>
	<i>Klebsiella pneumoniae</i>	M6H 78578	Genome project ²	<i>tuf</i>
	<i>Klebsiella pneumoniae</i>	M6H 78578	Genome project ²	<i>tuf</i> (EF-G)
30	<i>Lactobacillus paracasei</i>		E13922	<i>tuf</i>
	<i>Legionella pneumophila</i>	Philadelphia-1	Genome project ²	<i>tuf</i>
	<i>Leptospira interrogans</i>		AF115283	<i>tuf</i>
	<i>Leptospira interrogans</i>		AF115283	<i>tuf</i> (EF-G)
	<i>Micrococcus luteus</i>	IFO 3333	M17788	<i>tuf</i> (EF-G)
35	<i>Micrococcus luteus</i>	IFO 3333	M17788	<i>tuf</i>
	<i>Moraxella</i> sp.	TAC II 25	AJ249258	<i>tuf</i>
	<i>Mycobacterium avium</i>	104	Genome project ²	<i>tuf</i>
	<i>Mycobacterium avium</i>	104	Genome project ²	<i>tuf</i> (EF-G)
	<i>Mycobacterium bovis</i>	AF2122/97	Genome project ²	<i>tuf</i>
40	<i>Mycobacterium bovis</i>	AF2122/97	Genome project ²	<i>tuf</i> (EF-G)
	<i>Mycobacterium leprae</i>		L13276	<i>tuf</i>
	<i>Mycobacterium leprae</i>		Z14314	<i>tuf</i>
	<i>Mycobacterium leprae</i>		Z14314	<i>tuf</i> (EF-G)
	<i>Mycobacterium leprae</i>	Thai 53	D13869	<i>tuf</i>
45	<i>Mycobacterium tuberculosis</i>	Erdmann	S40925	<i>tuf</i>
	<i>Mycobacterium tuberculosis</i>	H37Rv	AL021943	<i>tuf</i> (EF-G)
	<i>Mycobacterium tuberculosis</i>	H37Rv	Z84395	<i>tuf</i>
	<i>Mycobacterium tuberculosis</i>	y42	AD000005	<i>tuf</i>
	<i>Mycobacterium tuberculosis</i>	CSU#93	Genome project ²	<i>tuf</i>
50	<i>Mycobacterium tuberculosis</i>	CSU#93	Genome project ²	<i>tuf</i> (EF-G)
	<i>Mycoplasma capricolum</i>	PG-31	X16462	<i>tuf</i>
	<i>Mycoplasma genitalium</i>	G37	U39732	<i>tuf</i>
	<i>Mycoplasma genitalium</i>	G37	U39689	<i>tuf</i> (EF-G)
	<i>Mycoplasma hominis</i>		X57136	<i>tuf</i>
55	<i>Mycoplasma hominis</i>	PG21	M57675	<i>tuf</i>

Table 11. Microbial species for which *tuf* and/or *atpD* and/or *recA* sequences are available in public databases (continued).

	Species	Strain	Accession number	Coding gene*
	<i>Mycoplasma pneumoniae</i>	M129	AE000019	<i>tuf</i>
	<i>Mycoplasma pneumoniae</i>	M129	AE000058	<i>tuf</i> (EF-G)
	<i>Neisseria gonorrhoeae</i>	MS11	L36380	<i>tuf</i>
	<i>Neisseria gonorrhoeae</i>	MS11	L36380	<i>tuf</i> (EF-G)
5	<i>Neisseria meningitidis</i>	Z2491	Genome project ²	<i>tuf</i> (EF-G)
	<i>Neisseria meningitidis</i>	Z2491	Genome project ²	<i>tuf</i>
	<i>Pasteurella multocida</i>	Pm70	Genome project ²	<i>tuf</i>
	<i>Peptococcus niger</i>	DSM 20745	X76869	<i>tuf</i>
	<i>Phormidium ectocarp</i>	PCC 7375	U09443	<i>tuf</i>
10	<i>Planobispora rosea</i>	ATCC 53773	U67308	<i>tuf</i>
	<i>Planobispora rosea</i>	ATCC 53733	X98830	<i>tuf</i>
	<i>Planobispora rosea</i>	ATCC 53733	X98830	<i>tuf</i> (EF-G)
	<i>Plectonema boryanum</i>	PCC 73110	U09444	<i>tuf</i>
	<i>Porphyromonas gingivalis</i>	W83	Genome project ²	<i>tuf</i>
15	<i>Porphyromonas gingivalis</i>	W83	Genome project ²	<i>tuf</i> (EF-G)
	<i>Porphyromonas gingivalis</i>	FDC 381	AB035461	<i>tuf</i>
	<i>Porphyromonas gingivalis</i>	W83	AB035462	<i>tuf</i>
	<i>Porphyromonas gingivalis</i>	SUNY 1021	AB035463	<i>tuf</i>
	<i>Porphyromonas gingivalis</i>	A7A1-28	AB035464	<i>tuf</i>
20	<i>Porphyromonas gingivalis</i>	ATCC 33277	AB035465	<i>tuf</i>
	<i>Porphyromonas gingivalis</i>	ATCC 33277	AB035471	<i>tuf</i> (EF-G)
	<i>Prochlorothrix hollandica</i>		U09445	<i>tuf</i>
	<i>Pseudomonas aeruginosa</i>	PAO-1	Genome project ²	<i>tuf</i>
	<i>Pseudomonas putida</i>		Genome project ²	<i>tuf</i>
25	<i>Rickettsia prowazekii</i>	Madrid E	AJ235272	<i>tuf</i>
	<i>Rickettsia prowazekii</i>	Madrid E	AJ235270	<i>tuf</i> (EF-G)
	<i>Rickettsia prowazekii</i>	Madrid E	Z54171	<i>tuf</i> (EF-G)
	<i>Salmonella choleraesuis</i> subsp. <i>choleraesuis</i> serotype <i>Typhimurium</i>		X64591	<i>tuf</i> (EF-G)
30	<i>Salmonella choleraesuis</i> subsp. <i>choleraesuis</i> serotype <i>Typhimurium</i>	LT2 trpE91	X55116	<i>tuf</i>
	<i>Salmonella choleraesuis</i> subsp. <i>choleraesuis</i> serotype <i>Typhimurium</i>	LT2 trpE91	X55117	<i>tuf</i>
	<i>Serpulina hyodysenteriae</i>	B204	U51635	<i>tuf</i>
35	<i>Serratia marcescens</i>		AF058451	<i>tuf</i>
	<i>Shewanella putrefaciens</i>	DSM 50426		<i>tuf</i>
	<i>Shewanella putrefaciens</i>	MR-1	Genome project ²	<i>tuf</i>
	<i>Spirochaeta aurantia</i>	DSM 1902	X76874	<i>tuf</i>
	<i>Staphylococcus aureus</i>		AJ237696	<i>tuf</i> (EF-G)
40	<i>Staphylococcus aureus</i>	EMRSA-16	Genome project ²	<i>tuf</i>
	<i>Staphylococcus aureus</i>	NCTC 8325	Genome project ²	<i>tuf</i>
	<i>Staphylococcus aureus</i>	COL	Genome project ²	<i>tuf</i>
	<i>Staphylococcus aureus</i>	EMRSA-16	Genome project ²	<i>tuf</i> (EF-G)
	<i>Stigmatella aurantiaca</i>	DW4	X82820	<i>tuf</i>
45	<i>Stigmatella aurantiaca</i>	Sg a1	X76870	<i>tuf</i>
	<i>Streptococcus mutans</i>	GS-5 Kuramitsu	U75481	<i>tuf</i>
	<i>Streptococcus mutans</i>	UAB159	Genome project ²	<i>tuf</i>
	<i>Streptococcus oralis</i>	NTCC 11427	P331701	<i>tuf</i>
	<i>Streptococcus pyogenes</i>		Genome project ²	<i>tuf</i> (EF-G)
50	<i>Streptococcus pyogenes</i>	M1-GAS	Genome project ²	<i>tuf</i>
	<i>Streptomyces aureofaciens</i>	ATCC 10762	AF007125	<i>tuf</i>
	<i>Streptomyces cinnamomeus</i>	Tue89	X98831	<i>tuf</i>
	<i>Streptomyces coelicolor</i>	A3(2)	AL031013	<i>tuf</i> (EF-G)
	<i>Streptomyces coelicolor</i>	A3(2)	X77039	<i>tuf</i> (EF-G)
55	<i>Streptomyces coelicolor</i>	M145	X77039	<i>tuf</i>

Table 11. Microbial species for which *tuf* and/ or *atpD* and/or *recA* sequences are available in public databases (continued).

	Species	Strain	Accession number	Coding gene*
	<i>Streptomyces collinus</i>	BSM 40733	S79408	<i>tuf</i>
	<i>Streptomyces netropsis</i>	Tu1063	AF153618	<i>tuf</i>
	<i>Streptomyces ramocissimus</i>		X67057	<i>tuf</i>
	<i>Streptomyces ramocissimus</i>		X67058	<i>tuf</i>
5	<i>Streptomyces ramocissimus</i>		X67057	<i>tuf</i> (EF-G)
	<i>Synechococcus</i> sp.	PCC 6301	X17442	<i>tuf</i> (EF-G)
	<i>Synechococcus</i> sp.	PCC 6301	X17442	<i>tuf</i>
	<i>Synechocystis</i> sp.	PCC 6803	D90913	<i>tuf</i> (EF-G)
	<i>Synechocystis</i> sp.	PCC 6803	D90913	<i>tuf</i>
10	<i>Synechocystis</i> sp.	PCC 6803	X65159	<i>tuf</i> (EF-G)
	<i>Taxeobacter ocealeus</i>	Myx 2105	X77036	<i>tuf</i>
	<i>Thermotoga maritima</i>		Genome project ²	<i>tuf</i> (EF-G)
	<i>Thermotoga maritima</i>		M27479	<i>tuf</i>
	<i>Thermus aquaticus</i>	EP 00276	X66322	<i>tuf</i>
15	<i>Thermus thermophilus</i>	HB8	X16278	<i>tuf</i> (EF-G)
	<i>Thermus thermophilus</i>	HB8	X05977	<i>tuf</i>
	<i>Thermus thermophilus</i>	HB8	X06657	<i>tuf</i>
	<i>Thiomonas cuprina</i>	DSM 5495	U78300	<i>tuf</i>
	<i>Thiomonas cuprina</i>	DSM 5495	U78300	<i>tuf</i> (EF-G)
20	<i>Thiomonas cuprina</i>	Hoe5	X76871	<i>tuf</i>
	<i>Treponema denticola</i>		Genome project ²	<i>tuf</i>
	<i>Treponema denticola</i>		Genome project ²	<i>tuf</i> (EF-G)
	<i>Treponema pallidum</i>		AE001202	<i>tuf</i>
	<i>Treponema pallidum</i>		AE001222	<i>tuf</i> (EF-G)
25	<i>Treponema pallidum</i>		AE001248	<i>tuf</i> (EF-G)
	<i>Ureaplasma urealyticum</i>	ATCC 33697	Z34275	<i>tuf</i>
	<i>Ureaplasma urealyticum</i>	serovar 3 biovar 1	AE002151	<i>tuf</i>
	<i>Ureaplasma urealyticum</i>	serovar 3 biovar 1	AE002151	<i>tuf</i> (EF-G)
	<i>Vibrio cholerae</i>	N16961	Genome project ²	<i>tuf</i>
30	<i>Wolinella succinogenes</i>	DSM 1740	X76872	<i>tuf</i>
	<i>Yersinia pestis</i>	CO-92	Genome project ²	<i>tuf</i>
	<i>Yersinia pestis</i>	CO-92	Genome project ²	<i>tuf</i> (EF-G)
35	Archaeobacteria			
	<i>Archaeoglobus fulgidus</i>		Genome project ²	<i>tuf</i> (EF-G)
	<i>Halobacterium marismortui</i>		X16677	<i>tuf</i>
	<i>Methanobacterium thermoautotrophicum</i>	delta H	AE000877	<i>tuf</i>
40	<i>Methanococcus jannaschii</i>	ATCC 43067	U67486	<i>tuf</i>
	<i>Methanococcus vannielii</i>		X05698	<i>tuf</i>
	<i>Pyrococcus abyssi</i>	Orsay	AJ248285	<i>tuf</i>
	<i>Thermoplasma acidophilum</i>	DSM 1728	X53866	<i>tuf</i>
45	Fungi			
	<i>Absidia glauca</i>	CBS 101.48	X54730	<i>tuf</i> (EF-1)
	<i>Arxula adeninivorans</i>	Ls3	Z47379	<i>tuf</i> (EF-1)
50	<i>Aspergillus oryzae</i>	KBN616	AB007770	<i>tuf</i> (EF-1)
	<i>Aureobasidium pullulans</i>	R106	U19723	<i>tuf</i> (EF-1)
	<i>Candida albicans</i>	SC5314	Genome project ²	<i>tuf</i> (M)
	<i>Candida albicans</i>	SC5314	M29934	<i>tuf</i> (EF-1)
	<i>Candida albicans</i>	SC5314	M29935	<i>tuf</i> (EF-1)
55	<i>Cryptococcus neoformans</i>	B3501	U81803	<i>tuf</i> (EF-1)

Table 11. Microbial species for which *tuf* and/or *atpD* and/or *recA* sequences are available in public databases (continued).

	Species	Strain	Accession number	Coding gene*
	<i>Cryptococcus neoformans</i>	M1-106	U81804	<i>tuf</i> (EF-1)
	<i>Eremothecium gossypii</i>	ATCC 10895	X73978	<i>tuf</i> (EF-1)
	<i>Eremothecium gossypii</i>		A29820	<i>tuf</i> (EF-1)
	<i>Fusarium oxysporum</i>	NRRL-26037	AF008498	<i>tuf</i> (EF-1)
5	<i>Histoplasma capsulatum</i>	186AS	U14100	<i>tuf</i> (EF-1)
	<i>Podospora anserina</i>		X74799	<i>tuf</i> (EF-1)
	<i>Podospora curvicolle</i>	VLV	X96614	<i>tuf</i> (EF-1)
	<i>Prototheca wickerhamii</i>	263-11	AJ245645	<i>tuf</i> (EF-1)
	<i>Puccinia graminis</i>	race 32	X73529	<i>tuf</i> (EF-1)
10	<i>Reclinomonas americana</i>	ATCC 50394	AF007261	<i>tuf</i> (M)
	<i>Rhizomucor racemosus</i>	ATCC 1216B	X17475	<i>tuf</i> (EF-1)
	<i>Rhizomucor racemosus</i>	ATCC 1216B	J02605	<i>tuf</i> (EF-1)
	<i>Rhizomucor racemosus</i>	ATCC 1216B	X17476	<i>tuf</i> (EF-1)
	<i>Rhodotorula mucilaginosa</i>		AF016239	<i>tuf</i> (EF-1)
15	<i>Saccharomyces cerevisiae</i>		K00428	<i>tuf</i> (M)
	<i>Saccharomyces cerevisiae</i>		M59369	<i>tuf</i> (EF-G)
	<i>Saccharomyces cerevisiae</i>		X00779	<i>tuf</i> (EF-1)
	<i>Saccharomyces cerevisiae</i>		X01638	<i>tuf</i> (EF-1)
	<i>Saccharomyces cerevisiae</i>		M10992	<i>tuf</i> (EF-1)
20	<i>Saccharomyces cerevisiae</i>	Alpha S288	X78993	<i>tuf</i> (EF-1)
	<i>Saccharomyces cerevisiae</i>		M15666	<i>tuf</i> (EF-1)
	<i>Saccharomyces cerevisiae</i>		Z35987	<i>tuf</i> (EF-1)
	<i>Saccharomyces cerevisiae</i>	S288C (AB972)	U51033	<i>tuf</i> (EF-1)
	<i>Schizophyllum commune</i>	1-40	X94913	<i>tuf</i> (EF-1)
25	<i>Schizosaccharomyces pombe</i>	972h-	AL021816	<i>tuf</i> (EF-1)
	<i>Schizosaccharomyces pombe</i>	972h-	AL021813	<i>tuf</i> (EF-1)
	<i>Schizosaccharomyces pombe</i>	972h-	D82571	<i>tuf</i> (EF-1)
	<i>Schizosaccharomyces pombe</i>		U42189	<i>tuf</i> (EF-1)
	<i>Schizosaccharomyces pombe</i>	PR745	D89112	<i>tuf</i> (EF-1)
30	<i>Sordaria macrospora</i>	OOO	X96615	<i>tuf</i> (EF-1)
	<i>Trichoderma reesei</i>	QM9414	Z23012	<i>tuf</i> (EF-1)
	<i>Yarrowia lipolytica</i>		AF054510	<i>tuf</i> (EF-1)
35	Parasites			
	<i>Blastocystis hominis</i>	HE87-1	D64080	<i>tuf</i> (EF-1)
	<i>Cryptosporidium parvum</i>		U69697	<i>tuf</i> (EF-1)
	<i>Eimeria tenella</i>	LS18	AI755521	<i>tuf</i> (EF-1)
40	<i>Entamoeba histolytica</i>	HM1:IMSS	X83565	<i>tuf</i> (EF-1)
	<i>Entamoeba histolytica</i>	NIH 200	M92073	<i>tuf</i> (EF-1)
	<i>Giardia lamblia</i>		D14342	<i>tuf</i> (EF-1)
	<i>Kentrophoros</i> sp.		AF056101	<i>tuf</i> (EF-1)
	<i>Leishmania amazonensis</i>	IFLA/BR/67/PH8	M92653	<i>tuf</i> (EF-1)
45	<i>Leishmania braziliensis</i>		U72244	<i>tuf</i> (EF-1)
	<i>Onchocerca volvulus</i>		M64333	<i>tuf</i> (EF-1)
	<i>Porphyra purpurea</i>	Avonport	U08844	<i>tuf</i> (EF-1)
	<i>Plasmodium berghei</i>	ANKA	AJ224150	<i>tuf</i> (EF-1)
	<i>Plasmodium falciparum</i>	K1	X60488	<i>tuf</i> (EF-1)
50	<i>Plasmodium knowlesi</i>	line H	AJ224153	<i>tuf</i> (EF-1)
	<i>Toxoplasma gondii</i>	RH	Y11431	<i>tuf</i> (EF-1)
	<i>Trichomonas tenax</i>	ATCC 30207	D78479	<i>tuf</i> (EF-1)
	<i>Trypanosoma brucei</i>	LVH/75/	U10562	<i>tuf</i> (EF-1)
55	<i>Trypanosoma cruzi</i>	USAMRU-K/18 Y	L76077	<i>tuf</i> (EF-1)

Table 11. Microbial species for which *tuf* and/or *atpD* and/or *recA* sequences are available in public databases (continued).

	Species	Strain	Accession number	Coding gene*
Human and plants				
	<i>Arabidopsis thaliana</i>	Columbia	X89227	<i>tuf</i> (EF-1)
5	<i>Glycine max</i>	Ceresia	X89058	<i>tuf</i> (EF-1)
	<i>Glycine max</i>	Ceresia	Y15107	<i>tuf</i> (EF-1)
	<i>Glycine max</i>	Ceresia	Y15108	<i>tuf</i> (EF-1)
	<i>Glycine max</i>	Maple Arrow	X66062	<i>tuf</i> (EF-1)
	<i>Homo sapiens</i>		X03558	<i>tuf</i> (EF-1)
10	<i>Pyramimonas disomata</i>		AB008010	<i>tuf</i>
<u>atpD sequences</u>				
15	Bacteria			
	<i>Acetobacterium woodii</i>	DSM 1030	U10505	<i>atpD</i>
	<i>Actinobacillus actinomycetemcomitans</i>	HK1651	Genome project ²	<i>atpD</i>
	<i>Bacillus anthracis</i>	Ames	Genome project ²	<i>atpD</i>
20	<i>Bacillus firmus</i>	OF4	M60117	<i>atpD</i>
	<i>Bacillus megaterium</i>	QM B1551	M20255	<i>atpD</i>
	<i>Bacillus stearothermophilus</i>		D38058	<i>atpD</i>
	<i>Bacillus stearothermophilus</i>	IFO1035	D38060	<i>atpD</i>
	<i>Bacillus subtilis</i>	168	Z28592	<i>atpD</i>
25	<i>Bacteroides fragilis</i>	DSM 2151	M22247	<i>atpD</i>
	<i>Bordetella bronchiseptica</i>	RB50	Genome project ²	<i>atpD</i>
	<i>Bordetella pertussis</i>	Tohama 1	Genome project ²	<i>atpD</i>
	<i>Borrelia burgdorferi</i>	B31	AE001122	<i>atpD</i> (V)
	<i>Burkholderia cepacia</i>	DSM50181	X76877	<i>atpD</i>
30	<i>Burkholderia pseudomallei</i>	K96243	Genome project ²	<i>atpD</i>
	<i>Campylobacter jejuni</i>	NCTC 11168	CJ11168X1	<i>atpD</i>
	<i>Chlamydia pneumoniae</i>		Genome project ²	<i>atpD</i> (V)
	<i>Chlamydia trachomatis</i>	MoPn	Genome project ²	<i>atpD</i> (V)
	<i>Chlorobium vibrioforme</i>	DSM 263	X76873	<i>atpD</i>
35	<i>Citrobacter freundii</i>	JEO503	AF037156	<i>atpD</i>
	<i>Clostridium acetobutylicum</i>	ATCC 824	Genome project ²	<i>atpD</i>
	<i>Clostridium acetobutylicum</i>	DSM 792	AF101055	<i>atpD</i>
	<i>Clostridium difficile</i>	630	Genome project ²	<i>atpD</i>
	<i>Corynebacterium diphtheriae</i>	NCTC13129	Genome project ²	<i>atpD</i>
40	<i>Corynebacterium glutamicum</i>	ASO 19	X76875	<i>atpD</i>
	<i>Corynebacterium glutamicum</i>	MJ-233	E09634	<i>atpD</i>
	<i>Cytophaga lytica</i>	DSM 2039	M22535	<i>atpD</i>
	<i>Enterobacter aerogenes</i>	DSM 30053	- ³	<i>atpD</i>
	<i>Enterococcus faecalis</i>	V583	Genome project ²	<i>atpD</i> (V)
45	<i>Enterococcus hirae</i>		M90060	<i>atpD</i>
	<i>Enterococcus hirae</i>	ATCC 9790	D17462	<i>atpD</i> (V)
	<i>Escherichia coli</i>		J01594	<i>atpD</i>
	<i>Escherichia coli</i>		M25464	<i>atpD</i>
	<i>Escherichia coli</i>		V00267	<i>atpD</i>
50	<i>Escherichia coli</i>		V00311	<i>atpD</i>
	<i>Escherichia coli</i>	K12 MG1655	L10328	<i>atpD</i>
	<i>Flavobacterium ferrugineum</i>	DSM 13524	- ³	<i>atpD</i>
	<i>Haemophilus actinomycetemcomitans</i>		Genome project ²	<i>atpD</i>
	<i>Haemophilus influenzae</i>	Rd	U32730	<i>atpD</i>
55	<i>Helicobacter pylori</i>	NCTC 11638	AF004014	<i>atpD</i>

Table 11. Microbial species for which *tuf* and/or *atpD* and/or *recA* sequences are available in public databases (continued).

	Species	Strain	Accession number	Coding gene*
	<i>Helicobacter pylori</i>	26695	Genome project ²	<i>atpD</i>
	<i>Helicobacter pylori</i>	J99	Genome project ²	<i>atpD</i>
	<i>Klebsiella pneumoniae</i>	M6H 78578	Genome project ²	<i>atpD</i>
	<i>Lactobacillus casei</i>	DSM 20021	X64542	<i>atpD</i>
5	<i>Legionella pneumophila</i>	Philadelphia-1	Genome project ²	<i>atpD</i>
	<i>Moorella thermoacetica</i>	ATCC 39073	U64318	<i>atpD</i>
	<i>Mycobacterium avium</i>	104	Genome project ²	<i>atpD</i>
	<i>Mycobacterium bovis</i>	AF2122/97	Genome project ²	<i>atpD</i>
	<i>Mycobacterium leprae</i>		U15186	<i>atpD</i>
10	<i>Mycobacterium leprae</i>		Genome project ²	<i>atpD</i>
	<i>Mycobacterium tuberculosis</i>	H37Rv	Z73419	<i>atpD</i>
	<i>Mycobacterium tuberculosis</i>	CSU#93	Genome project ²	<i>atpD</i>
	<i>Mycoplasma gallisepticum</i>		X64256	<i>atpD</i>
	<i>Mycoplasma genitalium</i>	G37	U39725	<i>atpD</i>
15	<i>Mycoplasma pneumoniae</i>	M129	U43738	<i>atpD</i>
	<i>Neisseria gonorrhoeae</i>	FA 1090	Genome project ²	<i>atpD</i>
	<i>Neisseria meningitidis</i>	Z2491	Genome project ²	<i>atpD</i>
	<i>Pasteurella multocida</i>	Pm70	Genome project ²	<i>atpD</i>
	<i>Pectinatus frisingensis</i>	DSM 20465	X64543	<i>atpD</i>
20	<i>Peptococcus niger</i>	DSM 20475	X76878	<i>atpD</i>
	<i>Pirellula marina</i>	IFAM 1313	X57204	<i>atpD</i>
	<i>Porphyromonas gingivalis</i>	W83	Genome project ²	<i>atpD</i> (V)
	<i>Propionigenium modestum</i>	DSM 2376	X58461	<i>atpD</i>
	<i>Pseudomonas aeruginosa</i>	PAO1	Genome project ²	<i>atpD</i>
25	<i>Pseudomonas putida</i>		Genome project ²	<i>atpD</i>
	<i>Rhodobacter capsulatus</i>	B100	X99599	<i>atpD</i>
	<i>Rhodospirillum rubrum</i>		X02499	<i>atpD</i>
	<i>Rickettsia prowazekii</i>	F-12	AF036246	<i>atpD</i>
	<i>Rickettsia prowazekii</i>	Madrid	Genome project ²	<i>atpD</i>
30	<i>Ruminococcus albus</i>	7ATCC	AB006151	<i>atpD</i>
	<i>Salmonella bongori</i>	JEO4162	AF037155	<i>atpD</i>
	<i>Salmonella bongori</i>	BR1859	AF037154	<i>atpD</i>
	<i>Salmonella choleraesuis</i>	S83769	AF037146	<i>atpD</i>
	subsp. <i>arizonae</i>			
35	<i>Salmonella choleraesuis</i>	u24	AF037147	<i>atpD</i>
	subsp. <i>arizonae</i>			
	<i>Salmonella choleraesuis</i> subsp.	K228	AF037140	<i>atpD</i>
	<i>choleraesuis</i> serotype Dublin			
	<i>Salmonella choleraesuis</i> subsp.	K771	AF037139	<i>atpD</i>
40	<i>choleraesuis</i> serotype Dublin			
	<i>Salmonella choleraesuis</i> subsp.	Div36-86	AF037142	<i>atpD</i>
	<i>choleraesuis</i> serotype Infantis			
	<i>Salmonella choleraesuis</i> subsp.	Div95-86	AF037143	<i>atpD</i>
	<i>choleraesuis</i> serotype Tennessee			
45	<i>Salmonella choleraesuis</i> subsp.	LT2	AF037141	<i>atpD</i>
	<i>choleraesuis</i> serotype Typhimurium			
	<i>Salmonella choleraesuis</i>	DS210/89	AF037149	<i>atpD</i>
	subsp. <i>diarizonae</i>			
	<i>Salmonella choleraesuis</i>	JEO307	AF037148	<i>atpD</i>
50	subsp. <i>diarizonae</i>			
	<i>Salmonella choleraesuis</i>	S109671	AF037150	<i>atpD</i>
	subsp. <i>diarizonae</i>			
	<i>Salmonella choleraesuis</i>	S84366	AF037151	<i>atpD</i>
	subsp. <i>houtenae</i>			
55	<i>Salmonella choleraesuis</i>	S84098	AF037152	<i>atpD</i>

Table 11. Microbial species for which *tuf* and/or *atpD* and/or *recA* sequences are available in public databases (continued).

	Species	Strain	Accession number	Coding gene*
	subsp. <i>houteanae</i>			
	<i>Salmonella choleraesuis</i>	BR2047	AF037153	<i>atpD</i>
	subsp. <i>indica</i>			
	<i>Salmonella choleraesuis</i>	NSC72	AF037144	<i>atpD</i>
5	subsp. <i>salamae</i>			
	<i>Salmonella choleraesuis</i>	S114655	AF037145	<i>atpD</i>
	subsp. <i>salamae</i>			
	<i>Shewanella putrefaciens</i>	MR-1	Genome project ²	<i>atpD</i>
	<i>Staphylococcus aureus</i>	COL	Genome project ²	<i>atpD</i>
10	<i>Stigmatella aurantiaca</i>	Sga1	X76879	<i>atpD</i>
	<i>Streptococcus bovis</i>	JB-1	AB009314	<i>atpD</i>
	<i>Streptococcus mutans</i>	GS-5	U31170	<i>atpD</i>
	<i>Streptococcus mutans</i>	UAB159	Genome project ²	<i>atpD</i>
	<i>Streptococcus pneumoniae</i>	Type 4	Genome project ²	<i>atpD</i> (V)
15	<i>Streptococcus pneumoniae</i>	Type 4	Genome project ²	<i>atpD</i>
	<i>Streptococcus pyogenes</i>	M1-GAS	Genome project ²	<i>atpD</i> (V)
	<i>Streptococcus pyogenes</i>	M1-GAS	Genome project ²	<i>atpD</i>
	<i>Streptococcus sanguinis</i>	10904	AF001955	<i>atpD</i>
	<i>Streptomyces lividans</i>	1326	Z22606	<i>atpD</i>
20	<i>Thermus thermophilus</i>	HB8	D63799	<i>atpD</i> (V)
	<i>Thiobacillus ferrooxidans</i>	ATCC 33020	M81087	<i>atpD</i>
	<i>Treponema pallidum</i>	Nichols	AE001228	<i>atpD</i> (V)
	<i>Vibrio alginolyticus</i>		X16050	<i>atpD</i>
	<i>Vibrio cholerae</i>	N16961	Genome project ²	<i>atpD</i>
25	<i>Wolinella succinogenes</i>	DSM 1470	X76880	<i>atpD</i>
	<i>Yersinia enterocolitica</i>	NCTC 10460	AF037157	<i>atpD</i>
	<i>Yersinia pestis</i>	CO-92	Genome project ²	<i>atpD</i>
30	Archaeobacteria			
	<i>Archaeoglobus fulgidus</i>	DSM 4304	AE001023	<i>atpD</i> (V)
	<i>Halobacterium salinarum</i>		S56356	<i>atpD</i> (V)
	<i>Haloferax volcanii</i>	WR 340	X79516	<i>atpD</i>
35	<i>Methanococcus jannaschii</i>	DSM 2661	U67477	<i>atpD</i> (V)
	<i>Methanosarcina barkeri</i>	DSM 800	J04836	<i>atpD</i> (V)
	Fungi			
40	<i>Candida albicans</i>	SC5314	Genome project ²	<i>atpD</i>
	<i>Candida tropicalis</i>		M64984	<i>atpD</i> (V)
	<i>Kluyveromyces lactis</i>	2359/152	U37764	<i>atpD</i>
	<i>Neurospora crassa</i>		X53720	<i>atpD</i>
45	<i>Saccharomyces cerevisiae</i>		M12082	<i>atpD</i>
	<i>Saccharomyces cerevisiae</i>	X2180-1A	J05409	<i>atpD</i> (V)
	<i>Schizosaccharomyces pombe</i>	972 h-	S47814	<i>atpD</i> (V)
	<i>Schizosaccharomyces pombe</i>	972 h-	M57956	<i>atpD</i>
50	Parasites			
	<i>Giardia lamblia</i>	WB	U18938	<i>atpD</i>
	<i>Plasmodium falciparum</i>	3D7	L08200	<i>atpD</i> (V)
55	<i>Trypanosoma congolense</i>	IL3000	Z25814	<i>atpD</i> (V)

Table 11. Microbial species for which *tuf* and/or *atpD* and/or *recA* sequences are available in public databases (continued).

	Species	Strain	Accession number	Coding gene*
Human and plants				
5	<i>Homo sapiens</i> <i>Homo sapiens</i>		L09234 M27132	<i>atpD</i> (V) <i>atpD</i>
<u>recA sequences</u>				
10	Bacteria			
	<i>Acetobacter aceti</i>	no. 1023	S60630	<i>recA</i>
	<i>Acetobacter altoacetigenes</i>	MH-24	E05290	<i>recA</i>
15	<i>Acetobacter polyoxogenes</i>	NBI 1028	D13183	<i>recA</i>
	<i>Acholeplasma laidlawii</i>	8195	M81465	<i>recA</i>
	<i>Acidiphilium facilis</i>	ATCC 35904	D16538	<i>recA</i>
	<i>Acidothermus cellulolyticus</i>	ATCC 43068	AJ006705	<i>recA</i>
	<i>Acinetobacter calcoaceticus</i>	BD413/ADP1	L26100	<i>recA</i>
20	<i>Actinobacillus actinomycetemcomitans</i>	HK1651	Genome project ²	<i>recA</i>
	<i>Aeromonas salmonicida</i>	A449	U83688	<i>recA</i>
	<i>Agrobacterium tumefaciens</i>	C58	L07902	<i>recA</i>
	<i>Allochroa matium vinosum</i>		AJ000677	<i>recA</i>
	<i>Aquifex aeolicus</i>	VF5	AE000775	<i>recA</i>
25	<i>Aquifex pyrophilus</i>	Kol5a	L23135	<i>recA</i>
	<i>Azotobacter vinelandii</i>		S96898	<i>recA</i>
	<i>Bacillus stearothermophilus</i>	10	Genome project ²	<i>recA</i>
	<i>Bacillus subtilis</i>	PB1831	U87792	<i>recA</i>
	<i>Bacillus subtilis</i>	168	Z99112	<i>recA</i>
30	<i>Bacteroides fragilis</i>		M63029	<i>recA</i>
	<i>Bifidobacterium breve</i>	NCFB 2258	AF094756	<i>recA</i>
	<i>Blastochloris viridis</i>	DSM 133	AF022175	<i>recA</i>
	<i>Bordetella pertussis</i>	165	X53457	<i>recA</i>
	<i>Bordetella pertussis</i>	Tohama I	Genome project ²	<i>recA</i>
35	<i>Borrelia burgdorferi</i>	Sh-2-82	U23457	<i>recA</i>
	<i>Borrelia burgdorferi</i>	B31	AE001124	<i>recA</i>
	<i>Brevibacterium flavum</i>	MJ-233	E10390	<i>recA</i>
	<i>Brucella abortus</i>	2308	L00679	<i>recA</i>
	<i>Burkholderia cepacia</i>	ATCC 17616	U70431	<i>recA</i>
40	<i>Burkholderia cepacia</i>		D90120	<i>recA</i>
	<i>Burkholderia pseudomallei</i>	K96243	Genome project ²	<i>recA</i>
	<i>Campylobacter fetus</i> subsp. <i>fetus</i>	23D	AF020677	<i>recA</i>
	<i>Campylobacter jejuni</i>	81-176	U03121	<i>recA</i>
	<i>Campylobacter jejuni</i>	NCTC 11168	AL139079	<i>recA</i>
45	<i>Chlamydia trachomatis</i>	L2	U16739	<i>recA</i>
	<i>Chlamydia trachomatis</i>	D/UW-3/CX	AE001335	<i>recA</i>
	<i>Chlamydia pneumoniae</i>	CWL029	AE001658	<i>recA</i>
	<i>Chloroflexus aurantiacus</i>	J-10-fl	AF037259	<i>recA</i>
	<i>Clostridium acetobutylicum</i>		M94057	<i>recA</i>
50	<i>Clostridium perfringens</i>	13	U61497	<i>recA</i>
	<i>Corynebacterium diphtheriae</i>	NCTC13129	Genome project ²	<i>recA</i>
	<i>Corynebacterium glutamicum</i>	AS019	U14965	<i>recA</i>
	<i>Corynebacterium pseudotuberculosis</i>	C231	U30387	<i>recA</i>
	<i>Deinococcus radiodurans</i>	KD8301	AB005471	<i>recA</i>
55	<i>Deinococcus radiodurans</i>	R1	U01876	<i>recA</i>

Table 11. Microbial species for which *tuf* and/or *atpD* and/or *recA* sequences are available in public databases (continued).

	Species	Strain	Accession number	Coding gene*
	<i>Enterobacter agglomerans</i>	339	L03291	<i>recA</i>
	<i>Enterococcus faecalis</i>	OGIX	M81466	<i>recA</i>
	<i>Erwinia carotovora</i>		X55554	<i>recA</i>
	<i>Escherichia coli</i>		J01672	<i>recA</i>
5	<i>Escherichia coli</i>		X55552	<i>recA</i>
	<i>Escherichia coli</i>	K-12	AE000354	<i>recA</i>
	<i>Frankia alni</i>	Arl3	AJ006707	<i>recA</i>
	<i>Gluconobacter oxydans</i>		U21001	<i>recA</i>
	<i>Haemophilus influenzae</i>	Rd	U32687	<i>recA</i>
10	<i>Haemophilus influenzae</i>	Rd	U32741	<i>recA</i>
	<i>Haemophilus influenzae</i>	Rd	L07529	<i>recA</i>
	<i>Helicobacter pylori</i>	69A	Z35478	<i>recA</i>
	<i>Helicobacter pylori</i>	26695	AE000536	<i>recA</i>
	<i>Helicobacter pylori</i>	J99	AE001453	<i>recA</i>
15	<i>Klebsiella pneumoniae</i>	M6H 78578	Genome project ²	<i>recA</i>
	<i>Lactococcus lactis</i>	ML3	M88106	<i>recA</i>
	<i>Legionella pneumophila</i>		X55453	<i>recA</i>
	<i>Leptospira biflexa</i>	serovar patoc	U32625	<i>recA</i>
	<i>Leptospira interrogans</i>	serovar pomona	U29169	<i>recA</i>
20	<i>Magnetospirillum magnetotacticum</i>	MS-1	X17371	<i>recA</i>
	<i>Methylobacillus flagellatus</i>	MFK1	M35325	<i>recA</i>
	<i>Methylomonas clara</i>	ATCC 31226	X59514	<i>recA</i>
	<i>Mycobacterium avium</i>	104	Genome project ²	<i>recA</i>
	<i>Mycobacterium bovis</i>	AF122/97	Genome project ²	<i>recA</i>
25	<i>Mycobacterium leprae</i>		X73822	<i>recA</i>
	<i>Mycobacterium tuberculosis</i>	H37Rv	X58485	<i>recA</i>
	<i>Mycobacterium tuberculosis</i>	CSU#93	Genome project ²	<i>recA</i>
	<i>Mycoplasma genitalium</i>	G37	U39717	<i>recA</i>
	<i>Mycoplasma mycoides</i>	GM9	L22073	<i>recA</i>
30	<i>Mycoplasma pneumoniae</i>	ATCC 29342	MPAE000033	<i>recA</i>
	<i>Mycoplasma pulmonis</i>	KD735	L22074	<i>recA</i>
	<i>Myxococcus xanthus</i>		L40368	<i>recA</i>
	<i>Myxococcus xanthus</i>		L40367	<i>recA</i>
	<i>Neisseria animalis</i>	NCTC 10212	U57910	<i>recA</i>
35	<i>Neisseria cinerea</i>	LCDC 81-176	AJ223869	<i>recA</i>
	<i>Neisseria cinerea</i>	LNP 1646	U57906	<i>recA</i>
	<i>Neisseria cinerea</i>	NCTC 10294	AJ223871	<i>recA</i>
	<i>Neisseria cinerea</i>	Vedros M601	AJ223870	<i>recA</i>
	<i>Neisseria elongata</i>	CCUG 2131	AJ223882	<i>recA</i>
40	<i>Neisseria elongata</i>	CCUG 4165A	AJ223880	<i>recA</i>
	<i>Neisseria elongata</i>	NCTC 10660	AJ223881	<i>recA</i>
	<i>Neisseria elongata</i>	NCTC 11050	AJ223878	<i>recA</i>
	<i>Neisseria elongata</i>	NHITCC 2376	AJ223877	<i>recA</i>
	<i>Neisseria elongata</i>	CCUG 4557	AJ223879	<i>recA</i>
45	subsp. <i>intermedia</i>			
	<i>Neisseria flava</i>	Bangor 9	AJ223873	<i>recA</i>
	<i>Neisseria flavescens</i>	LNP 444	U57907	<i>recA</i>
	<i>Neisseria gonorrhoeae</i>	CH95	U57902	<i>recA</i>
	<i>Neisseria gonorrhoeae</i>	FA19	X64842	<i>recA</i>
50	<i>Neisseria gonorrhoeae</i>	MS11	X17374	<i>recA</i>
	<i>Neisseria gonorrhoeae</i>		Genome project ²	<i>recA</i>
	<i>Neisseria lactamica</i>	CCUC 7757	AJ223866	<i>recA</i>
	<i>Neisseria lactamica</i>	CCUG 7852	Y11819	<i>recA</i>
	<i>Neisseria lactamica</i>	LCDC 77-143	Y11818	<i>recA</i>
55	<i>Neisseria lactamica</i>	LCDC 80-111	AJ223864	<i>recA</i>

Table 11. Microbial species for which *tuf* and/or *atpD* and/or *recA* sequences are available in public databases (continued).

	Species	Strain	Accession number	Coding gene*
	<i>Neisseria lactamica</i>	LCDC 845	AJ223865	<i>recA</i>
	<i>Neisseria lactamica</i>	NCTC 10617	U57905	<i>recA</i>
	<i>Neisseria lactamica</i>	NCTC 10618	AJ223863	<i>recA</i>
	<i>Neisseria meningitidis</i>	44/46	X64849	<i>recA</i>
5	<i>Neisseria meningitidis</i>	Bangor 13	AJ223868	<i>recA</i>
	<i>Neisseria meningitidis</i>	HF116	X64848	<i>recA</i>
	<i>Neisseria meningitidis</i>	HF130	X64844	<i>recA</i>
	<i>Neisseria meningitidis</i>	HF46	X64847	<i>recA</i>
	<i>Neisseria meningitidis</i>	M470	X64850	<i>recA</i>
10	<i>Neisseria meningitidis</i>	N94II	X64846	<i>recA</i>
	<i>Neisseria meningitidis</i>	NCTC 8249	AJ223867	<i>recA</i>
	<i>Neisseria meningitidis</i>	P63	X64845	<i>recA</i>
	<i>Neisseria meningitidis</i>	S3446	U57903	<i>recA</i>
	<i>Neisseria meningitidis</i>	FAM18	Genome project ²	<i>recA</i>
15	<i>Neisseria mucosa</i>	LNP 405	U57908	<i>recA</i>
	<i>Neisseria mucosa</i>	Vedros M1801	AJ223875	<i>recA</i>
	<i>Neisseria perflava</i>	CCUG 17915	AJ223876	<i>recA</i>
	<i>Neisseria perflava</i>	LCDC 85402	AJ223862	<i>recA</i>
	<i>Neisseria pharyngis</i> var. <i>flava</i>	NCTC 4590	U57909	<i>recA</i>
20	<i>Neisseria polysaccharea</i>	CCUG 18031	Y11815	<i>recA</i>
	<i>Neisseria polysaccharea</i>	CCUG 24845	Y11816	<i>recA</i>
	<i>Neisseria polysaccharea</i>	CCUG 24846	Y11814	<i>recA</i>
	<i>Neisseria polysaccharea</i>	INS MA 3008	Y11817	<i>recA</i>
	<i>Neisseria polysaccharea</i>	NCTC 11858	U57904	<i>recA</i>
25	<i>Neisseria sicca</i>	NRL 30016	AJ223872	<i>recA</i>
	<i>Neisseria subflava</i>	NRL 30017	AJ223874	<i>recA</i>
	<i>Paracoccus denitrificans</i>	DSM 413	U59631	<i>recA</i>
	<i>Pasteurella multocida</i>		X99324	<i>recA</i>
	<i>Porphyromonas gingivalis</i>	W83	U70054	<i>recA</i>
30	<i>Prevotella ruminicola</i>	JCM 8958	U61227	<i>recA</i>
	<i>Proteus mirabilis</i>	pG1300	X14870	<i>recA</i>
	<i>Proteus vulgaris</i>		X55555	<i>recA</i>
	<i>Pseudomonas aeruginosa</i>		X05691	<i>recA</i>
	<i>Pseudomonas aeruginosa</i>	PAM 7	X52261	<i>recA</i>
35	<i>Pseudomonas aeruginosa</i>	PAO12	D13090	<i>recA</i>
	<i>Pseudomonas fluorescens</i>	OE 28.3	M96558	<i>recA</i>
	<i>Pseudomonas putida</i>		L12684	<i>recA</i>
	<i>Pseudomonas putida</i>	PpS145	U70864	<i>recA</i>
	<i>Rhizobium leguminosarum</i>	VF39	X59956	<i>recA</i>
40	biovar <i>viciae</i>			
	<i>Rhizobium phaseoli</i>	CNPAF512	X62479	<i>recA</i>
	<i>Rhodobacter capsulatus</i>	J50	X82183	<i>recA</i>
	<i>Rhodobacter sphaeroides</i>	2.4.1	X72705	<i>recA</i>
	<i>Rhodopseudomonas palustris</i>	N 7	D84467	<i>recA</i>
45	<i>Rickettsia prowazekii</i>	Madrid E	AJ235273	<i>recA</i>
	<i>Rickettsia prowazekii</i>	Madrid E	U01959	<i>recA</i>
	<i>Serratia marcescens</i>		M22935	<i>recA</i>
	<i>Shigella flexneri</i>		X55553	<i>recA</i>
	<i>Shigella sonnei</i>	KNIH104S	AF101227	<i>recA</i>
50	<i>Sinorhizobium meliloti</i>	2011	X59957	<i>recA</i>
	<i>Staphylococcus aureus</i>		L25893	<i>recA</i>
	<i>Streptococcus gordonii</i>	Challis V288	L20574	<i>recA</i>
	<i>Streptococcus mutans</i>	UA96	M81468	<i>recA</i>
	<i>Streptococcus mutans</i>	GS-5	M61897	<i>recA</i>
55	<i>Streptococcus pneumoniae</i>		Z17307	<i>recA</i>

Table 11. Microbial species for which *tuf* and/or *atpD* and/ *r recA* sequences are available in public databases (continued).

	Species	Strain	Accession number	Coding gene*
	<i>Streptococcus pneumoniae</i>	R800	Z34303	<i>recA</i>
	<i>Streptococcus pyogenes</i>	NZ131	U21934	<i>recA</i>
	<i>Streptococcus pyogenes</i>	D471	M81469	<i>recA</i>
	<i>Streptococcus salivarius</i>		M94062	<i>recA</i>
5	subsp. <i>thermophilus</i>			
	<i>Streptomyces ambofaciens</i>	DSM 40697	Z30324	<i>recA</i>
	<i>Streptomyces coelicolor</i>	A3(2)	AL020958	<i>recA</i>
	<i>Streptomyces lividans</i>	TK24	X76076	<i>recA</i>
	<i>Streptomyces rimosus</i>	R6	X94233	<i>recA</i>
10	<i>Streptomyces venezuelae</i>	ATCC10712	U04837	<i>recA</i>
	<i>Synechococcus</i> sp.	PR6	M29495	<i>recA</i>
	<i>Synechocystis</i> sp.	PCC6803	D90917	<i>recA</i>
	<i>Thermotoga maritima</i>		L23425	<i>recA</i>
	<i>Thermotoga maritima</i>		AE001823	<i>recA</i>
15	<i>Thermus aquaticus</i>		L20095	<i>recA</i>
	<i>Thermus thermophilus</i>	HB8	D17392	<i>recA</i>
	<i>Thiobacillus ferrooxidans</i>		M26933	<i>recA</i>
	<i>Treponema denticola</i>		Genome project ²	<i>recA</i>
	<i>Treponema pallidum</i>	Nichols	AE001243	<i>recA</i>
20	<i>Vibrio anguillarum</i>		M80525	<i>recA</i>
	<i>Vibrio cholerae</i>	017	X71969	<i>recA</i>
	<i>Vibrio cholerae</i>	2740-80	U10162	<i>recA</i>
	<i>Vibrio cholerae</i>	569B	L42384	<i>recA</i>
	<i>Vibrio cholerae</i>	M549	AF117881	<i>recA</i>
25	<i>Vibrio cholerae</i>	M553	AF117882	<i>recA</i>
	<i>Vibrio cholerae</i>	M645	AF117883	<i>recA</i>
	<i>Vibrio cholerae</i>	M793	AF117878	<i>recA</i>
	<i>Vibrio cholerae</i>	M794	AF117880	<i>recA</i>
	<i>Vibrio cholerae</i>	M967	AF117879	<i>recA</i>
30	<i>Xanthomonas citri</i>	XW47	AF006590	<i>recA</i>
	<i>Xanthomonas oryzae</i>		AF013600	<i>recA</i>
	<i>Xenorhabdus bovienii</i>	T228/1	U87924	<i>recA</i>
	<i>Xenorhabdus nematophilus</i>	AN6	AF127333	<i>recA</i>
	<i>Yersinia pestis</i>	231	X75336	<i>recA</i>
35	<i>Yersinia pestis</i>	CO-92	Genome project ²	<i>recA</i>
Fungi, parasites, human and plants				
40	<i>Anabaena variabilis</i>	ATCC 29413	M29680	<i>recA</i>
	<i>Arabidopsis thaliana</i>		U43652	<i>recA</i> (Rad51)
	<i>Candida albicans</i>		U39808	<i>recA</i> (Dmc1)
	<i>Coprinus cinereus</i>	Okayama-7	U21905	<i>recA</i> (Rad51)
	<i>Emericella nidulans</i>		Z80341	<i>recA</i> (Rad51)
45	<i>Gallus gallus</i>		L09655	<i>recA</i> (Rad51)
	<i>Homo sapiens</i>		D13804	<i>recA</i> (Rad51)
	<i>Homo sapiens</i>		D63882	<i>recA</i> (Dmc1)
	<i>Leishmania major</i>	Friedlin	AF062379	<i>recA</i> (Rad51)
	<i>Leishmania major</i>	Friedlin	AF062380	<i>recA</i> (Dmc1)
50	<i>Mus musculus</i>		D58419	<i>recA</i> (Dmc1)
	<i>Neurospora crassa</i>	74-OR23-1A	D29638	<i>recA</i> (Rad51)
	<i>Saccharomyces cerevisiae</i>		D10023	<i>recA</i> (Rad51)
	<i>Schizosaccharomyces pombe</i>		Z22691	<i>recA</i> (Rad51)
	<i>Schizosaccharomyces pombe</i>	972h-	AL021817	<i>recA</i> (Dmc1)
55	<i>Tetrahymena thermophila</i>	PB9R	AF064516	<i>recA</i> (Rad51)

Table 11. Microbial species for which *tuf* and/or *atpD* and/or *recA* sequences are available in public databases (continued).

Species	Strain	Accession number	Coding gene*
<i>Trypanosoma brucei</i>	stock 427	Y13144	<i>recA</i> (Rad51)
<i>Ustilago maydis</i>		U62484	<i>recA</i> (Rad51)
<i>Xenopus laevis</i>		D38488	<i>recA</i> (Rad51)
5 <i>Xenopus laevis</i>		D38489	<i>recA</i> (Rad51)

* *tuf* indicates *tuf* sequences, including *tuf* genes, *fusA* genes and *fusA-tuf* intergenic spacers.

tuf (C) indicates *tuf* sequences divergent from main (usually A and B) copies of the elongation factor-Tu

10 *tuf* (EF-1) indicates *tuf* sequences of the eukaryotic type (elongation factor 1 α)

tuf (M) indicates *tuf* sequences from organellar (mostly mitochondrial) origin

atpD indicates *atpD* sequences of the F-type

atpD (V) indicates *atpD* sequences of the V-Type

recA indicates *recA* sequences

15 *recA* (Rad51) indicates *rad51* sequences or homologs

recA (Dmc1) indicates *dmc1* sequences or homologs

¹ Nucleotide sequences published in Arch. Microbiol. 1990 153:241-247

² These sequences are from the TIGR database (<http://www.tigr.org/tdb/tdb.html>)

³ Nucleotide sequences published in FEMS Microbiology Letters 1988 50:101-106

Table 12. Bacterial species used to test the specificity of the *Staphylococcus*-specific amplification primers derived from *tuf* sequences.

	Strain	Reference number	Strain	Reference number
5	Staphylococcal species (n=27)		Other Gram-positive bacteria (n=20)	
	<i>Staphylococcus arlettae</i>	ATCC 43957	<i>Bacillus subtilis</i>	ATCC 27370
	<i>Staphylococcus aureus</i>	ATCC 35844	<i>Enterococcus avium</i>	ATCC 14025
	subsp. <i>anaerobius</i>			
10	<i>Staphylococcus aureus</i>	ATCC 43300	<i>Enterococcus durans</i>	ATCC 19432
	subsp. <i>aureus</i>			
	<i>Staphylococcus auricularis</i>	ATCC 33753	<i>Enterococcus faecalis</i>	ATCC 19433
	<i>Staphylococcus capitis</i>	ATCC 27840	<i>Enterococcus faecium</i>	ATCC 19434
	subsp. <i>capitis</i>			
15	<i>Staphylococcus caprae</i>	ATCC 35538	<i>Enterococcus flavescens</i>	ATCC 49996
	<i>Staphylococcus carnosus</i>	ATCC 51365	<i>Enterococcus gallinarum</i>	ATCC 49573
	<i>Staphylococcus chromogenes</i>	ATCC 43764	<i>Lactobacillus acidophilus</i>	ATCC 4356
	<i>Staphylococcus cohnii</i>	DSM 20260	<i>Lactococcus lactis</i>	ATCC 11454
	subsp. <i>urealyticum</i>			
20	<i>Staphylococcus delphini</i>	ATCC 49171	<i>Listeria innocua</i>	ATCC 33090
	<i>Staphylococcus epidermidis</i>	ATCC 14990	<i>Listeria ivanovii</i>	ATCC 19119
	<i>Staphylococcus equorum</i>	ATCC 43958	<i>Listeria monocytogenes</i>	ATCC 15313
	<i>Staphylococcus felis</i>	ATCC 49168	<i>Macrococcus caseolyticus</i>	ATCC 13548
	<i>Staphylococcus gallinarum</i>	ATCC 35539	<i>Streptococcus agalactiae</i>	ATCC 13813
25	<i>Staphylococcus haemolyticus</i>	ATCC 29970	<i>Streptococcus anginosus</i>	ATCC 33397
	<i>Staphylococcus hominis</i>	ATCC 27844	<i>Streptococcus bovis</i>	ATCC 33317
	<i>Staphylococcus hyicus</i>	ATCC 11249	<i>Streptococcus mutans</i>	ATCC 25175
	<i>Staphylococcus intermedius</i>	ATCC 29663	<i>Streptococcus pneumoniae</i>	ATCC 6303
	<i>Staphylococcus kloosii</i>	ATCC 43959	<i>Streptococcus pyogenes</i>	ATCC 19615
30	<i>Staphylococcus lentus</i>	ATCC 29070	<i>Streptococcus salivarius</i>	ATCC 7073
	<i>Staphylococcus lugdunensis</i>	ATCC 43809		
	<i>Staphylococcus saprophyticus</i>	ATCC 15305		
	<i>Staphylococcus schleiferi</i>	ATCC 49545		
	subsp. <i>coagulans</i>			
35	<i>Staphylococcus sciuri</i>	ATCC 29060		
	subsp. <i>sciuri</i>			
	<i>Staphylococcus simulans</i>	ATCC 27848		
	<i>Staphylococcus warneri</i>	ATCC 27836		
	<i>Staphylococcus xylosus</i>	ATCC 29971		
40	Gram-negative bacteria (n=33)			
	<i>Acinetobacter baumannii</i>	ATCC 19606	<i>Morganella morganii</i>	ATCC 25830
	<i>Bacteroides distasonis</i>	ATCC 8503	<i>Neisseria gonorrhoeae</i>	ATCC 35201
	<i>Bacteroides fragilis</i>	ATCC 25285	<i>Neisseria meningitidis</i>	ATCC 13077
	<i>Bulkholderia cepacia</i>	ATCC 25416	<i>Proteus mirabilis</i>	ATCC 25933
45	<i>Bordetella pertussis</i>	ATCC 9797	<i>Proteus vulgaris</i>	ATCC 13315
	<i>Citrobacter freundii</i>	ATCC 8090	<i>Providencia rettgeri</i>	ATCC 9250
	<i>Enterobacter aerogenes</i>	ATCC 13048	<i>Providencia stuartii</i>	ATCC 29914
	<i>Enterobacter cloacae</i>	ATCC 13047	<i>Pseudomonas aeruginosa</i>	ATCC 27853
	<i>Escherichia coli</i>	ATCC 25922	<i>Pseudomonas fluorescens</i>	ATCC 13525
50	<i>Haemophilus influenzae</i>	ATCC 8907	<i>Salmonella choleraesuis</i>	ATCC 7001
	<i>Haemophilus parahaemolyticus</i>	ATCC 10014	<i>Salmonella typhimurium</i>	ATCC 14028
	<i>Haemophilus parainfluenzae</i>	ATCC 7901	<i>Serratia marcescens</i>	ATCC 8100
	<i>Hafnia alvei</i>	ATCC 13337	<i>Shigella flexneri</i>	ATCC 12022
	<i>Kingella indologenes</i>	ATCC 25869	<i>Shigella sonnei</i>	ATCC 29930
55	<i>Klebsiella oxytoca</i>	ATCC 13182	<i>Stenotrophomonas maltophilia</i>	ATCC 13843
	<i>Klebsiella pneumoniae</i>	ATCC 13883	<i>Yersinia enterocolitica</i>	ATCC 9610
	<i>Moraxella catarrhalis</i>	ATCC 25240		

Table 13. Bacterial species used to test the specificity of the penicillin-resistant *Streptococcus pneumoniae* assay.

	Strain	Reference number	Strain	Reference number
5	Gram-positive species (n=67)			
	<i>Abiotrophia adiacens</i>	ATCC 49175	<i>Staphylococcus hominis</i>	ATCC 27844
	<i>Abiotrophia defectiva</i>	ATCC 49176	<i>Staphylococcus lugdunensis</i>	ATCC 43809
	<i>Actinomyces pyogenes</i>	ATCC 19411	<i>Staphylococcus saprophyticus</i>	ATCC 15305
10	<i>Bacillus anthracis</i>	ATCC 4229	<i>Staphylococcus simulans</i>	ATCC 27848
	<i>Bacillus cereus</i>	ATCC 14579	<i>Staphylococcus warneri</i>	ATCC 27836
	<i>Bifidobacterium breve</i>	ATCC 15700	<i>Streptococcus acidominimus</i>	ATCC 51726
	<i>Clostridium difficile</i>	ATCC 9689	<i>Streptococcus agalactiae</i>	ATCC 12403
	<i>Enterococcus avium</i>	ATCC 14025	<i>Streptococcus anginosus</i>	ATCC 33397
15	<i>Enterococcus casseliflavus</i>	ATCC 25788	<i>Streptococcus bovis</i>	ATCC 33317
	<i>Enterococcus dispar</i>	ATCC 51266	<i>Streptococcus constellatus</i>	ATCC 27823
	<i>Enterococcus durans</i>	ATCC 19432	<i>Streptococcus cricetus</i>	ATCC 19624
	<i>Enterococcus faecalis</i>	ATCC 29212	<i>Streptococcus cristatus</i>	ATCC 51100
	<i>Enterococcus faecium</i>	ATCC 19434	<i>Streptococcus downei</i>	ATCC 33748
20	<i>Enterococcus flavescens</i>	ATCC 49996	<i>Streptococcus dysgalactiae</i>	ATCC 43078
	<i>Enterococcus gallinarum</i>	ATCC 49573	<i>Streptococcus equi</i>	ATCC 9528
	<i>Enterococcus hirae</i>	ATCC 8043	<i>Streptococcus ferus</i>	ATCC 33477
	<i>Enterococcus mundtii</i>	ATCC 43186	<i>Streptococcus gordonii</i>	ATCC 10558
	<i>Enterococcus raffinosus</i>	ATCC 49427	<i>Streptococcus intermedius</i>	ATCC 27335
25	<i>Lactobacillus lactis</i>	ATCC 19435	<i>Streptococcus mitis</i>	ATCC 903
	<i>Lactobacillus monocytogenes</i>	ATCC 15313	<i>Streptococcus mitis</i>	LSPQ 2583
	<i>Mobiluncus curtisii</i>	ATCC 35242	<i>Streptococcus mitis</i>	ATCC 49456
	<i>Peptococcus niger</i>	ATCC 27731	<i>Streptococcus mutans</i>	ATCC 27175
	<i>Peptostreptococcus acones</i>	ATCC 6919	<i>Streptococcus oralis</i>	ATCC 10557
30	<i>Peptostreptococcus anaerobius</i>	ATCC 27337	<i>Streptococcus oralis</i>	ATCC 9811
	<i>Peptostreptococcus asaccharolyticus</i>	ATCC 2639	<i>Streptococcus oralis</i>	ATCC 35037
	<i>Peptostreptococcus lactolyticus</i>	ATCC 51172	<i>Streptococcus parasanguinis</i>	ATCC 15912
	<i>Peptostreptococcus magnus</i>	ATCC 15794	<i>Streptococcus parauberis</i>	ATCC 6631
35	<i>Peptostreptococcus prevotii</i>	ATCC 9321	<i>Streptococcus rattus</i>	ATCC 15912
	<i>Peptostreptococcus tetradius</i>	ATCC 35098	<i>Streptococcus salivarius</i>	ATCC 7073
	<i>Staphylococcus aureus</i>	ATCC 25923	<i>Streptococcus sanguinis</i>	ATCC 10556
	<i>Staphylococcus capitis</i>	ATCC 27840	<i>Streptococcus suis</i>	ATCC 43765
	<i>Staphylococcus epidermidis</i>	ATCC 14990	<i>Streptococcus uberis</i>	ATCC 19436
40	<i>Staphylococcus haemolyticus</i>	ATCC 29970	<i>Streptococcus vestibularis</i>	ATCC 49124
	Gram-negative species (n=33)			
	<i>Actinobacter baumannii</i>	ATCC 19606	<i>Moraxella morganii</i>	ATCC 13077
	<i>Bordetella pertussis</i>	ATCC 9797	<i>Neisseria gonorrhoeae</i>	ATCC 35201
	<i>Citrobacter diversus</i>	ATCC 27028	<i>Neisseria meningitidis</i>	ATCC 13077
45	<i>Citrobacter freundii</i>	ATCC 8090	<i>Proteus mirabilis</i>	ATCC 25933
	<i>Enterobacter aerogenes</i>	ATCC 13048	<i>Proteus vulgaris</i>	ATCC 13315
	<i>Enterobacter agglomerans</i>	ATCC 27155	<i>Providencia alcalifaciens</i>	ATCC 9886
	<i>Enterobacter cloacae</i>	ATCC 13047	<i>Providencia rettgeri</i>	ATCC 9250
	<i>Escherichia coli</i>	ATCC 25922	<i>Providencia rustigianii</i>	ATCC 33673
50	<i>Haemophilus ducreyi</i>	ATCC 33940	<i>Providencia stuartii</i>	ATCC 33672
	<i>Haemophilus haemolyticus</i>	ATCC 33390	<i>Pseudomonas aeruginosa</i>	ATCC 35554
	<i>Haemophilus influenzae</i>	ATCC 9007	<i>Pseudomonas fluorescens</i>	ATCC 13525
	<i>Haemophilus parainfluenzae</i>	ATCC 7901	<i>Pseudomonas stutzeri</i>	ATCC 17588
	<i>Hafnia alvei</i>	ATCC 13337	<i>Salmonella typhimurium</i>	ATCC 14028
55	<i>Klebsiella oxytoca</i>	ATCC 13182	<i>Serratia marcescens</i>	ATCC 13880
	<i>Klebsiella pneumoniae</i>	ATCC 13883	<i>Shigella flexneri</i>	ATCC 12022
	<i>Moraxella atlantae</i>	ATCC 29525	<i>Yersinia enterocolitica</i>	ATCC 9610
	<i>Moraxella catarrhalis</i>	ATCC 43628		

Table 14. Bacterial species (n=104) detected by the platelet contaminants assay. Bold characters indicate the major bacterial contaminants found in platelet concentrates.

5	<i>Abiotrophia adiacens</i>	<i>Klebsiella oxytoca</i>	<i>Staphylococcus simulans</i>
	<i>Abiotrophia defectiva</i>	<i>Klebsiella pneumoniae</i>	<i>Staphylococcus warneri</i>
	<i>Acinetobacter baumannii</i>	<i>Legionella pneumophila</i>	<i>Stenotrophomonas maltophilia</i>
	<i>Acinetobacter lwoffii</i>	<i>Megamonas hypermegale</i>	80 <i>Streptococcus acidominimus</i>
	<i>Aerococcus viridans</i>	45 <i>Moraxella atlantae</i>	<i>Streptococcus agalactiae</i>
10	<i>Bacillus anthracis</i>	<i>Moraxella catarrhalis</i>	<i>Streptococcus anginosus</i>
	<i>Bacillus cereus</i>	<i>Morganella morganii</i>	<i>Streptococcus bovis</i>
	<i>Bacillus subtilis</i>	<i>Neisseria gonorrhoeae</i>	<i>Streptococcus constellatus</i>
	<i>Brucella abortus</i>	<i>Neisseria meningitidis</i>	85 <i>Streptococcus cricetus</i>
	<i>Burkholderia cepacia</i>	50 <i>Pasteurella aerogenes</i>	<i>Streptococcus cristatus</i>
15	<i>Citrobacter diversus</i>	<i>Pasteurella multocida</i>	<i>Streptococcus dysgalactiae</i>
	<i>Citrobacter freundii</i>	<i>Peptostreptococcus magnus</i>	<i>Streptococcus equi</i>
	<i>Enterobacter aerogenes</i>	<i>Proteus mirabilis</i>	<i>Streptococcus ferus</i>
	<i>Enterobacter agglomerans</i>	<i>Providencia alcalifaciens</i>	90 <i>Streptococcus gordonii</i>
	<i>Enterobacter cloacae</i>	55 <i>Providencia rettgeri</i>	<i>Streptococcus intermedius</i>
20	<i>Enterococcus avium</i>	<i>Providencia rustigianii</i>	<i>Streptococcus macacae</i>
	<i>Enterococcus casseliflavus</i>	<i>Providencia stuartii</i>	<i>Streptococcus mitis</i>
	<i>Enterococcus dispar</i>	<i>Pseudomonas aeruginosa</i>	<i>Streptococcus mutans</i>
	<i>Enterococcus durans</i>	<i>Pseudomonas fluorescens</i>	95 <i>Streptococcus oralis</i>
	<i>Enterococcus faecalis</i>	60 <i>Pseudomonas stutzeri</i>	<i>Streptococcus parasanguinis</i>
25	<i>Enterococcus faecium</i>	<i>Salmonella bongori</i>	<i>Streptococcus parauberis</i>
	<i>Enterococcus flavescens</i>	<i>Salmonella choleraesuis</i>	<i>Streptococcus pneumoniae</i>
	<i>Enterococcus gallinarum</i>	<i>Salmonella enteritidis</i>	<i>Streptococcus pyogenes</i>
	<i>Enterococcus mundtii</i>	<i>Salmonella gallinarum</i>	100 <i>Streptococcus rattii</i>
	<i>Enterococcus raffinosus</i>	65 <i>Salmonella typhimurium</i>	<i>Streptococcus salivarius</i>
30	<i>Enterococcus solitarius</i>	<i>Serratia liquefaciens</i>	<i>Streptococcus sanguinis</i>
	<i>Escherichia coli</i>	<i>Serratia marcescens</i>	<i>Streptococcus sobrinus</i>
	<i>Gemella morbillorum</i>	<i>Shigella flexneri</i>	<i>Streptococcus uberis</i>
	<i>Haemophilus ducreyi</i>	<i>Shigella sonnei</i>	105 <i>Streptococcus vestibularis</i>
	<i>Haemophilus haemolyticus</i>	70 <i>Staphylococcus aureus</i>	<i>Vibrio cholerae</i>
35	<i>Haemophilus influenzae</i>	<i>Staphylococcus capitis</i>	<i>Yersinia enterocolitica</i>
	<i>Haemophilus</i>	<i>Staphylococcus epidermidis</i>	<i>Yersinia pestis</i>
	<i>parahaemolyticus</i>	<i>Staphylococcus haemolyticus</i>	<i>Yersinia pseudotuberculosis</i>
	<i>Haemophilus parainfluenzae</i>	<i>Staphylococcus hominis</i>	
	<i>Hafnia alvei</i>	75 <i>Staphylococcus lugdunensis</i>	
40	<i>Kingella kingae</i>	<i>Staphylococcus saprophyticus</i>	

Table 15. Microorganism identified by commercial systems¹.

5	<i>Abiotrophia adiacens</i> (<i>Streptococcus adiacens</i>) <i>Abiotrophia defectiva</i> (<i>Streptococcus defectivus</i>) <i>Achromobacter</i> species <i>Acidaminococcus fermentans</i> <i>Acinetobacter alkaligenes</i> <i>Acinetobacter anitratus</i> <i>Acinetobacter baumannii</i> <i>Acinetobacter calcoaceticus</i> <i>Acinetobacter calcoaceticus biovar anitratus</i> <i>Acinetobacter calcoaceticus biovar lwoffii</i> <i>Acinetobacter genomospecies</i> <i>Acinetobacter haemolyticus</i> <i>Acinetobacter johnsonii</i> <i>Acinetobacter junii</i> <i>Acinetobacter lwoffii</i> <i>Acinetobacter radiorensistens</i> <i>Acinetobacter</i> species <i>Actinobacillus actinomycetemcomitans</i> <i>Actinobacillus capsulatus</i> <i>Actinobacillus equuli</i> <i>Actinobacillus hominis</i> <i>Actinobacillus lignieresii</i> <i>Actinobacillus pleuropneumoniae</i> <i>Actinobacillus</i> species <i>Actinobacillus suis</i> <i>Actinobacillus ureae</i> <i>Actinomyces bovis</i> <i>Actinomyces israelii</i> <i>Actinomyces meyeri</i> <i>Actinomyces naeslundii</i> <i>Actinomyces neuii</i> subsp. <i>anitratus</i> <i>Actinomyces neuii</i> subsp. <i>neuii</i> <i>Actinomyces odontolyticus</i> <i>Actinomyces pyogenes</i> <i>Actinomyces radingae</i> <i>Actinomyces</i> species <i>Actinomyces turicensis</i> <i>Actinomyces viscosus</i> <i>Aerococcus</i> species <i>Aerococcus viridans</i> <i>Aeromonas caviae</i> <i>Aeromonas hydrophila</i> <i>Aeromonas hydrophila</i> group <i>Aeromonas jandaei</i> <i>Aeromonas salmonicida</i> <i>Aeromonas salmonicida</i> subsp. <i>achromogenes</i> <i>Aeromonas salmonicida</i> subsp. <i>masoucida</i> <i>Aeromonas salmonicida</i> subsp. <i>salmonicida</i> <i>Aeromonas schubertii</i> <i>Aeromonas sobria</i> <i>Aeromonas</i> species <i>Aeromonas trola</i> <i>Aeromonas veronii</i> <i>Aeromonas veronii</i> biovar <i>sobria</i> <i>Aeromonas veronii</i> biovar <i>veronii</i> <i>Agrobacterium radiobacter</i> <i>Agrobacterium</i> species <i>Agrobacterium tumefaciens</i> <i>Alcaligenes denitrificans</i> <i>Alcaligenes faecalis</i> <i>Alcaligenes odorans</i> <i>Alcaligenes odorans</i> (<i>Alcaligenes faecalis</i>) <i>Alcaligenes</i> species <i>Alcaligenes xylosoxidans</i> <i>Alcaligenes xylosoxidans</i> subsp. <i>denitrificans</i>	75 80 85 90 95 100 105 110 115 120 125 130 135 140 145	<i>Alcaligenes xylosoxidans</i> subsp. <i>xylosoxidans</i> <i>Alloicoccus otitis</i> <i>Anaerobiospirillum succiniciproducens</i> <i>Anaerovibrio lipolytica</i> <i>Arachnia propionica</i> <i>Arcanobacterium</i> (<i>Actinomyces</i>) <i>bernardiae</i> <i>Arcanobacterium</i> (<i>Actinomyces</i>) <i>pyogenes</i> <i>Arcanobacterium haemolyticum</i> <i>Arcobacter cryaerophilus</i> (<i>Campylobacter cryaerophila</i>) <i>Arthrobacter globiformis</i> <i>Arthrobacter</i> species <i>Arxiozyma telluris</i> (<i>Torulopsis pintolopesii</i>) <i>Atopobium minutum</i> (<i>Lactobacillus minutus</i>) <i>Aureobacterium</i> species <i>Bacillus amyloliquefaciens</i> <i>Bacillus anthracis</i> <i>Bacillus badius</i> <i>Bacillus cereus</i> <i>Bacillus circulans</i> <i>Bacillus coagulans</i> <i>Bacillus firmus</i> <i>Bacillus lentus</i> <i>Bacillus licheniformis</i> <i>Bacillus megaterium</i> <i>Bacillus mycoides</i> <i>Bacillus pantothenicus</i> <i>Bacillus pumilus</i> <i>Bacillus</i> species <i>Bacillus sphaericus</i> <i>Bacillus stearothermophilus</i> <i>Bacillus subtilis</i> <i>Bacillus thuringiensis</i> <i>Bacteroides caccae</i> <i>Bacteroides capillosus</i> <i>Bacteroides distasonis</i> <i>Bacteroides eggerthii</i> <i>Bacteroides fragilis</i> <i>Bacteroides merdae</i> <i>Bacteroides ovatus</i> <i>Bacteroides</i> species <i>Bacteroides splanchnicus</i> <i>Bacteroides stercoris</i> <i>Bacteroides thetaiotaomicron</i> <i>Bacteroides uniformis</i> <i>Bacteroides ureolyticus</i> (<i>B. corrodens</i>) <i>Bacteroides vulgatus</i> <i>Bergeyella</i> (<i>Weeksella</i>) <i>zooheicum</i> <i>Bifidobacterium adolescentis</i> <i>Bifidobacterium bifidum</i> <i>Bifidobacterium breve</i> <i>Bifidobacterium dentium</i> <i>Bifidobacterium infantis</i> <i>Bifidobacterium</i> species <i>Blastoschizomyces</i> (<i>Dipodascus</i>) <i>capitatus</i> <i>Bordetella avium</i> <i>Bordetella bronchiseptica</i> <i>Bordetella parapertussis</i> <i>Bordetella pertussis</i> <i>Bordetella</i> species <i>Borrelia</i> species <i>Branhamella</i> (<i>Moraxella</i>) <i>cetarrhalis</i> <i>Branhamella</i> species <i>Brevibacillus brevis</i> <i>Brevibacillus laterosporus</i> <i>Brevibacterium casei</i> <i>Brevibacterium epidermidis</i> <i>Brevibacterium linens</i>	150 155 160 165 170 175 180 185 190 195 200 205 210 215 220	<i>Brevibacterium</i> species <i>Brevundimonas</i> (<i>Pseudomonas</i>) <i>diminuta</i> <i>Brevundimonas</i> (<i>Pseudomonas</i>) <i>vesicularis</i> <i>Brevundimonas</i> species <i>Brochothrix thermosphacta</i> <i>Brucella abortus</i> <i>Brucella canis</i> <i>Brucella melitensis</i> <i>Brucella ovis</i> <i>Brucella</i> species <i>Brucella suis</i> <i>Budvicia aquatica</i> <i>Burkholderia</i> (<i>Pseudomonas</i>) <i>cepacia</i> <i>Burkholderia</i> (<i>Pseudomonas</i>) <i>gladioli</i> <i>Burkholderia</i> (<i>Pseudomonas</i>) <i>mallei</i> <i>Burkholderia</i> (<i>Pseudomonas</i>) <i>pseudomallei</i> <i>Burkholderia</i> species <i>Buttiauxella agrestis</i> <i>Campylobacter coli</i> <i>Campylobacter concisus</i> <i>Campylobacter fetus</i> <i>Campylobacter fetus</i> subsp. <i>fetus</i> <i>Campylobacter fetus</i> subsp. <i>venerealis</i> <i>Campylobacter hyointestinalis</i> <i>Campylobacter jejuni</i> subsp. <i>doylei</i> <i>Campylobacter jejuni</i> subsp. <i>jejuni</i> <i>Campylobacter lari</i> <i>Campylobacter lari</i> subsp. <i>UPTC</i> <i>Campylobacter mucosalis</i> <i>Campylobacter</i> species <i>Campylobacter sputorum</i> <i>Campylobacter sputorum</i> subsp. <i>bubulus</i> <i>Campylobacter sputorum</i> subsp. <i>fecalis</i> <i>Campylobacter sputorum</i> subsp. <i>sputorum</i> <i>Campylobacter upsaliensis</i> <i>Candida</i> (<i>Clavispora</i>) <i>lusitanae</i> <i>Candida</i> (<i>Pichia</i>) <i>guilliermondii</i> <i>Candida</i> (<i>Torulopsis</i>) <i>glabrata</i> <i>Candida albicans</i> <i>Candida boidinii</i> <i>Candida catenulata</i> <i>Candida ciferrii</i> <i>Candida colliculosa</i> <i>Candida conglobata</i> <i>Candida curvata</i> (<i>Cryptococcus curvatus</i>) <i>Candida datilia</i> <i>Candida dubliniensis</i> <i>Candida famata</i> <i>Candida globosa</i> <i>Candida hellenica</i> <i>Candida holmii</i> <i>Candida humicola</i> <i>Candida inconspicua</i> <i>Candida intermedia</i> <i>Candida kefyr</i> <i>Candida krusei</i> <i>Candida lambica</i> <i>Candida magnoliae</i> <i>Candida maris</i> <i>Candida melibiosica</i> <i>Candida membranifaciens</i> <i>Candida norvegensis</i> <i>Candida norvegica</i> <i>Candida parapsilosis</i> <i>Candida paratropicalis</i> <i>Candida pelliculosa</i>
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Table 15. Microorganism identified by commercial systems (continued)

<i>Candida pseudotropicalis</i>		<i>Clostridium hastiforme</i>		<i>Corynebacterium urealyticum</i> (group D2)
<i>Candida pulcherrima</i>		<i>Clostridium histolyticum</i>		<i>Corynebacterium xerosis</i>
<i>Candida ravautii</i>		<i>Clostridium innocuum</i>	160	<i>Cryptococcus albidus</i>
<i>Candida rugosa</i>		<i>Clostridium limosum</i>		<i>Cryptococcus ater</i>
5 <i>Candida sake</i>		<i>Clostridium novyi</i>		<i>Cryptococcus cereanus</i>
<i>Candida silvicola</i>		<i>Clostridium novyi</i> A		<i>Cryptococcus gastricus</i>
<i>Candida species</i>		<i>Clostridium parapatritificum</i>		<i>Cryptococcus humicolus</i>
<i>Candida sphaerica</i>		<i>Clostridium perfringens</i>	165	<i>Cryptococcus lactivorius</i>
<i>Candida stellatoidea</i>		<i>Clostridium putrificum</i>		<i>Cryptococcus laurentii</i>
10 <i>Candida tenuis</i>		<i>Clostridium ramosum</i>		<i>Cryptococcus luteolus</i>
<i>Candida tropicalis</i>		<i>Clostridium septicum</i>		<i>Cryptococcus melibiosum</i>
<i>Candida utilis</i>		<i>Clostridium sordellii</i>		<i>Cryptococcus neoformans</i>
<i>Candida valida</i>		<i>Clostridium species</i>	170	<i>Cryptococcus species</i>
<i>Candida vini</i>		<i>Clostridium sphenoides</i>		<i>Cryptococcus terreus</i>
15 <i>Candida viswanathii</i>		<i>Clostridium sporogenes</i>		<i>Cryptococcus uniguttulatus</i>
<i>Candida zeylanoides</i>		<i>Clostridium subterminale</i>		<i>Debaryomyces hansenii</i>
<i>Capnocytophaga gingivalis</i>		<i>Clostridium tertium</i>		<i>Debaryomyces maramba</i>
<i>Capnocytophaga ochracea</i>		<i>Clostridium tetani</i>	175	<i>Debaryomyces polymorphus</i>
<i>Capnocytophaga species</i>		<i>Clostridium tyrobutyricum</i>		<i>Debaryomyces species</i>
20 <i>Capnocytophaga sputigena</i>		<i>Comamonas (Pseudomonas) acidovorans</i>		<i>Dermabacter hominis</i>
<i>Cardiobacterium hominis</i>		<i>Comamonas (Pseudomonas) testosteroni</i>		<i>Dermacoccus (Micrococcus) nishinomiyaensis</i>
<i>Camobacterium divergens</i>		<i>Comamonas species</i>	180	<i>Dietzia species</i>
<i>Camobacterium piscicola</i>		<i>Corynebacterium accolens</i>		<i>Edwardsiella hoshinae</i>
CDC group ED-2		<i>Corynebacterium afermentans</i>		<i>Edwardsiella ictaluri</i>
25 CDC group EF4 (<i>Pasteurella</i> sp.)		<i>Corynebacterium amycolatum</i>		<i>Edwardsiella species</i>
CDC group EF-4A		<i>Corynebacterium aquaticum</i>		<i>Edwardsiella tarda</i>
CDC group EF-4B		<i>Corynebacterium argentoratense</i>	185	<i>Eikenella corrodens</i>
CDC group EQ-Z		<i>Corynebacterium auris</i>		<i>Empedobacter brevis</i> (<i>Flavobacterium breve</i>)
CDC group HB-5		<i>Corynebacterium bovis</i>		<i>Enterobacter aerogenes</i>
30 CDC group II K-2		<i>Corynebacterium coyleae</i>		<i>Enterobacter agglomerans</i>
CDC group IV C-2 (<i>Bordetella</i> -like)		<i>Corynebacterium cystitidis</i>		<i>Enterobacter amnigenus</i>
CDC group M5		<i>Corynebacterium diphtheriae</i>	190	<i>Enterobacter amnigenus asburiae</i>
CDC group M6		<i>Corynebacterium diphtheriae</i> biotype <i>belanti</i>		(CDC enteric group 17)
<i>Cedecea davisae</i>		<i>Corynebacterium diphtheriae</i> biotype <i>gravis</i>		<i>Enterobacter amnigenus biogroup 1</i>
35 <i>Cedecea lapagei</i>		<i>Corynebacterium diphtheriae</i> biotype <i>intermedius</i>		<i>Enterobacter amnigenus biogroup 2</i>
<i>Cedecea neteri</i>		<i>Corynebacterium diphtheriae</i> biotype <i>mitis</i>	195	<i>Enterobacter asburiae</i>
<i>Cedecea species</i>		<i>Corynebacterium diphtheriae</i> biotype <i>seminale</i>		<i>Enterobacter cancerogenus</i>
<i>Cellulomonas (Oerskovia) turbata</i>		<i>Corynebacterium flavescens</i>	200	<i>Enterobacter cloacae</i>
<i>Cellulomonas species</i>		<i>Corynebacterium glucuronolyticum</i>		<i>Enterobacter gergoviae</i>
40 <i>Chlamydia species</i>		<i>Corynebacterium glucuronolyticum</i>		<i>Enterobacter hormaechei</i>
<i>Chromobacterium violaceum</i>		<i>Corynebacterium group A</i>		<i>Enterobacter intermedius</i>
<i>Chryseobacterium (Flavobacterium) indologenes</i>		<i>Corynebacterium group A-4</i>	205	<i>Enterobacter sakazakii</i>
<i>Chryseobacterium (Flavobacterium) meningosepticum</i>		<i>Corynebacterium group A-5</i>		<i>Enterobacter species</i>
<i>Chryseobacterium gleum</i>		<i>Corynebacterium group ANF</i>		<i>Enterobacter taylorae</i>
<i>Chryseobacterium species</i>		<i>Corynebacterium group B</i>		<i>Enterobacter taylorae</i> (CDC enteric group 19)
<i>Chryseomonas indologenes</i>		<i>Corynebacterium group B-3</i>		<i>Enterococcus (Streptococcus) cecorum</i>
<i>Citeromyces matritensis</i>		<i>Corynebacterium group F</i>		<i>Enterococcus (Streptococcus) faecalis</i> (Group D)
50 <i>Citrobacter amalonaticus</i>		<i>Corynebacterium group F-1</i>		<i>Enterococcus (Streptococcus) faecium</i> (Group D)
<i>Citrobacter braakii</i>		<i>Corynebacterium group F-2</i>	210	<i>Enterococcus (Streptococcus) saccharolyticus</i>
<i>Citrobacter diversus</i>		<i>Corynebacterium group G</i>		<i>Enterococcus avium</i> (Group D)
<i>Citrobacter farmeri</i>		<i>Corynebacterium group G-1</i>		<i>Enterococcus casseliflavus</i> (Streptococcus faecium subsp. casseliflavus)
<i>Citrobacter freundii</i>		<i>Corynebacterium group G-2</i>		<i>Enterococcus durans</i> (Streptococcus faecium subsp. durans) (Group D)
55 <i>Citrobacter freundii</i> complex		<i>Corynebacterium group I</i>		<i>Enterococcus gallinarum</i>
<i>Citrobacter koseri</i>		<i>Corynebacterium group I-2</i>		<i>Enterococcus hirae</i>
<i>Citrobacter sedlakii</i>		<i>Corynebacterium jeikeium</i> (group JK)		<i>Enterococcus malodoratus</i>
<i>Citrobacter species</i>		<i>Corynebacterium kutscheri</i> (<i>C. murium</i>)	215	<i>Enterococcus mundtii</i>
<i>Citrobacter werkmanii</i>		<i>Corynebacterium macginleyi</i>		<i>Enterococcus raffinosus</i>
60 <i>Citrobacter youngae</i>		<i>Corynebacterium minutissimum</i>		<i>Enterococcus species</i>
<i>Clostridium acetobutylicum</i>		<i>Corynebacterium pilosum</i>	225	<i>Erwinia amylovora</i>
<i>Clostridium barati</i>		<i>Corynebacterium propinquum</i>		<i>Erwinia carotovora</i>
<i>Clostridium beijerinckii</i>		<i>Corynebacterium pseudodiphtheriticum</i>		<i>Erwinia carotovora</i> subsp. <i>atroseptica</i>
<i>Clostridium bifementans</i>		<i>Corynebacterium pseudotuberculosis</i>		<i>Erwinia carotovora</i> subsp. <i>betavascularum</i>
65 <i>Clostridium botulinum</i>		<i>Corynebacterium pyogenes</i>		<i>Erwinia carotovora</i> subsp. <i>carotovora</i>
<i>Clostridium botulinum</i> (NP) B&F		<i>Corynebacterium renale</i>	230	<i>Erwinia chrysanthemi</i>
<i>Clostridium botulinum</i> (NP) E		<i>Corynebacterium renale</i> group		<i>Erwinia cypripedii</i>
<i>Clostridium botulinum</i> (P) A&H		<i>Corynebacterium seminale</i>		<i>Erwinia maltotivora</i>
<i>Clostridium botulinum</i> (P) F		<i>Corynebacterium species</i>		
<i>Clostridium botulinum</i> G2		<i>Corynebacterium striatum</i> (<i>C. flavidum</i>)		
<i>Clostridium butyricum</i>		<i>Corynebacterium ulcerans</i>		
<i>Clostridium cadaveris</i>				
<i>Clostridium chauvoei</i>				
75 <i>Clostridium clostridioforme</i>				
<i>Clostridium difficile</i>				
<i>Clostridium fallax</i>				
<i>Clostridium glycolicum</i>				

Table 15. Microorganism identified by commercial systems (continued)

<i>Erwinia nigrifluens</i>	VII	<i>Lactobacillus paracasei</i> subsp. <i>paracasei</i>
<i>Erwinia quercina</i>	80	<i>Haemophilus parainfluenzae</i> biotype
<i>Erwinia raphanistrum</i>	VIII	<i>Haemophilus paraphrohaemolyticus</i>
<i>Erwinia rubrifaciens</i>		160
<i>Erwinia salicis</i>		<i>Haemophilus paraphrophilus</i>
<i>Erwinia species</i>		<i>Haemophilus segnis</i>
<i>Erysipelothrix rhusiopathiae</i>	85	<i>Haemophilus somnus</i>
<i>Erysipelothrix species</i>		<i>Haemophilus species</i>
<i>Escherichia blattae</i>		<i>Hafnia alvei</i>
10 <i>Escherichia coli</i>		165
<i>Escherichia coli</i> A-D		<i>Hanseniaspora guilliermondii</i>
<i>Escherichia coli</i> O157:H7		<i>Hanseniaspora uvarum</i>
<i>Escherichia fergusonii</i>	90	<i>Hanseniaspora valbyensis</i>
<i>Escherichia hermannii</i>		<i>Hansenula anomala</i>
15 <i>Escherichia species</i>		<i>Hansenula holstii</i>
<i>Escherichia vulneris</i>		<i>Hansenula polymorpha</i>
<i>Eubacterium aerofaciens</i>	95	<i>Helicobacter (Campylobacter) cinaedi</i>
<i>Eubacterium alactolyticum</i>		<i>Helicobacter (Campylobacter)</i>
<i>Eubacterium lentum</i>		<i>fennelliae</i>
20 <i>Eubacterium limosum</i>		<i>Helicobacter (Campylobacter) pylori</i>
<i>Eubacterium species</i>		175
<i>Ewingella americana</i>	100	<i>Issatchenkia orientalis</i>
<i>Filobasidium neoformans</i>		<i>Kingella denitrificans</i>
<i>Filobasidium floriforme</i>		<i>Kingella indologenes</i>
25 <i>Filobasidium uniguttulatum</i>		<i>Kingella kingae</i>
<i>Flavimonas oryzae</i>		<i>Kingella species</i>
<i>Flavobacterium glauum</i>	105	<i>Klebsiella ornithinolytica</i>
<i>Flavobacterium indologenes</i>		<i>Klebsiella oxytoca</i>
<i>Flavobacterium odoratum</i>		<i>Klebsiella planticola</i>
30 <i>Flavobacterium species</i>		<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>
<i>Francisella novicida</i>		<i>Klebsiella pneumoniae</i> subsp. <i>pneumoniae</i>
<i>Francisella philomiragia</i>	110	<i>Klebsiella pneumoniae</i> subsp. <i>rhinoscleromatis</i>
<i>Francisella species</i>		<i>Klebsiella species</i>
<i>Francisella tularensis</i>		<i>Klebsiella terrigena</i>
35 <i>Fusobacterium montiferum</i>		<i>Kloekera apiculata</i>
<i>Fusobacterium necrogenes</i>		<i>Kloekera apis</i>
<i>Fusobacterium necrophorum</i>	115	<i>Kloekera japonica</i>
<i>Fusobacterium nucleatum</i>		<i>Kloekera species</i>
<i>Fusobacterium species</i>		<i>Kluyvera ascorbata</i>
40 <i>Fusobacterium varium</i>		<i>Kluyvera cryocrescens</i>
<i>Gaffkya species</i>		<i>Kluyvera species</i>
<i>Gardnerella vaginalis</i>	120	<i>Kluyveromyces lactis</i>
<i>Gemella haemolysans</i>		<i>Kluyveromyces marxianus</i>
<i>Gemella morbillorum</i>		<i>Kluyveromyces thermotolerans</i>
45 <i>Gemella species</i>		<i>Kocuria (Micrococcus) kristinae</i>
<i>Geotrichum candidum</i>		<i>Kocuria (Micrococcus) rosea</i>
<i>Geotrichum fermentans</i>	125	<i>Kocuria (Micrococcus) varians</i>
<i>Geotrichum penicillarium</i>		<i>Koserella trabulsi</i>
<i>Geotrichum penicillatum</i>		<i>Kytococcus (Micrococcus) sedentarius</i>
50 <i>Geotrichum species</i>		<i>Lactobacillus (Weissella) viridescens</i>
<i>Gordana species</i>		130
<i>Haemophilus aegyptius</i>		<i>Lactobacillus A</i>
<i>Haemophilus aphrophilus</i>		<i>Lactobacillus acidophilus</i>
<i>Haemophilus ducreyi</i>		<i>Lactobacillus B</i>
55 <i>Haemophilus haemoglobinophilus</i>		<i>Lactobacillus brevis</i>
<i>Haemophilus haemolyticus</i>		<i>Lactobacillus buchneri</i>
<i>Haemophilus influenzae</i>	135	<i>Lactobacillus casei</i>
<i>Haemophilus influenzae</i> biotype I		<i>Lactobacillus casei</i> subsp. <i>casei</i>
<i>Haemophilus influenzae</i> biotype II		<i>Lactobacillus casei</i> subsp. <i>lactosus</i>
60 <i>Haemophilus influenzae</i> biotype III		<i>Lactobacillus casei</i> subsp. <i>thamnosus</i>
<i>Haemophilus influenzae</i> biotype IV		<i>Lactobacillus cateniformis</i>
<i>Haemophilus influenzae</i> biotype V	140	<i>Lactobacillus cellobiosus</i>
<i>Haemophilus influenzae</i> biotype VI		<i>Lactobacillus collinoides</i>
<i>Haemophilus influenzae</i> biotype VII		<i>Lactobacillus coprophilus</i>
65 <i>Haemophilus influenzae</i> biotype VIII		<i>Lactobacillus crispatus</i>
<i>Haemophilus paragaillinarum</i>		<i>Lactobacillus curvatus</i>
<i>Haemophilus parahemolyticus</i>	145	<i>Lactobacillus delbrueckii</i> subsp. <i>bulgaricus</i>
<i>Haemophilus parainfluenzae</i>		<i>Lactobacillus delbrueckii</i> subsp. <i>delbrueckii</i>
<i>Haemophilus parainfluenzae</i> biotype I		<i>Lactobacillus delbrueckii</i> subsp. <i>lactis</i>
<i>Haemophilus parainfluenzae</i> biotype II	150	<i>Lactobacillus fermentum</i>
<i>Haemophilus parainfluenzae</i> biotype III		<i>Lactobacillus fructivorans</i>
<i>Haemophilus parainfluenzae</i> biotype IV		<i>Lactobacillus helveticus</i>
75 <i>Haemophilus parainfluenzae</i> biotype V		<i>Lactobacillus helveticus</i> subsp. <i>jugurti</i>
<i>Haemophilus parainfluenzae</i> biotype VI	155	<i>Lactobacillus jensenii</i>
<i>Haemophilus parainfluenzae</i> biotype VII		<i>Lactobacillus lindneri</i>
		<i>Lactobacillus minutus</i>
		<i>Lactobacillus paracasei</i> subsp. <i>paracasei</i>
		<i>Lactobacillus pentosus</i>
		<i>Lactobacillus plantarum</i>
		<i>Lactobacillus salivarius</i>
		<i>Lactobacillus salivarius</i> var. <i>salicinius</i>
		<i>Lactobacillus species</i>
		<i>Lactococcus diacetylactis</i>
		<i>Lactococcus garvieae</i>
		<i>Lactococcus lactis</i> subsp. <i>cremoris</i>
		<i>Lactococcus lactis</i> subsp. <i>diacetylactis</i>
		<i>Lactococcus lactis</i> subsp. <i>hordniae</i>
		<i>Lactococcus lactis</i> subsp. <i>lactis</i>
		<i>Lactococcus plantarum</i>
		<i>Lactococcus raffinolactis</i>
		<i>Leclercia adecarboxylata</i>
		<i>Legionella species</i>
		<i>Leminorella species</i>
		<i>Leptospira species</i>
		<i>Leptotrichia buccalis</i>
		<i>Leuconostoc (Weissella)</i>
		<i>paramesenteroides</i>
		<i>Leuconostoc carnosum</i>
		<i>Leuconostoc citreum</i>
		<i>Leuconostoc gelidum</i>
		<i>Leuconostoc lactis</i>
		<i>Leuconostoc mesenteroides</i>
		<i>Leuconostoc mesenteroides</i> subsp. <i>cremoris</i>
		<i>Leuconostoc mesenteroides</i> subsp. <i>dextranicum</i>
		<i>Leuconostoc mesenteroides</i> subsp. <i>mesenteroides</i>
		<i>Leuconostoc species</i>
		<i>Listeria grayi</i>
		<i>Listeria innocua</i>
		<i>Listeria ivanovii</i>
		<i>Listeria monocytogenes</i>
		<i>Listeria murrayi</i>
		<i>Listeria seeligeri</i>
		<i>Listeria species</i>
		<i>Listeria welshimeri</i>
		<i>Megasphaera elsdenii</i>
		<i>Methylobacterium mesophilicum</i>
		<i>Metschnikowia pulcherrima</i>
		<i>Microbacterium species</i>
		<i>Micrococcus luteus</i>
		<i>Micrococcus lysodeikticus</i>
		<i>Micrococcus species</i>
		<i>Mobiluncus curtisi</i>
		<i>Mobiluncus mulleris</i>
		<i>Mobiluncus species</i>
		<i>Moraxella (Branhamella) catarrhalis</i>
		<i>Moraxella atlantae</i>
		<i>Moraxella bovis</i>
		<i>Moraxella lacunata</i>
		<i>Moraxella nonliquefaciens</i>
		<i>Moraxella osloensis</i>
		<i>Moraxella phenylpyruvica</i>
		<i>Moraxella species</i>
		<i>Morganella morganii</i>
		<i>Morganella morganii</i> subsp. <i>morganii</i>
		<i>Morganella morganii</i> subsp. <i>sibirica</i>
		<i>Mycobacterium africanum</i>
		<i>Mycobacterium asiaticum</i>
		<i>Mycobacterium avium</i>
		<i>Mycobacterium bovis</i>
		<i>Mycobacterium chelonae</i>
		<i>Mycobacterium fortuitum</i>
		<i>Mycobacterium gordonae</i>
		<i>Mycobacterium kansasii</i>
		<i>Mycobacterium mageritense</i>
		<i>Mycobacterium marinum</i>
		<i>Mycobacterium phlei</i>
		<i>Mycobacterium scrofulaceum</i>
		<i>Mycobacterium smegmatis</i>
		<i>Mycobacterium species</i>

Tabl 15. Microorganisms notified by commercial systems (continued)¹

	<i>Mycobacterium tuberculosis</i>		<i>Pichia fermentans</i>		<i>Saccharomyces exiguus</i>
	<i>Mycobacterium ulcerans</i>	80	<i>Pichia membranaefaciens</i>		<i>Saccharomyces kluyveri</i>
	<i>Mycobacterium xenopi</i>		<i>Pichia norvegensis</i>	160	<i>Saccharomyces species</i>
	<i>Mycoplasma fermentans</i>		<i>Pichia ohmeri</i>		<i>Sakaguchia dacryoides</i>
5	<i>Mycoplasma hominis</i>		<i>Pichia spartinae</i>		(<i>Rhodospiridium dacryoidum</i>)
	<i>Mycoplasma orale</i>		<i>Pichia species</i>		<i>Salmonella ansonae</i>
	<i>Mycoplasma pneumoniae</i>	85	<i>Plesiomonas shigelloides</i>		<i>Salmonella choleraesuis</i>
	<i>Mycoplasma species</i>		<i>Porphyromonas asaccharolytica</i>		<i>Salmonella enteritidis</i>
	<i>Myroides species</i>		<i>Porphyromonas endodontalis</i>	165	<i>Salmonella gallinarum</i>
10	<i>Neisseria cinerea</i>		<i>Porphyromonas gingivalis</i>		<i>Salmonella paratyphi A</i>
	<i>Neisseria elongata</i> subsp. <i>elongata</i>		<i>Porphyromonas levii</i>		<i>Salmonella paratyphi B</i>
	<i>Neisseria flava</i>	90	<i>Prevotella (Bacteroides) buccae</i>		<i>Salmonella pullorum</i>
	<i>Neisseria flavescens</i>		<i>Prevotella (Bacteroides) buccalis</i>		<i>Salmonella species</i>
	<i>Neisseria gonorrhoeae</i>		<i>Prevotella (Bacteroides) corporis</i>	170	<i>Salmonella typhi</i>
15	<i>Neisseria lactamica</i>		<i>Prevotella (Bacteroides) denticola</i>		<i>Salmonella typhimurium</i>
	<i>Neisseria meningitidis</i>		<i>Prevotella (Bacteroides) loeschii</i>		<i>Salmonella typhisuis</i>
	<i>Neisseria mucosa</i>	95	<i>Prevotella (Bacteroides) oralis</i>		<i>Salmonella/Arlzona</i>
	<i>Neisseria perflava</i>		<i>Prevotella (Bacteroides) disiens</i>		<i>Serratia ficaria</i>
	<i>Neisseria polysaccharea</i>		<i>Prevotella (Bacteroides) oris</i>	175	<i>Serratia fonticola</i>
20	<i>Neisseria saprophytes</i>		<i>Prevotella bivia (Bacteroides bivius)</i>		<i>Serratia grimesii</i>
	<i>Neisseria sicca</i>		<i>Prevotella intermedia (Bacteroides</i>		<i>Serratia liquefaciens</i>
	<i>Neisseria subflava</i>	100	<i>intermedius)</i>		<i>Serratia marcescens</i>
	<i>Neisseria weaveri</i>		<i>Prevotella melaninogenica</i>		<i>Serratia odorifera</i>
	<i>Neisseria weaveri</i> (CDC group M5)		(<i>Bacteroides melaninogenicus</i>)	180	<i>Serratia odorifera</i> type 1
25	<i>Nocardia species</i>		<i>Prevotella ruminicola</i>		<i>Serratia odorifera</i> type 2
	<i>Ochrobactrum anthropi</i>		<i>Propionibacterium acnes</i>		<i>Serratia phymuthica</i>
	<i>Oerskovia species</i>	105	<i>Propionibacterium avidum</i>		<i>Serratia proteamaculans</i>
	<i>Oerskovia xanthineolytica</i>		<i>Propionibacterium granulosum</i>		<i>Serratia proteamaculans</i> subsp.
	<i>Oligella (Moraxella) urethralis</i>		<i>Propionibacterium propionicum</i>	185	<i>proteamaculans</i>
30	<i>Oligella species</i>		<i>Propionibacterium species</i>		<i>Serratia proteamaculans</i> subsp.
	<i>Oligella ureolytica</i>		<i>Proteus mirabilis</i>		<i>quinovora</i>
	<i>Paenibacillus alvei</i>	110	<i>Proteus penneri</i>		<i>Serratia rubidaea</i>
	<i>Paenibacillus macerans</i>		<i>Proteus species</i>		<i>Serratia species</i>
	<i>Paenibacillus polymyxa</i>		<i>Proteus vulgaris</i>	190	<i>Shewanella (Pseudomonas,</i>
35	<i>Pantoea agglomerans</i>		<i>Prototheca species</i>		<i>Alteromonas) putrefaciens</i>
	<i>Pantoea ananas (Erwinia uredovora)</i>		<i>Prototheca wickerhamii</i>		<i>Shigella boydii</i>
	<i>Pantoea dispersa</i>	115	<i>Prototheca zopfii</i>		<i>Shigella dysenteriae</i>
	<i>Pantoea species</i>		<i>Providencia alcalifaciens</i>		<i>Shigella flexneri</i>
	<i>Pantoea stewartii</i>		<i>Providencia helmabachae</i>	195	<i>Shigella sonnei</i>
40	<i>Pasteurella (Haemophilus) avium</i>		<i>Providencia rettgeri</i>		<i>Shigella species</i>
	<i>Pasteurella aerogenes</i>		<i>Providencia rustigianii</i>		<i>Sphingobacterium multivorum</i>
	<i>Pasteurella gallinarum</i>	120	<i>Providencia species</i>		<i>Sphingobacterium species</i>
	<i>Pasteurella haemolytica</i>		<i>Providencia stuartii</i>		<i>Sphingobacterium spiritivorum</i>
	<i>Pasteurella haemolytica</i>		<i>Providencia stuartii urea +</i>	200	<i>Sphingobacterium thalophilum</i>
45	<i>Pasteurella multocida</i>		<i>Pseudomonas (Chryseomonas)</i>		<i>Sphingomonas (Pseudomonas)</i>
	<i>Pasteurella multocida</i> SF		<i>luteola</i>		<i>paucimobilis</i>
	<i>Pasteurella multocida</i> subsp.	125	<i>Pseudomonas acidovorans</i>		<i>Sporidiobolus salmonicolor</i>
	<i>multocida</i>		<i>Pseudomonas aeruginosa</i>		<i>Sporobolomyces roseus</i>
	<i>Pasteurella multocida</i> subsp. <i>septica</i>		<i>Pseudomonas alcaligenes</i>	205	<i>Sporobolomyces salmonicolor</i>
50	<i>Pasteurella pneumotropica</i>		<i>Pseudomonas cepacia</i>		<i>Sporobolomyces species</i>
	<i>Pasteurella species</i>		<i>Pseudomonas chlororaphis (P.</i>		<i>Staphylococcus (Peptococcus)</i>
	<i>Pasteurella ureae</i>	130	<i>aureofaciens)</i>		<i>saccharolyticus</i>
	<i>Pediococcus acidilactici</i>		<i>Pseudomonas fluorescens</i>		<i>Staphylococcus erlathae</i>
	<i>Pediococcus damnosus</i>		<i>Pseudomonas fluorescens</i> group	210	<i>Staphylococcus aureus</i>
55	<i>Pediococcus pentosaceus</i>		<i>Pseudomonas mendocina</i>		<i>Staphylococcus aureus</i> (Coagulase-
	<i>Pediococcus species</i>		<i>Pseudomonas pseudoalcaligenes</i>		<i>negative)</i>
	<i>Peptococcus niger</i>	135	<i>Pseudomonas putida</i>		<i>Staphylococcus auricularis</i>
	<i>Peptococcus species</i>		<i>Pseudomonas species</i>		<i>Staphylococcus capitis</i>
	<i>Peptostreptococcus anaerobius</i>		<i>Pseudomonas stutzeri</i>	215	<i>Staphylococcus capitis</i> subsp. <i>capitis</i>
60	<i>Peptostreptococcus asaccharolyticus</i>		<i>Pseudomonas testosteroni</i>		<i>Staphylococcus capitis</i> subsp.
	<i>Peptostreptococcus indolicus</i>		<i>Pseudomonas vesicularis</i>		<i>ureolyticus</i>
	<i>Peptostreptococcus magnus</i>	140	<i>Pseudoramibacter (Eubacterium)</i>		<i>Staphylococcus caprae</i>
	<i>Peptostreptococcus micros</i>		<i>alactolyticus</i>		<i>Staphylococcus carnosus</i>
	<i>Peptostreptococcus parvulus</i>		<i>Psychrobacter (Moraxella)</i>	220	<i>Staphylococcus caseolyticus</i>
65	<i>Peptostreptococcus prevotii</i>		<i>phenylpyruvicus</i>		<i>Staphylococcus chromogenes</i>
	<i>Peptostreptococcus productus</i>		<i>Rahnella aquatilis</i>		<i>Staphylococcus cohnii</i>
	<i>Peptostreptococcus species</i>	145	<i>Ralstonia (Pseudomonas,</i>		<i>Staphylococcus cohnii</i> subsp. <i>cohnii</i>
	<i>Peptostreptococcus tetradius</i>		<i>Burkholderia) pickettii</i>		<i>Staphylococcus cohnii</i> subsp.
	<i>Phaeococcomyces exophialiae</i>		<i>Rhodococcus (Corynebacterium) equi</i>	225	<i>urealyticum</i>
70	<i>Photobacterium damsela</i>		<i>Rhodococcus species</i>		<i>Staphylococcus epidermidis</i>
	<i>Pichia (Hansenula) anomala</i>		<i>Rhodospiridium toruloides</i>		<i>Staphylococcus equorum</i>
	<i>Pichia (Hansenula) jadinii</i>	150	<i>Rhodotorula glutinis</i>		<i>Staphylococcus gallinarum</i>
	<i>Pichia (Hansenula) petersonii</i>		<i>Rhodotorula minuta</i>		<i>Staphylococcus haemolyticus</i>
	<i>Pichia angusta (Hansenula</i>		<i>Rhodotorula mucilaginosa (R. rubra)</i>	230	<i>Staphylococcus hominis</i>
75	<i>polymorpha)</i>		<i>Rhodotorula species</i>		<i>Staphylococcus hominis</i> subsp.
	<i>Pichia carsonii (P. vini)</i>		<i>Rickettsia species</i>		<i>hominis</i>
	<i>Pichia etchellsii</i>	155	<i>Rothia dentocariosa</i>		<i>Staphylococcus hominis</i> subsp.
	<i>Pichia farinosa</i>		<i>Saccharomyces cerevisiae</i>		<i>novobioceticus</i>

Table 15. Microorganisms identified by commercial systems (continued)¹

		60	<i>Streptococcus</i> Gamma (non)-hemolytic	120	<i>Tetragenococcus</i> (<i>Pediococcus</i>) <i>halophilus</i>
	<i>Staphylococcus hyicus</i>		<i>Streptococcus gordonii</i>		<i>Torulaspora delbrueckii</i>
	<i>Staphylococcus intermedius</i>		<i>Streptococcus</i> Group B		(<i>Saccharomyces rosei</i>)
5	<i>Staphylococcus kloosii</i>		<i>Streptococcus</i> Group C		<i>Torulopsis candida</i>
	<i>Staphylococcus lentus</i>		<i>Streptococcus</i> Group D		<i>Torulopsis haemulonii</i>
	<i>Staphylococcus lugdunensis</i>	65	<i>Streptococcus</i> Group E	125	<i>Torulopsis inconspicua</i>
	<i>Staphylococcus saprophyticus</i>		<i>Streptococcus</i> Group F		<i>Treponema</i> species
	<i>Staphylococcus schleiferi</i>		<i>Streptococcus</i> Group G		<i>Trichosporon asahii</i>
	<i>Staphylococcus sciuri</i>		<i>Streptococcus</i> Group L		<i>Trichosporon asteroides</i>
10	<i>Staphylococcus simulans</i>		<i>Streptococcus</i> Group P		<i>Trichosporon beigeli</i>
	<i>Staphylococcus species</i>	70	<i>Streptococcus</i> Group U	130	<i>Trichosporon cutaneum</i>
	<i>Staphylococcus warneri</i>		<i>Streptococcus intermedius</i>		<i>Trichosporon inkin</i>
	<i>Staphylococcus xylosum</i>		<i>Streptococcus intermedius</i>		<i>Trichosporon mucoides</i>
	<i>Stenotrophomonas</i> (<i>Xanthomonas</i>) <i>maltophila</i>		(<i>Streptococcus milleri</i> II)		<i>Trichosporon ovoides</i>
15	<i>Stephanosaurus citreus</i>	75	<i>Streptococcus intermedius</i> (<i>viridans</i>)		<i>Trichosporon pullulans</i>
	<i>Stomatococcus mucilaginosus</i>		<i>Streptococcus</i>	135	<i>Trichosporon</i> species
	<i>Streptococcus acidominimus</i>		<i>Streptococcus milleri</i> group		<i>Turicella otitidis</i>
	<i>Streptococcus agalactiae</i>		<i>Streptococcus mitis</i>		<i>Ureaplasma</i> species
20	<i>Streptococcus agalactiae</i> (Group B)		<i>Streptococcus mitis</i> (<i>viridans</i>)		<i>Ureaplasma urealyticum</i>
	<i>Streptococcus agalactiae</i> hemolytic	80	<i>Streptococcus</i>		<i>Veillonella parvula</i> (<i>V. alcalescens</i>)
	<i>Streptococcus agalactiae</i> non-hemolytic		<i>Streptococcus mitis</i> group	140	<i>Veillonella</i> species
	<i>Streptococcus alactolyticus</i>		<i>Streptococcus mutans</i>		<i>Vibrio alginolyticus</i>
25	<i>Streptococcus anginosus</i>		<i>Streptococcus mutans</i> (<i>viridans</i>)		<i>Vibrio cholerae</i>
	<i>Streptococcus anginosus</i> (Group D, nonenterococci)	85	<i>Streptococcus</i>		<i>Vibrio damsela</i>
	<i>Streptococcus beta-hemolytic</i> group A		<i>Streptococcus oralis</i>		<i>Vibrio fluvialis</i>
	<i>Streptococcus beta-hemolytic</i> non-group A or B		<i>Streptococcus parasanguis</i>	145	<i>Vibrio furnissii</i>
30	<i>Streptococcus beta-hemolytic</i> non-group A		<i>Streptococcus pneumoniae</i>		<i>Vibrio harveyi</i>
	<i>Streptococcus beta-hemolytic</i>		<i>Streptococcus porcineus</i>		<i>Vibrio hollisae</i>
	<i>Streptococcus bovis</i> (Group D, nonenterococci)	90	<i>Streptococcus pyogenes</i>		<i>Vibrio metschnikovii</i>
35	<i>Streptococcus bovis</i> I		<i>Streptococcus pyogenes</i> (Group A)	150	<i>Vibrio mimicus</i>
	<i>Streptococcus bovis</i> II		<i>Streptococcus salivarius</i>		<i>Vibrio parahaemolyticus</i>
	<i>Streptococcus canis</i>		<i>Streptococcus salivarius</i> (<i>viridans</i>)		<i>Vibrio</i> species
	<i>Streptococcus constellatus</i>		<i>Streptococcus</i>		<i>Vibrio</i> species SF
40	<i>Streptococcus constellatus</i> (<i>Streptococcus milleri</i> I)	95	<i>Streptococcus salivarius</i> subsp.		<i>Vibrio vulnificus</i>
	<i>Streptococcus constellatus</i> (<i>viridans</i>)		<i>Streptococcus salivarius</i> subsp.	155	<i>Weeksella</i> (<i>Bergeyella</i>) <i>virosa</i>
	<i>Streptococcus downei</i>		<i>Streptococcus salivarius</i> subsp. <i>thermophilus</i>		<i>Weeksella</i> species
45	<i>Streptococcus dysgalactiae</i> subsp. <i>dysgalactiae</i>	100	<i>Streptococcus sanguis</i>		<i>Weeksella virosa</i>
	<i>Streptococcus dysgalactiae</i> subsp. <i>equisimilis</i>		<i>Streptococcus sanguis</i> I (<i>viridans</i>)		<i>Williopsis</i> (<i>Hansenula</i>) <i>saturum</i>
	<i>Streptococcus equi</i> (Group C/Group G)		<i>Streptococcus</i>		<i>Xanthomonas campestris</i>
50	<i>Streptococcus equi</i> subsp. <i>equi</i>	105	<i>Streptococcus sanguis</i> II (<i>viridans</i>)	160	<i>Xanthomonas</i> species
	<i>Streptococcus equi</i> subsp. <i>zooepidemicus</i>		<i>Streptococcus</i>		<i>Yarrowia</i> (<i>Candida</i>) <i>lipolytica</i>
	<i>Streptococcus equinus</i>		<i>Streptococcus sobrinus</i>		<i>Yersinia aldovae</i>
55	<i>Streptococcus equinus</i> (Group D, nonenterococci)		<i>Streptococcus species</i>		<i>Yersinia enterocolitica</i>
	<i>Streptococcus equisimilis</i>		<i>Streptococcus suis</i> I	165	<i>Yersinia enterocolitica</i> group
	<i>Streptococcus equisimilis</i> (Group C/Group G <i>Streptococcus</i>)		<i>Streptococcus suis</i> II		<i>Yersinia frederiksenii</i>
			<i>Streptococcus uberis</i>		<i>Yersinia intermedia</i>
			<i>Streptococcus uberis</i> (<i>viridans</i>)		<i>Yersinia intermedius</i>
		110	<i>Streptococcus</i>		<i>Yersinia kristensenii</i>
			<i>Streptococcus vestibularis</i>		<i>Yersinia pestis</i>
			<i>Streptococcus zooepidemicus</i>	170	<i>Yersinia pseudotuberculosis</i>
			<i>Streptococcus zooepidemicus</i> (Group C)		<i>Yersinia pseudotuberculosis</i> SF
		115	<i>Streptomyces somaliensis</i>		<i>Yersinia ruckeri</i>
			<i>Streptomyces species</i>		<i>Yersinia</i> species
			<i>Suttonella</i> (<i>Kingella</i>) <i>indologenes</i>	175	<i>Yokenella regensburgeri</i>
			<i>Tatumella ptyseos</i>		<i>Yokenella regensburgeri</i> (<i>Koserella</i>) <i>trabulsi</i>
					<i>Zygoascus hellenicus</i>
					<i>Zygosaccharomyces</i> species

¹ The list includes microorganisms that may be identified by API identification test systems and VITEK[®] automated identification system from bioMérieux Inc., or by the MicroScan - WalkAway[®] automated systems from Dade Behring. Identification relies on classical identification methods using batteries of biochemical and other phenotypical tests.

Table 16. *tuf* gene sequences obtained in our laboratory (Example 42).

Species	Strain no.	Gene	GenBank Accession no.*
<i>Abiotrophia adiacens</i>	ATCC49175	<i>tuf</i>	AF124224
<i>Enterococcus avium</i>	ATCC14025	<i>tufA</i>	AF124220
		<i>tufB</i>	AF274715
<i>Enterococcus casseliflavus</i>	ATCC25788	<i>tufA</i>	AF274716
		<i>tufB</i>	AF274717
<i>Enterococcus cecorum</i>	ATCC43198	<i>tuf</i>	AF274718
<i>Enterococcus columbae</i>	ATCC51263	<i>tuf</i>	AF274719
<i>Enterococcus dispar</i>	ATCC51266	<i>tufA</i>	AF274720
		<i>tufB</i>	AF274721
<i>Enterococcus durans</i>	ATCC19432	<i>tufA</i>	AF274722
		<i>tufB</i>	AF274723
<i>Enterococcus faecalis</i>	ATCC29212	<i>tuf</i>	AF124221
<i>Enterococcus faecium</i>	ATCC 19434	<i>tufA</i>	AF124222
		<i>tufB</i>	AF274724
<i>Enterococcus gallinarum</i>	ATCC49573	<i>tufA</i>	AF124223
		<i>tufB</i>	AF274725
<i>Enterococcus hirae</i>	ATCC8043	<i>tufA</i>	AF274726
		<i>tufB</i>	AF274727
<i>Enterococcus malodoratus</i>	ATCC43197	<i>tufA</i>	AF274728
		<i>tufB</i>	AF274729
<i>Enterococcus mundtii</i>	ATCC43186	<i>tufA</i>	AF274730
		<i>tufB</i>	AF274731
<i>Enterococcus pseudoavium</i>	ATCC49372	<i>tufA</i>	AF274732
		<i>tufB</i>	AF274733
<i>Enterococcus raffinosus</i>	ATCC49427	<i>tufA</i>	AF274734
		<i>tufB</i>	AF274735
<i>Enterococcus saccharolyticus</i>	ATCC43076	<i>tuf</i>	AF274736
<i>Enterococcus solitarius</i>	ATCC49428	<i>tuf</i>	AF274737
<i>Enterococcus sulfureus</i>	ATCC49903	<i>tuf</i>	AF274738
<i>Lactococcus lactis</i>	ATCC11154	<i>tuf</i>	AF274745
<i>Listeria monocytogenes</i>	ATCC15313	<i>tuf</i>	AF274746
<i>Listeria seeligeri</i>	ATCC35967	<i>tuf</i>	AF274747
<i>Staphylococcus aureus</i>	ATCC25923	<i>tuf</i>	AF274739
<i>Staphylococcus epidermidis</i>	ATCC14990	<i>tuf</i>	AF274740
<i>Streptococcus mutans</i>	ATCC25175	<i>tuf</i>	AF274741
<i>Streptococcus pneumoniae</i>	ATCC6303	<i>tuf</i>	AF274742
<i>Streptococcus pyogenes</i>	ATCC19615	<i>tuf</i>	AF274743
<i>Streptococcus suis</i>	ATCC43765	<i>tuf</i>	AF274744

*Corresponding sequence ID NO. for the above ATCC strains are given in table 7.

Table 17. tuf gene sequences selected from databases for Example 42.

Species	Gene	Accession no.*
<i>Agrobacterium tumefaciens</i>	tufA	X99673
	tufB	X99674
<i>Anacystis nidulans</i>	tuf	X17442
<i>Aquifex aeolicus</i>	tufA	AE000657
	tufB	AE000657
<i>Bacillus stearothermophilus</i>	tuf	AJ000260
<i>Bacillus subtilis</i>	tuf	AL009126
<i>Bacteroides fragilis</i>	tuf	P33165
<i>Borrelia burgdorferi</i>	tuf	AE000783
<i>Brevibacterium linens</i>	tuf	X76863
<i>Bulkholderia cepacia</i>	tuf	P33167
<i>Campylobacter jejuni</i>	tufB	Y17167
<i>Chlamydia pneumoniae</i>	tuf	AE001363
<i>Chlamydia trachomatis</i>	tuf	M74221
<i>Corynebacterium glutamicum</i>	tuf	X77034
<i>Cytophaga lytica</i>	tuf	X77035
<i>Deinococcus radiodurans</i>	tuf	AE000513
<i>Escherichia coli</i>	tufA	J01690
	tufB	J01717
<i>Fervidobacterium islandicum</i>	tuf	Y15788
<i>Haemophilus influenzae</i>	tufA	L42023
	tufB	L42023
<i>Helicobacter pylori</i>	tuf	AE000511
<i>Homo sapiens</i> (Human)	EF-1 α	X03558
<i>Methanococcus jannaschii</i>	EF-1 α	U67486
<i>Mycobacterium leprae</i>	tuf	D13869
<i>Mycobacterium tuberculosis</i>	tuf	X63539
<i>Mycoplasma genitalium</i>	tuf	L43967
<i>Mycoplasma pneumoniae</i>	tuf	U00089
<i>Neisseria gonorrhoeae</i>	tufA	L36380
<i>Nicotiana tabacum</i> (Tobacco)	EF-1 α	U04632
<i>Peptococcus niger</i>	tuf	X76869
<i>Planobispora rosea</i>	tuf1	U67308
<i>Saccharomyces cerevisiae</i> (Yeast)	EF-1 α	X00779
<i>Salmonella typhimurium</i>	tufA	X55116
	tufB	X55117
<i>Shewanella putrefaciens</i>	tuf	P33169
<i>Spirochaeta aurantia</i>	tuf	X76874
<i>Spirulina platensis</i>	tufA	X15646
<i>Streptomyces aureofaciens</i>	tuf1	AF007125
<i>Streptomyces cinnamomeus</i>	tuf1	X98831
<i>Streptomyces coelicolor</i>	tuf1	X77039
	tuf3	X77040
<i>Streptomyces collinus</i>	tuf1	S79408
<i>Streptomyces ramocissimus</i>	tuf1	X67057
	tuf2	X67058
	tuf3	X67059
<i>Synechocystis</i> sp.	tuf	AB001339
<i>Taxobacter ocellatus</i>	tuf	X77036
<i>Thermotoga maritima</i>	tuf	AE000512
<i>Thermus aquaticus</i>	tuf	X66322
<i>Thermus thermophilus</i>	tuf	X06657
<i>Thiobacillus cuprinus</i>	tuf	U78300
<i>Treponema pallidum</i>	tuf	AE000520
<i>Wolinella succinogenes</i>	tuf	X76872

* Sequence data were obtained from GenBank, EMBL, and SWISSPROT databases. Genes were designated as appeared in the references.

Table 18. Nucleotide and amino acid sequence identities of EF-Tu between different enterococci and other low G+C gram-positive bacteria.

The upper right triangle represents the deduced amino acid sequence identities of gram-positive bacterial EF-Tu, while the lower left triangle represents the DNA sequence identities of the corresponding *tuf* genes. The sequence identities between different enterococcal *tufA* genes are boxed while those between enterococcal *tufB* genes are shaded.

Bacterial <i>tuf</i> gene	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	
1. <i>E. avium</i> <i>tufA</i>		96	98	96	96	96	97	95	98	99	95	95	96	94	96	93	86	87	85	88	88	86	86	85	86	87	86	82	91	90	90	90	92	84	85	84	82	83		
2. <i>E. casseliflavus</i> <i>tufA</i>	90		97	96	96	96	95	96	96	96	95	95	96	95	96	93	87	88	86	87	87	86	87	87	87	87	87	87	87	87	87	87	87	87	87	87	87	87	87	
3. <i>E. dispar</i> <i>tufA</i>	93	90		95	95	95	95	95	97	97	91	90	95	95	95	93	86	87	85	87	87	86	87	87	87	87	87	87	87	87	87	87	87	87	87	87	87	87	87	
4. <i>E. durans</i> <i>tufA</i>	90	89	90		99	96	99	93	95	95	96	90	91	94	95	94	92	87	87	86	86	86	85	86	87	87	87	87	87	87	87	87	87	87	87	87	87	87	87	
5. <i>E. faecium</i> <i>tufA</i>	88	90	89	96		96	98	93	98	95	96	89	91	88	94	92	87	86	86	86	86	85	86	87	87	87	87	87	87	87	87	87	87	87	87	87	87	87	87	87
6. <i>E. gallinarum</i> <i>tufA</i>	90	87	89	89	89		96	93	95	96	96	88	89	89	96	93	82	87	87	86	87	87	87	87	87	87	87	87	87	87	87	87	87	87	87	87	87	87	87	87
7. <i>E. hirae</i> <i>tufA</i>	90	90	89	99	96	89		93	99	95	96	91	91	89	95	94	92	86	87	86	86	85	86	86	87	87	87	87	87	87	87	87	87	87	87	87	87	87	87	87
8. <i>E. melitensis</i> <i>tufA</i>	96	91	94	90	89	90	89		92	97	97	89	89	90	93	96	92	86	85	82	85	85	85	85	85	85	85	85	85	85	85	85	85	85	85	85	85	85	85	85
9. <i>E. mundtii</i> <i>tufA</i>	89	88	96	93	89	96	88	94		95	88	90	88	94	94	92	87	87	86	86	86	85	86	87	87	87	87	87	87	87	87	87	87	87	87	87	87	87	87	87
10. <i>E. pseudovarum</i> <i>tufA</i>	97	92	93	90	89	91	89	97	88		97	91	90	90	91	95	96	94	87	87	86	87	87	87	87	87	87	87	87	87	87	87	87	87	87	87	87	87	87	87
11. <i>E. raffinosus</i> <i>tufA</i>	97	91	93	90	89	89	89	97	88	97		91	90	90	94	95	93	88	87	85	86	85	85	85	85	85	85	85	85	85	85	85	85	85	85	85	85	85	85	85
12. <i>E. pedorum</i> <i>tufA</i>	90	90	95	96	95	96	92	95	95	95	97		98	95	93	93	88	88	87	87	87	86	88	89	87	87	87	87	87	87	87	87	87	87	87	87	87	87	87	87
13. <i>E. columbae</i> <i>tufA</i>	90	90	95	96	97	96	93	95	95	95	97	98		95	94	92	92	89	88	87	88	88	87	87	87	87	87	87	87	87	87	87	87	87	87	87	87	87	87	87
14. <i>E. faecalis</i> <i>tufA</i>	91	91	90	89	96	97	94	94	94	95	96	90	89		94	93	87	87	88	87	87	86	88	87	87	87	87	87	87	87	87	87	87	87	87	87	87	87	87	87
15. <i>E. saccharolyticus</i> <i>tufA</i>	91	91	91	90	87	90	89	91	89	92	91	89	89	82	94		92	86	87	85	87	86	84	85	85	87	87	87	87	87	87	87	87	87	87	87	87	87	87	87
16. <i>E. sulfureus</i> <i>tufA</i>	91	89	90	91	88	88	90	91	89	92	91	88	89	91	94	91		85	84	81	84	85	84	84	81	84	85	85	81	90	87	88	89	91	82	83	82	82	82	
17. <i>E. solitarius</i> <i>tuf</i>	83	84	83	83	84	83	82	84	83	84	84	84	83	84	83	83	88		87	85	87	87	86	87	88	88	88	88	88	88	88	88	88	88	88	88	88	88	88	88
18. <i>E. avium</i> <i>tufB</i>	77	77	78	78	75	77	78	78	77	78	77	78	78	78	77	76	77	77		93	93	94	94	94	92	98	93	99	97	87	86	87	85	86	88	87	85	86		
19. <i>E. casseliflavus</i> <i>tufB</i>	71	72	72	72	70	72	72	70	71	72	72	72	70	72	72	72	78	78	78		93	95	95	96	95	93	95	94	94	87	86	88	88	84	85	90	89	88		
20. <i>E. dispar</i> <i>tufB</i>	76	78	77	77	77	77	77	77	77	77	77	77	77	77	77	78	78	75	75	83	80	82		98	95	97	94	97	95	94	87	86	88	88	84	85	90	89	88	
21. <i>E. durans</i> <i>tufB</i>	77	78	78	78	77	78	77	78	77	78	77	77	77	78	78	75	75	83	80	82		98	95	97	94	97	95	94	87	86	88	88	84	85	90	89	88	88		
22. <i>E. faecium</i> <i>tufB</i>	76	75	76	76	75	77	76	76	76	76	77	77	77	77	76	74	74	76	78	79	86		96	97	95	97	95	94	87	87	88	88	84	86	90	90	89	87		
23. <i>E. gallinarum</i> <i>tufB</i>	72	73	72	73	72	74	72	71	72	72	72	72	72	73	73	72	72	78	81	77	81	82		94	94	95	95	94	85	87	89	89	84	86	90	90	89	87		
24. <i>E. hirae</i> <i>tufB</i>	75	74	75	75	75	75	75	75	76	76	75	74	74	74	75	72	74	80	79	79	84	83	79		93	97	93	94	87	85	86	88	83	83	88	90	88	88		
25. <i>E. melitensis</i> <i>tufB</i>	76	76	76	77	77	77	74	77	76	76	77	75	77	77	73	78	90	79	83	81	80	77	79		93	98	97	87	86	87	87	85	86	88	89	87	85	86		
26. <i>E. mundtii</i> <i>tufB</i>	74	74	74	73	74	74	74	74	74	74	74	74	74	74	75	74	71	73	80	80	78	85	85	80	84	80		94	87	86	88	84	86	90	90	89	88			
27. <i>E. pseudovarum</i> <i>tufB</i>	77	77	78	77	78	77	77	76	78	78	77	77	78	78	77	76	78	80	81	79	80	81	80		96	98	97	88	87	85	87	87	85	87	88	89	88	86	87	
28. <i>E. raffinosus</i> <i>tufB</i>	78	79	79	78	77	77	78	78	77	79	79	78	78	78	79	77	79	80	79	84	84	81	77	80	80	81	82		87	85	87	88	84	86	90	89	88	88		
29. <i>E. adiacens</i> <i>tuf</i>	68	67	67	66	68	66	66	69	66	68	68	67	68	68	68	62	77	70	70	77	76	71	73	77	73	78	78		90	88	89	90	81	85	88	84	85	83		
30. <i>E. subitans</i> <i>tuf</i>	61	60	79	79	80	80	79	79	79	80	81	60	81	81	80	78	78	73	69	73	71	70	71	72	71	74	78		91	92	90	90	82	82	83	82	84			
31. <i>E. monocytiogenes</i> <i>tuf</i>	62	61	62	62	62	62	62	61	61	61	61	61	61	61	61	61	61	61	61	61	61	61	61	61	61	61	61		99	98	90	90	84	84	84	84	84			
32. <i>E. sociogen</i> <i>tuf</i>	62	61	62	62	62	62	61	62	61	62	61	62	61	62	60	81	79	76	71	76	75	74	73	75	75	73	77	76		98	90	81	84	85	85	84	85			
33. <i>E. aureus</i> <i>tuf</i>	64	64	63	63	63	64	64	62	64	63	64	66	66	64	62	61	79	75	69	75	75	73	69	72	74	72	74		94	87	86	88	84	86	90	89	88			
34. <i>E. epidermidis</i> <i>tuf</i>	63	63	63	64	63	64	64	62	64	63	63	66	67	65	63	62	79	75	69	75	75	73	68	72	74	72	74		94	87	86	88	84	86	90	89	88			
35. <i>E. mutans</i> <i>tuf</i>	76	77	76	76	76	77	76	75	76	76	76	77	76	76	76	74	78	79	72	77	78	77	74	75	78	75	78		77	75	76	77	74	73	97	96	94			
36. <i>E. pneumoniae</i> <i>tuf</i>	76	77	76	77	77	77	77	75	78	76	76	77	76	77	75	74	75	76	72	78	78	76	73	74	77	75	75		76	76	74	74	87	96	96	96				
37. <i>E. pyogenes</i> <i>tuf</i>	76	77	76	77	76	75	77	74	77	76	75	76	75	77	75	73	75	74	71	75	78	75	73	74	75	75	75		77	76	75	73	72	87	93	94	89			
38. <i>E. ana</i> <i>tuf</i>	74	78	76	76	74	75	76	74	76	76	77	77	75	78	76	73	75	74	71	75	78	74	70	74	75	73	73		77	77	77	77	72	88	93	91	88			
39. <i>E. leclii</i> <i>tuf</i>	75	76	75	76	75	75	76	75	76	76	77	78	76	78	75	72	74	75	72	75	77	76	71	75	74	75	75		75	75	75	75	74	80	83	82	81			

Table 19. Strains analyzed in Example 43.

Taxon	Strain*	Strain†	16S rDNA sequence accession number
<i>Cedecea</i>	ATCC 33431 ^T		
<i>Cedecea lapagei</i>	ATCC 33432 ^T		
<i>Cedecea neteri</i>	ATCC 33855 ^T		
<i>Citrobacter amalonaticus</i>	ATCC 25405 ^T	CDC 9020-77 ^T	AF025370
<i>Citrobacter braakii</i>	ATCC 43162		
		CDC 080-58 ^T	AF025368
<i>Citrobacter farmeri</i>	ATCC 51112 ^T	CDC 2991-81 ^T	AF025371
<i>Citrobacter freundii</i>	ATCC 8090 ^T	DSM 30039 ^T	AJ233408
<i>Citrobacter koseri</i>	ATCC 27156 ^T		
<i>Citrobacter sedlakii</i>	ATCC 51115 ^T	CDC 4696-86 ^T	AF025364
<i>Citrobacter werkmanii</i>	ATCC 51114 ^T	CDC 0876-58 ^T	AF025373
<i>Citrobacter youngae</i>	ATCC 29935 ^T		
<i>Edwardsiella hoshinae</i>	ATCC 33379 ^T		
<i>Edwardsiella tarda</i>	ATCC 15947 ^T		
		CDC 4411-68	AF015259
<i>Enterobacter aerogenes</i>	ATCC 13048 ^T	JCM 1235 ^T	AB004750
<i>Enterobacter agglomerans</i>	ATCC 27989		
<i>Enterobacter amnigenus</i>	ATCC 33072 ^T	JCM 1237 ^T	AB004749
<i>Enterobacter asburiae</i>	ATCC 35953 ^T	JCM 6051 ^T	AB004744
<i>Enterobacter cancerogenus</i>	ATCC 35317 ^T		
<i>Enterobacter cloacae</i>	ATCC 13047 ^T		
<i>Enterobacter gergoviae</i>	ATCC 33028 ^T	JCM 1234 ^T	AB004748
<i>Enterobacter hormaechei</i>	ATCC 49162 ^T		
<i>Enterobacter sakazakii</i>	ATCC 29544 ^T	JCM 1233 ^T	AB004746
<i>Escherichia coli</i>	ATCC 11775 ^T	ATCC 11775 ^T	X80725
<i>Escherichia coli</i>	ATCC 25922	ATCC 25922	X80724
<i>Escherichia coli</i> (ETEC)	ATCC 35401		
<i>Escherichia coli</i> (O157:H7)	ATCC 43895	ATCC 43895	Z83205
<i>Escherichia fergusonii</i>	ATCC 35469 ^T		
<i>Escherichia hermanii</i>	ATCC 33650 ^T		
<i>Escherichia vulneris</i>	ATCC 33821 ^T	ATCC 33821 ^T	X80734
<i>Ewingella americana</i>	ATCC 33852 ^T		
		NCPPB 3905	X88848
<i>Hafnia alvei</i>	ATCC 13337 ^T	ATCC 13337 ^T	M59155
<i>Klebsiella omithinolytica</i>	ATCC 31898		
		CIP 103.364	U78182
<i>Klebsiella oxytoca</i>	ATCC 33496		
		ATCC 13182 ^T	U78183
<i>Klebsiella planticola</i>	ATCC 33531 ^T	JCM 7251 ^T	AB004755
<i>Klebsiella pneumoniae</i>			
subsp. <i>pneumoniae</i>	ATCC 13883 ^T	DSM 30104 ^T	AJ233420
subsp. <i>ozaenae</i>	ATCC 11296 ^T	ATCC 11296 ^T	Y17654
subsp. <i>rhinoscleromatis</i>	ATCC 13884 ^T		

Table 19. Strains analyzed in Example 43 (continued).

Taxon	Strain*	Strain†	16S rDNA sequence accession number
<i>Kluyvera ascorbata</i>	ATCC 33433 ^T	ATCC 14236	Y07650
<i>Kluyvera cryocrescens</i>	ATCC 33435 ^T		
<i>Kluyvera georgiana</i>	ATCC 51603 ^T		
<i>Leclercia adecarboxylata</i>	ATCC 23216 ^T		
<i>Leminorella grimonii</i>	ATCC 33999 ^T	DSM 5078 ^T	AJ233421
<i>Moellerella wisconsensis</i>	ATCC 35017 ^T		
<i>Morganella morganii</i>	ATCC 25830 ^T		
<i>Pantoea agglomerans</i>	ATCC 27155 ^T	DSM 3493 ^T	AJ233423
<i>Pantoea dispersa</i>	ATCC 14589 ^T		
<i>Plesiomonas shigelloides</i>	ATCC 14029 ^T		
<i>Pragia fontium</i>	ATCC 49100 ^T	DSM 5563 ^T	AJ233424
<i>Proteus mirabilis</i>	ATCC 25933		
<i>Proteus penneri</i>	ATCC 33519 ^T		
<i>Proteus vulgaris</i>	ATCC 13315 ^T	DSM 30118 ^T	AJ233425
<i>Providencia alcalifaciens</i>	ATCC 9886 ^T		
<i>Providencia rettgeri</i>	ATCC 9250		
<i>Providencia rustigianii</i>	ATCC 33673 ^T		
<i>Providencia stuartii</i>	ATCC 33672		
<i>Rahnella aquatilis</i>	ATCC 33071 ^T	DSM 4594 ^T	AJ233426
<i>Salmonella choleraesuis</i>			
subsp. <i>arizonae</i>	ATCC 13314 ^T		
subsp. <i>choleraesuis</i>			
serotype <i>Choleraesuis</i>	ATCC 7001		
serotype <i>Enteritidis</i> ‡	ATCC 13076 ^T		
		SE22	SE22
serotype <i>Gallinarum</i>	ATCC 9184		
serotype <i>Heidelberg</i>	ATCC 8326		
serotype <i>Paratyphi A</i>	ATCC 9150		
serotype <i>Paratyphi B</i>	ATCC 8759		
serotype <i>Typhi</i> ‡	ATCC 10749		
		SI111	U88545
serotype <i>Typhimurium</i> ‡	ATCC 14028		
serotype <i>Virchow</i>	ATCC 51955		
subsp. <i>dianzonae</i>	ATCC 43973 ^T		
subsp. <i>houtenae</i>	ATCC 43974 ^T		
subsp. <i>indica</i>	ATCC 43976 ^T		
subsp. <i>salamae</i>	ATCC 43972 ^T		
<i>Serratia fonticola</i>	DSM 4576 ^T	DSM 4576 ^T	AJ233429
<i>Serratia grimesii</i>	ATCC 14460 ^T	DSM 30063 ^T	AJ233430
<i>Serratia liquefaciens</i>	ATCC 27592 ^T		
<i>Serratia marcescens</i>	ATCC 13880 ^T	DSM 30121 ^T	AJ233431
<i>Serratia odorifera</i>	ATCC 33077 ^T	DSM 4582 ^T	AJ233432
<i>Serratia plymuthica</i>	DSM 4540 ^T	DSM 4540 ^T	AJ233433
<i>Serratia rubidaea</i>	DSM 4480 ^T	DSM 4480 ^T	AJ233436
<i>Shigella boydii</i>	ATCC 9207	ATCC 9207	X96965
<i>Shigella dysenteriae</i>	ATCC 11835		
		ATCC 13313 ^T	X96966
		ATCC 25931	X96964

Table 19. Strains analyzed in Example 43 (continued).

Taxon	Strain*	Strain†	16S rDNA sequence accession number
<i>Shigella flexneri</i>	ATCC 12022	ATCC 12022	X96963
<i>Shigella sonnei</i>	ATCC 29930 ^T		
<i>Tatumella ptyseos</i>	ATCC 33301 ^T	DSM 5000 ^T	AJ233437
<i>Trabulsiella guamensis</i>	ATCC 49490 ^T		
<i>Yersinia enterocolitica</i>	ATCC 9610 ^T	ATCC 9610 ^T	M59292
<i>Yersinia frederiksenii</i>	ATCC 33641 ^T		
<i>Yersinia intermedia</i>	ATCC 29909 ^T		
<i>Yersinia pestis</i>	RRB KIMD27		
		ATCC 19428 ^T	X75274
<i>Yersinia pseudotuberculosis</i>	ATCC 29833 ^T		
<i>Yersinia rohdei</i>	ATCC 43380 ^T	ER-2935 ^T	X75276
<i>Shewanella putrefaciens</i>	ATCC 8071 ^T		
<i>Vibrio cholerae</i>	ATCC 25870		
		ATCC 14035 ^T	X74695

T Type strain

5 *Strains used in this study for sequencing of partial *tuf* and *atpD* genes. SEQ ID NOs. for *tuf* and *atpD* sequences corresponding to the above reference strains are given in table 7.

†Strains used in other studies for sequencing of 16S rDNA gene. When both strain numbers are on the same row, both strains are considered to be the same although strain numbers may be different.

‡Phylogenetic serotypes considered species by the Bacteriological Code (1990 Revision).

Table 20. PCR primer pairs used in this study

Primer SEQ ID NO.	Sequence	Nucleotide positions*	Amplicon length (bp)
<i>tuf</i>			
664	5'-AAYATGATACIGGIGCIGCICARATGGA- 3'	271-299	884
697	5'-CCIACIGTICKICCRCCYTCRCG-3'	1132-1156	
<i>atpD</i>			
568	5'-RTIATIGGIGCIGTIRTIGAYGT-3'	25-47	884
567	5'-TCRTCIGCIGGIACRTAIAYIGCYTG-3'	883-908	
700	5'-TIRTIGAYGTCGARTTCCCTCARG-3'	38-61	871
567	5'-TCRTCIGCIGGIACRTAIAYIGCYTG-3'	883-908	

- 5 *The nucleotide positions given are for *E. coli tuf* and *atpD* sequences (GenBank accession no. AE000410 and V00267, respectively). Numbering starts from the first base of the initiation codon.

Table 21. Selection of *M. catarrhalis*-specific primer pairs from SEQ ID NO: 29¹ (466 pb DNA fragment) other than those previously tested².

Primer	Sequence	Amplicon size (bp)	<i>Moraxella catarrhalis</i> ATCC 43628	<i>Moraxella catarrhalis</i> ATCC 53879	<i>Moraxella nonliquefaciens</i>	<i>Moraxella lacunata</i>	<i>Moraxella osloensis</i>	<i>Moraxella atlantae</i>	<i>Moraxella phenylpyruvica</i>	<i>Kingella indologenes</i>	<i>Kingella kingae</i>	<i>Neisseria meningitidis</i>	<i>Neisseria gonorrhoeae</i>	<i>Escherichia coli</i>	<i>Staphylococcus aureus</i>
SEQ ID NO:118	CGCTGACGGCTTGTGTGTACCA	118	+	+
SEQ ID NO:119	TGTTTGTAGCTTTTATTATTGA														
VBmcat1	TGCTTAAGATTCTACTCTGCCATTTT	93	+	+
VBmcat2	TAAGTCGCTGACGGCTTGT														
VBmcat3	CCTGCACCAACAGTCATCAT	140	+	+
VBmcat4	AATCACCAACAATGTCAAAGC														
VBmcat5	AATGATAACCAAGTCAAGCAAGC	219	+	+
VBmcat6	GGTGATGGTGATTTGTAAAA														
VBmcat7	GTGTGCGTTTCACTTTTACAAAT	160	+	+
VBmcat8	GGTGTAAAGCTGATGATGAGAG														
VBmcat9	TGACCATGCACACCCCTTATT	167	+	+
VBmcat10	TCATTGGGATGAAAGTATCGTT														

¹ SEQ ID NO. from US patent 6,001,564.² All PCR assays were performed with 1 ng of purified genomic DNA by using an annealing temperature of 55°C and 30 cycles of amplification. The genomic DNA from the various bacterial species above was always isolated from reference strains obtained from ATCC.³ All positive results showed a strong amplification signal with genomic DNA from the target species *M. catarrhalis*.

Table 22. Sequence of *S. epidermidis*-specific primer pairs from SEQ ID NO: 36¹ (705 pb DNA fragment) other than those previously tested.

Primer	Sequence (all 25 nucleotides)	Amplicon size (bp)	<i>Staphylococcus epidermidis</i> ATCC 14990	<i>Staphylococcus epidermidis</i> ATCC 12228	<i>Staphylococcus capitis</i>	<i>Staphylococcus cohnii</i>	<i>Staphylococcus aureus</i>	<i>Staphylococcus auricularis</i>	<i>Staphylococcus</i>	<i>Staphylococcus hominis</i>	<i>Staphylococcus</i>	<i>Staphylococcus simulans</i>	<i>Staphylococcus warnei</i>	<i>Bacillus subtilis</i>	<i>Enterococcus faecalis</i>	<i>Enterococcus faecium</i>	<i>Enterococcus gallinarum</i>	<i>Listeria monocytogenes</i>	<i>Streptococcus agalactiae</i>	<i>Streptococcus pneumoniae</i>	<i>Streptococcus pyogenes</i>	Annealing temperature ² (°C)
SEQ ID NO:145	ATCAAAAAGTTGGGAACCTTTTCA	125	+	+	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	55
SEQ ID NO:146	CAAAAGAGCGTGGAGAAAAGTATCA				-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	55
VBsep3	CATAGTCTGATTGCTCAAAAGTCTTG	208	+	+	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	60
VBsep4	GCGAATAGTGAACATACATTCTGTTG				-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	55
VBsep5	CACGCTCTTTTGCAATTCCATTGA	208	+	+	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	65
VBsep6	GAAGCAAAATATTCAAAATGCACCAG				-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	55
VBsep7	AAAGTCTTTTGCTTCTTCAGATTCA	177	+	+	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	65
VBsep8	GTGTTACAGGTATGGATGCTCTTA				-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	60
VBsep9	GAGCATCCATACCTGTGAACACAGA	153	+	+	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	55
VBsep10	TTTTCCAAATTACAAAGACATCAGT				-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	60
VBsep11	TTTGAAATTCGCATGTACTTTGTTTG	135	+	+	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	65
VBsep12	CCCCGGGTTTCGAAATCGATAAAAAG				-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	55

¹ SEQ ID NO. from US patent 6,001,564.² All PCR assays were performed with 1 ng of purified genomic DNA by using an annealing temperature of 55 to 65°C and 30 cycles of amplification. The genomic DNA from the various bacterial species above was always isolated from reference strains obtained from ATCC.³ All positive results showed a strong amplification signal with genomic DNA from the target species *S. epidermidis*. The intensity of the positive amplification signal with species other than *S. epidermidis* was variable.

NT = not tested.

Table 23. Influence of nucleotide variation(s) on the efficiency of the PCR amplification: Example with SEQ ID NO: 146 from *S. epidermidis*.

Primer ¹	Sequence (all 25 nucleotides)	Number of mutation	<i>Staphylococcus epidermidis</i> ² ATCC 14990					<i>Staphylococcus aureus</i>
			50°C		55°C			
			1	1	0,1	0,01	1	1
SEQ ID NO:145	ATCAAAAAGTTGGCGAACCTTTTCA	0						
SEQ ID NO:146	CAAAAGAGCGTGGAGAAAAGTATCA	0	3 ⁴	3+	2+	+		-
VBmut1	CAAAAGAGCGTGGAGAAAAGTATCA	1	3+	3+	2+	+		-
VBmut2	CAAAAGAGCGTGGAGAAAAGTATCA	1	3+	3+	2+	+		-
VBmut3	CAAAAGAGCGTGGAGAAAAGTATCA	1	3+	3+	2+	+		-
VBmut4	CAAAAGAGCGTGGAGAAAAGTATCA	1	3+	3+	2+	+		-
VBmut5	CAAAAGAGCGTGGAGAAAAGTATCA	1	3+	3+	2+	+		-
VBmut6	CAAAAGAGCGTGGAGAAAAGTATCA	1	3+	3+	2+	+		-
VBmut7	CAAAAGAGCGTGGAGAAAAGTATCA	1	3+	3+	2+	+		-
VBmut8	CAAAAGAGCGTGGAGAAAAGTATCA	1	3+	3+	2+	+		-
VBmut9	CAAAAGAGCGTGGAGAAAAGTATCA	2	3+	3+	2+	+		-
VBmut10	CAAAAGAGCGTGGAGAAAAGTATCA	2	3+	3+	2+	+		-
VBmut11	CAAAAGAGCGTGGAGAAAAGTATCA	2	3+	3+	2+	+		-
VBmut12	CAAAAGAGCGTGGAGAAAAGTATCA	3	3+	3+	2+	+		-
VBmut13	CAAAAGAGCGTGGAGAAAAGTATCA	4	3+	2+	+			-

¹ All PCR tests were performed with SEQ ID NO:145 without modification combined with SEQ ID NO:146 or 13 modified versions of SEQ ID NO:146. Boxed nucleotides indicate changes in SEQ ID NO:146. All SEQ ID NOs. are from US patent 6,001,564.

² The tests with *S. epidermidis* were performed by using an annealing temperature of 55°C with 1, 0,1 and 0,01 ng of purified genomic DNA or at 50°C with 1 ng of purified genomic DNA.

³ The tests with *S. aureus* were performed only at 50°C with 1 ng of genomic DNA.

⁴ The intensity of the positive amplification signal was quantified as follows: 3+ = strong signal, 2+ = intermediate signal and + = weak signal.

Table 24. Effect of the primer length on the efficiency of the PCR amplification¹: Example with the AT-rich SEQ ID NO: 145² and SEQ ID NO: 146² from *S. epidermidis*.

Primer	Sequence	Length (nt)	45°C						55°C						Staphylococcus aureus ⁴				Staphylococcus haemolyticus				Staphylococcus capitis				Staphylococcus warneri			
			1			0,1			0,01			1																		
			1	0,1	0,01	1	0,1	0,01	1	0,1	0,01	1	0,1	0,01	1	0,1	0,01	45	55	45	55	45	55	45	55	45	55	45	55	
VBsep301	ATATCATCAAAAAGTTGGCGAACCTTTTCA	30																												
VBsep302	AATTGCAAAAAGAGCGTGGAGAAAAGTATCA	30	NT	NT	NT	4+	3+	2+	4+	3+	2+	NT	NT	NT	NT	NT	NT	NT	NT	NT	NT	NT	NT	NT	NT	NT	NT	NT		
SEQ ID NO:145	ATCAAAAAGTTGGCGAACCTTTTCA	25	4+ ⁵	3+	2+	4+	3+	2+	4+	3+	2+																			
SEQ ID NO:146	CAAAAAGAGCGTGGAGAAAAGTATCA	25																												
VBsep201	AAAGTTGGCGAACCTTTTCA	20																												
VBsep202	GAGCGTGGAGAAAAGTATCA	20	NT	NT	NT	4+	3+	2+	4+	3+	2+	NT	NT	NT	NT	NT	NT	NT	NT	NT	NT	NT	NT	NT	NT	NT	NT	NT		
VBsep171	GTTGGCGAACCTTTTCA	17																												
VBsep172	CGTGGAGAAAAGTATCA	17	4+	3+	2+	3+	2+	+	3+	2+	+																			
VBsep151	TGGCGAACCTTTTCA	15																												
VBsep152	TGGAGAAAAGTATCA	15	3+	2+	+	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-		

¹ All PCR tests were performed using an annealing temperature of 45 or 55°C and 30 cycles of amplification.

² All SEQ ID NOs. in this Table are from US patent 6,001,546.

³ The tests with *S. epidermidis* were made with 1, 0,1 and 0,01 ng of purified genomic DNA.

⁴ The tests with all other bacterial species were made only with 1 ng of purified genomic DNA.

⁵ The intensity of the positive amplification signal was quantified as follows: 4+ = very strong signal, 3+ = strong signal, 2+ = intermediate signal and + = weak signal.
NT = not tested.

Tabl 25. Effect of the primer length on the efficiency of the PCR amplification¹: Example with the GC-rich SEQ ID NO: 83² and SEQ ID NO: 84² from *P. aeruginosa*.

Primer	Sequence	Length (nt)	1	0,1	0,01	<i>Pseudomonas fluorescens</i> ⁴	<i>Burkholderia cepacia</i>	<i>Shewanella putida</i>	<i>Stenotrophomonas maltophilia</i>	<i>Neisseria meningitidis</i>	<i>Haemophilus parahaemolyticus</i>
SEQ ID NO 83	CGAGCGGGTGGTTCATC	19	2 ⁵	+	-
SEQ ID NO 84	CAAGTCGTCGTCGAGGGA	19			
Pse554-16a	CGAGCGGGTGGTGTTTC	16			
Pse674-16a	GTCGTCGTCGAGGGA	16	2+	+	-
Pse554-13b	GCGGGTGGTGTTTC	13			
Pse674-13a	GTCGTCGAGGGA	13	2+	+	-

¹ All PCR tests were performed using an annealing temperature of 55°C and 30 cycles of amplification.

² All SEQ ID NOs. in this Table are from US patent 6,001,546.

³ The tests with *P. aeruginosa* were made with 1, 0,1 and 0,01 ng of purified genomic DNA.

⁴ The tests with all other bacterial species were made only with 1 ng of purified genomic DNA.

⁵ The intensity of the positive amplification signal was quantified as follows: 2+ = strong signal and + = moderately strong signal.

Annex I: Specific and ubiquitous primers for nucleic acid amplification (tuf s quences).

			Originating DNA fragm nt	
5	SEQ ID NO.	Nucleotide sequence	SEQ ID NO.	Nucleotide position
10	Bacterial species: <i>Acinetobacter baumannii</i>			
	1692	5'-GGT GAG AAC TGT GGT ATC TTA CTT	1	478-501
	1693 ^a	5'-CAT TTC AAC GCC TTC TTT CAA CTG	1	691-714
15	Bacterial species: <i>Chlamydia pneumoniae</i>			
	630	5'-CGG AGC TAT CCT AGT CGT TTC A	20	2-23
	629 ^a	5'-AAG TTC CAT CTC AAC AAG GTC AAT A	20	146-170
20	2085	5'-CAA ACT AAA GAA CAT ATC TTG CTA	20	45-68
	2086 ^a	5'-ATA TAA TTT GCA TCA CCT TCA AG	20	237-259
	2087	5'-TCA GCT CGT GGG ATT AGG AGA G	20	431-452
	2088 ^a	5'-AGG CTT CAC GCT GTT AGG CTG A	20	584-605
25	Bacterial species: <i>Chlamydia trachomatis</i>			
	554	5'-GTT CCT TAC ATC GTT GTT TTT CTC	22	82-105
	555 ^a	5'-TCT CGA ACT TTC TCT ATG TAT GCA	22	249-272
30	Parasitical species: <i>Cryptosporidium parvum</i>			
	798	5'-TGG TTG TCC CAG CCG ATC GTT T	865	158-179
	804 ^a	5'-CCT GGG ACG GCC TCT GGC AT	865	664-683
35	799	5'-ACC TGT GAA TAC AAG CAA TCT	865	280-300
	805 ^a	5'-CTC TTG TCC ATC TTA GCA GT	865	895-914
	800	5'-GAT GAA ATC TTC AAC GAA GTT GAT	865	307-330
40	806 ^a	5'-AGC ATC ACC AGA CTT GAT AAG	865	946-966
	801	5'-ACA ACA CCG AGA AGA TCC CA	865	353-372
	803 ^a	5'-ACT TCA GTG GTA ACA CCA GC	865	616-635
45	802	5'-TTG CCA TTT CTG GTT TCG TT	865	377-396
	807 ^a	5'-AAA GTG GCT TCA AAG GTT GC	865	981-1000
	Bacterial species: <i>Enterococcus faecium</i>			
50	1696	5'-ATG TTC CTG TAG TTG CTG GA	64	189-208
	1697 ^a	5'-TTT CTT CAG CAA TAC CAA CAA C	64	422-443
	Bacterial species: <i>Klebsiella pneumoniae</i>			
55	1329	5'-TGT AGA GCG CGG TAT CAT CAA AGT A	103	352-377
	1330 ^a	5'-AGA TTC GAA CTT GGT GTG CGG G	103	559-571

^a These sequences are from the complementary DNA strand of the s quence of the originating fragment given in the Sequence Listing.

Ann x I: Specific and ubiquitous primers for nucleic acid amplification (tuf s quences) (continued).

			Originating DNA fragment	
5	SEQ ID NO.	Nucleotide sequence	SEQ ID NO.	Nucleotide position
10	<u>Bacterial species:</u> <i>Mycoplasma pneumoniae</i>			
	2093	5'-TGT TGG CAA TCG AAG ACA CC	2097 ^a	635-654
	2094 ^b	5'-TTC AAT TTC TTG ACC TAC TTT CAA	2097 ^a	709-732
15	<u>Bacterial species:</u> <i>Neisseria gonorrhoeae</i>			
	551	5'-GAA GAA AAA ATC TTC GAA CTG GCT A	126	256-280
	552 ^b	5'-TAC ACG GCC GGT GAC TAC G	126	378-396
20	2173	5'-AAG AAA AAA TCT TCG AAC TGG CTA	126	257-280
	2174 ^b	5'-TCT ACA CGG CCG GTG	126	384-398
	2175	5'-CCG CCA TAC CCC GTT T	126	654-669
	2176 ^b	5'-CGG CAT TAC CAT TTC CAC ACC TTT	126	736-759
25	<u>Bacterial species:</u> <i>Pseudomonas aeruginosa</i>			
	1694	5'-AAG GCA AGG ATG ACA ACG GC	153	231-250
	1695 ^b	5'-ACG ATT TCC ACT TCT TCC TGG	153	418-438
30	<u>Bacterial species:</u> <i>Streptococcus agalactiae</i>			
	549	5'-GAA CGT GAT ACT GAC AAA CCT TTA	207-210 ^c	308-331 ^d
	550 ^b	5'-GAA GAA GAA CAC CAA CGT TG	207-210 ^c	520-539 ^d
35	<u>Bacterial species:</u> <i>Streptococcus pyogenes</i>			
	999	5'-TTG ACC TTG TTG ATG ACG AAG AG	1002	143-165
	1000 ^b	5'-TTA GTG TGT GGG TTG ATT GAA CT	1002	622-644
40	1001	5'-AAG AGT TGC TTG AAT TAG TTG AG	1002	161-183
	1000 ^b	5'-TTA GTG TGT GGG TTG ATT GAA CT	1002	622-644
45	<u>Parasitical species:</u> <i>Trypanosoma brucei</i>			
	820	5'-GAA GGA GGT GTC TGC TTA CAC	864	513-533
	821 ^b	5'-GGC GCA AAC GTC ACC ACA TCA	864	789-809
	820	5'-GAA GGA GGT GTC TGC TTA CAC	864	513-533
50	822 ^b	5'-CGG CGG ATG TCC TTA ACA GAA	864	909-929

^a Sequence from databases.

^b These sequences are from the complementary DNA strand of the sequence of the originating fragment given in the Sequence Listing.

^c These sequences were aligned to derive the corresponding primer.

^d The nucleotide positions refer to the *S. agalactiae* tuf sequence fragment (SEQ ID NO. 209).

Annex I: Specific and ubiquitous primers for nucleic acid amplification (tuf sequences) (continued).

			Originating DNA fragment	
5	SEQ ID NO.	Nucleotide sequence	SEQ ID NO.	Nucleotide position
10	<u>Parasitical species:</u> <i>Trypanosoma cruzi</i>			
	794	5'-GAC GAC AAG TCG GTG AAC TT	840-842 ^a	281-300 ^c
	795 ^b	5'-ACT TGC ACG CGA TGT GGC AG	840-842 ^a	874-893 ^c
15	<u>Bacterial genus:</u> <i>Clostridium</i> sp.			
	796	5'-GGT CCA ATG CCW CAA ACW AGA	32,719-724,736 ^a	32-52 ^d
	797 ^b	5'-CAT TAA GAA TGG YTT ATC TGT SKC TCT	32,719-724,736 ^a	320-346 ^d
20	808	5'-GCI TTA IWR GCA TTA GAA RAY CCA	32,719-724,736 ^a	224-247 ^d
	809 ^b	5'-TCT TCC TGT WGC AAC TGT TCC TCT	32,719-724,736 ^a	337-360 ^d
25	810	5'-AGA GMW ACA GAT AAR SCA TTC TTA	32,719-724,736 ^a	320-343 ^d
	811 ^b	5'-TRA ART AGA ATT GTG GTC TRT ATC C	32,719-724,736 ^a	686-710 ^d
30	<u>Bacterial genus:</u> <i>Corynebacterium</i> sp.			
	545	5'-TAC ATC CTB GTY GCI CTI AAC AAG TG	34-44,662 ^a	89-114 ^e
	546 ^b	5'-CCR CGI CCG GTR ATG GTG AAG AT	34-44,662 ^a	350-372 ^e
35	<u>Bacterial genus:</u> <i>Enterococcus</i> sp.			
	656	5'-AAT TAA TGG CTG CAG TTG AYG A	58-72 ^a	273-294 ^f
	657 ^b	5'-TTG TCC ACG TTC GAT RTC TTC A	58-72 ^a	556-577 ^f
40	656	5'-AAT TAA TGG CTG CAG TTG AYG A	58-72 ^a	273-294 ^f
	271 ^b	5'-TTG TCC ACG TTG GAT RTC TTC A	58-72 ^a	556-577 ^f
	1137	5'-AAT TAA TGG CTG CWG TTG AYG AA	58-72 ^a	273-295 ^f
45	1136 ^b	5'-ACT TGT CCA CGT TSG ATR TCT	58-72 ^a	559-579 ^f

^a These sequences were aligned to derive the corresponding primer.

50 ^b These sequences are from the complementary DNA strand of the sequence of the originating fragment given in the Sequence Listing.

^c The nucleotide positions refer to the *T. cruzi* tuf sequence fragment (SEQ ID NO. 842).

^d The nucleotide positions refer to the *C. p rfringens* tuf sequence fragment (SEQ ID NO. 32).

55 ^e The nucleotide positions refer to the *C. diphtheriae* tuf sequence fragment (SEQ ID NO. 662).

^f The nucleotide positions refer to the *E. durans* tuf sequence fragment (SEQ ID NO. 61).

Annex I: Specific and ubiquitous primers for nucleic acid amplification (tuf sequences) (continued).

			Originating DNA fragment	
5	SEQ ID NO.	Nucleotide sequence	SEQ ID NO.	Nucleotide position
10	<u>Bacterial genus:</u> <i>Legionella</i> sp.			
	2081	5'-GRA TYR TYA AAG TTG GTG AGG AAG	111-112 ^a	411-434 ^b
	2082 ^c	5'-CMA CTT CAT CYC GCT TCG TAC C	111-112 ^a	548-569 ^b
15	<u>Bacterial genus:</u> <i>Staphylococcus</i> sp.			
	553	5'-GGC CGT GTT GAA CGT GGT CAA ATC A	176-203 ^a	313-337 ^d
	575 ^c	5'-TIA CCA TTT CAG TAC CTT CTG GTA A	176-203 ^a	653-677 ^d
20	553	5'-GGC CGT GTT GAA CGT GGT CAA ATC A	176-203 ^a	313-337 ^d
	707 ^c	5'-TWA CCA TTT CAG TAC CTT CTG GTA A	176-203 ^a	653-677 ^d
	<u>Bacterial genus:</u> <i>Streptococcus</i> sp.			
25	547	5'-GTA CAG TTG CTT CAG GAC GTA TC	206-231 ^a	372-394 ^e
	548 ^c	5'-ACG TTC GAT TTC ATC ACG TTG	206-231 ^a	548-568 ^e
	<u>Fungal genus:</u> <i>Candida</i> sp.			
30	576	5'-AAC TTC RTC AAG AAG GTY GGT TAC AA	407-426, 428-432 ^a	332-357 ^f
	632 ^c	5'-CCC TTT GGT GGR TCS TKC TTG GA	407-426, 428-432 ^a	791-813 ^f
35	631	5'-CAG ACC AAC YGA IAA RCC ATT RAG AT	407-426, 428-432 ^a	523-548 ^f
	632 ^c	5'-CCC TTT GGT GGR TCS TKC TTG GA	407-426, 428-432 ^a	791-813 ^f
40	633	5'-CAG ACC AAC YGA IAA RCC ITT RAG AT	407-426, 428-432 ^a	523-548 ^f
	632 ^c	5'-CCC TTT GGT GGR TCS TKC TTG GA	407-426, 428-432 ^a	791-813 ^f

45

^a These sequences were aligned to derive the corresponding primer.

^b The nucleotide positions refer to the *L. pneumophila* tuf sequence fragment (SEQ ID NO. 112).

50 ^c These sequences are from the complementary DNA strand of the sequence of the originating fragment given in the Sequence Listing.

^d The nucleotide positions refer to the *S. aureus* tuf sequence fragment (SEQ ID NO. 179).

^e The nucleotide positions refer to the *S. agalactiae* tuf sequence fragment (SEQ ID NO. 209).

55 ^f The nucleotide positions refer to the *C. albicans* tuf(EF-1) sequence fragment (SEQ ID NO. 408).

Annex I: Specific and ubiquitous primers for nucleic acid amplification (tuf sequences) (continued).

			Originating DNA fragment	
5	SEQ ID NO.	Nucleotide sequence	SEQ ID NO.	Nucleotide position
10	<u>Fungal genus:</u> <i>Cryptococcus</i> sp.			
	1971	5'-CYG ACT GYG CCA TCC TYA TCA	434,623,1281, 1985,1986 ^a	150-170 ^b
	1973 ^c	5'-RAC ACC RGI YTT GGW ITC CTT	434,623,1281, 1985,1986 ^a	464-484 ^b
15				
	1972	5'-MGI CAG CTC ATY ITT GCW KSC	434,623,1281, 1985,1986 ^a	260-280 ^b
	1973 ^c	5'-RAC ACC RGI YTT GGW ITC CTT	434,623,1281, 1985,1986 ^a	464-484 ^b
20				
	<u>Parasitical genus:</u> <i>Entamoeba</i> sp.			
	703	5'-TAT GGA AAT TCG AAA CAT CT	512	38-57
25	704 ^c	5'-AGT GCT CCA ATT AAT GTT GG	512	442-461
	703	5'-TAT GGA AAT TCG AAA CAT CT	512	38-57
	705 ^c	5'-GTA CAG TTC CAA TAC CTG AA	512	534-553
30	703	5'-TAT GGA AAT TCG AAA CAT CT	512	38-57
	706 ^c	5'-TGA AAT CTT CAC ATC CAA CA	512	768-787
	793	5'-TTA TTG TTG CTG CTG GTA CT	512	149-168
	704 ^c	5'-AGT GCT CCA ATT AAT GTT GG	512	442-461
35				
	<u>Parasitical genus:</u> <i>Giardia</i> sp.			
	816	5'-GCT ACG ACG AGA TCA AGG GC	513	305-324
	819 ^c	5'-TCG AGC TTC TGG AGG AAG AG	513	895-914
40				
	817	5'-TGG AAG AAG GCC GAG GAG TT	513	355-374
	818 ^c	5'-AGC CGG GCT GGA TCT TCT TC	513	825-844
	<u>Parasitical genus:</u> <i>Leishmania</i> sp.			
45				
	701	5'-GTG TTC ACG ATC ATC GAT GCG	514-526 ^a	94-114 ^d
	702 ^c	5'-CTC TCG ATA TCC GCG AAG CG	514-526 ^a	913-932 ^d

- 50 ^a These sequences were aligned to derive the corresponding primer.
- ^b The nucleotide positions refer to the *C. neoformans* tuf (EF-1) sequence fragment (SEQ ID NO. 623).
- ^c These sequences are from the complementary DNA strand of the sequence of the originating fragment given in the Sequence Listing.
- 55 ^d The nucleotide positions refer to the *L. tropica* tuf(EF-1) sequence fragment (SEQ ID NO. 526).

Annex I: Specific and ubiquitous primers for nucleic acid amplification (tuf sequences) (continued).

			Originating DNA fragment	
5	SEQ ID NO.	Nucleotide sequence	SEQ ID NO.	Nucleotide position
10	<u>Parasitical genus:</u> <i>Trypanosoma sp.</i>			
	823	5'-GAG CGG TAT GAY GAG ATT GT	529,840-842,864 ^a	493-512 ^b
	824 ^c	5'-GGC TTC TGC GGC ACC ATG CG	529,840-842,864 ^a	1171-1190 ^b
15	<u>Bacterial family:</u> <i>Enterobacteriaceae</i>			
	933	5'-CAT CAT CGT ITT CMT GAA CAA RTG	78,103,146,168,238,698 ^a	390-413 ^d
20	934 ^c	5'-TCA CGY TTR RTA CCA CGC AGI AGA	78,103,146,168,238,698 ^a	831-854 ^d
25	<u>Bacterial family:</u> <i>Mycobacteriaceae</i>			
	539	5'-CCI TAC ATC CTB GTY GCI CTI AAC AAG	122	85-111
	540 ^c	5'-GGD GCI TCY TCR TCG WAI TCC TG	122	181-203
30	<u>Bacterial group:</u> <i>Escherichia coli and Shigella</i>			
	1661	5'-TGG GAA GCG AAA ATC CTG	1668 ^e	283-300
	1665 ^c	5'-CAG TAC AGG TAG ACT TCT G	1668 ^e	484-502
35	<u>Bacterial group:</u> <i>Pseudomonads group</i>			
	541	5'-GTK GAA ATG TTC CGC AAG CTG CT	153-155 ^a	476-498 ^f
	542 ^c	5'-CGG AAR TAG AAC TGS GGA CGG TAG	153-155 ^a	679-702 ^f
	541	5'-GTK GAA ATG TTC CGC AAG CTG CT	153-155 ^a	476-498 ^f
40	544 ^c	5'-AYG TTG TCG CCM GGC ATT MCC AT	153-155 ^a	749-771 ^f

^a These sequences were aligned to derive the corresponding primer.

45 ^b The nucleotide positions refer to the *T. brucei* tuf (EF-1) sequence fragment (SEQ ID NO. 864).

^c These sequences are from the complementary DNA strand of the sequence of the originating fragment given in the Sequence Listing.

50 ^d The nucleotide positions refer to the *E. coli* tuf sequence fragment (SEQ ID NO. 698).

^e Sequence from databases.

^f The nucleotide positions refer to the *P. aeruginosa* tuf sequence fragment (SEQ ID NO. 153).

Annex I: Specific and ubiquitous primers for nucleic acid amplification (tuf s qu nc s) (continued).

			Originating DNA fragment	
5	SEQ ID NO.	Nucleotide sequence	SEQ ID NO.	Nucleotide position
10	<u>Parasitical group:</u> <i>Trypanosomatidae</i> family			
	923	5'-GAC GCI GCC ATC CTG ATG ATC	511,514-526, 529,840-842, 864 ^a	166-188 ^b
15	924 ^c	5'-ACC TCA GTC GTC ACG TTG GCG	511,514-526, 529,840-842, 864 ^a	648-668 ^b
20	925	5'-AAG CAG ATG GTT GTG TGC TG	511,514-526, 529,840-842, 864 ^a	274-293 ^b
	926 ^c	5'-CAG CTG CTC GTG GTG CAT CTC GAT	511,514-526, 529,840-842, 864 ^a	676-699 ^b
25	927	5'-ACG CGG AGA AGG TGC GCT T	511,514-526, 529,840-842, 864 ^a	389-407 ^b
30	928 ^c	5'-GGT CGT TCT TCG AGT CAC CGC A	511,514-526, 529,840-842, 864 ^a	778-799 ^b
Universal primers (bacteria)				
35	636	5'-ACT GGY GTT GAI ATG TTC CGY AA	7,54,78, 100,103,159, 209,224,227 ^b	470-492 ^d
	637 ^c	5'-ACG TCA GTI GTA CGG AAR TAG AA	7,54,78, 100,103,159, 209,224,227 ^b	692-714 ^d
40	638	5'-CCA ATG CCA CAA ACI CGT GAR CAC AT	7,54,78, 100,103,159, 209,224,227 ^b	35-60 ^e
45	639 ^c	5'-TTT ACG GAA CAT TTC WAC ACC WGT IAC A	7,54,78, 100,103,159, 209,224,227 ^b	469-496 ^e

- 50 ^a These sequences were aligned to derive the corresponding primer.
- ^b The nucleotide positions refer to the *L. tropica* tuf (EF-1) sequence fragment (SEQ ID NO. 526).
- ^c These sequences are from the complementary DNA strand of the sequence of the originating fragment given in the Sequence Listing.
- 55 ^d The nucleotide positions refer to the *E. coli* tuf sequence fragment (SEQ ID NO. 78).
- ^e The nucleotide positions refer to the *B. cereus* tuf sequence fragment (SEQ ID NO. 7).

Annex I: Specific and ubiquitous primers for nucleic acid amplification (tuf sequences) (continued).

		Originating DNA fragment	
5	SEQ ID NO.	Nucleotide sequence	SEQ ID NO. Nucl otide position
10	Universal primers (bacteria) (continued)		
15	643	5'-ACT GGI GTI GAR ATG TTC CGY AA	1,3,4,7,12,13,16,49,54,72,78,85,88,91,94,98,103,108,112,115,116,120,121,126,128,134,136,146,154,159,179,186,205,209,212,224,238 ^a 470-492 ^b
20	644 ^C	5'-ACG TCI GTI GTI CKG AAR TAG AA	same as SEQ ID NO. 643 692-714 ^b
25	643	5'-ACT GGI GTI GAR ATG TTC CGY AA	1,3,4,7,12,13,16,49,54,72,78,85,88,91,94,98,103,108,112,115,116,120,121,126,128,134,136,146,154,159,179,186,205,209,212,224,238 ^a 470-492 ^b
30	645 ^C	5'-ACG TCI GTI GTI CKG AAR TAR AA	same as SEQ ID NO. 643 692-714 ^b
35	646	5'-ATC GAC AAG CCI TTC YTI ATG SC	2,13,82,122,145 ^a 317-339 ^d
40	647 ^C	5'-ACG TCC GTS GTR CGG AAG TAG AAC TG	2,13,82,122,145 ^a 686-711 ^d
45	646	5'-ATC GAC AAG CCI TTC YTI ATG SC	2,13,82,122,145 ^a 317-339 ^d
	648 ^C	5'-ACG TCS GTS GTR CGG AAG TAG AAC TG	2,13,82,122,145 ^a 686-711 ^d

^a These sequences were aligned to derive the corresponding primer.

^b The nucleotide positions refer to the *E. coli* tuf sequence fragment (SEQ ID NO. 78).

^c These sequences are from the complementary DNA strand of the sequence of the originating fragment given in the Sequence Listing.

^d The nucleotide positions refer to the *A. meyeri* tuf sequence fragment (SEQ ID NO. 2)

Annex I: Specific and ubiquitous primers for nucleic acid amplification (tuf sequences) (continued).

			Originating DNA fragment	
5	SEQ ID NO.	Nucleotide sequence	SEQ ID NO.	Nucleotide position
10	Universal primers (bacteria) (continued)			
	649	5'-GTC CTA TGC CTC ARA CWC GIG AGC AC	8,86,141,143 ^a	33-58 ^b
	650 ^C	5'-TTA CGG AAC ATY TCA ACA CCI GT	8,86,141,143 ^a	473-495 ^b
15	636	5'-ACT GGY GTT GAI ATG TTC CGY AA	8,86,141,143 ^a	473-495 ^b
	651 ^C	5'-TGA CGA CCA CCI TCY TCY TTY TTC A	8,86,141,143 ^a	639-663 ^b
	Universal primers (fungi)			
20	1974	5'-ACA AGG GIT GGR MSA AGG AGA C	404,405,433, 445,898,1268, 1276,1986 ^a	443-464 ^d
	1975 ^C	5'-TGR CCR GGG TGG TTR AGG ACG	404,405,433, 445,898,1268, 1276,1986 ^a	846-866 ^d
25	1976	5'-GAT GGA YTC YGT YAA ITG GGA	407-412, 414-426,428- 431,439,443,447, 448,622,624,665, 1685,1987-1990 ^a	286-306 ^e
30	1978 ^C	5'-CAT CIT GYA ATG GYA ATC TYA AT	same as SEQ ID NO. 1976	553-575 ^e
35	1977	5'-GAT GGA YTC YGT YAA RTG GGA	same as SEQ ID NO. 1976	286-306 ^e
	1979 ^C	5'-CAT CYT GYA ATG GYA ASC TYA AT	same as SEQ ID NO. 1976	553-575 ^e
40	1981	5'-TGG ACA CCI SCA AGI GGK CYG	401-405, 433,435,436, 438,444,445,449, 453,455,457,779, 781-783,785,786, 788-790,897-903, 1267-1272,1274-1280, 1282-1287,1991-1998 ^a	281-301 ^d
45	1980 ^C	5'-TCR ATG GCI TCI AIR AGR GTY T	same as SEQ ID NO. 1981	488-509 ^d
50				

^a These sequences were aligned to derive the corresponding primer.

^b The nucleotide positions refer to the *B. distasonis* tuf sequence fragment (SEQ ID NO. 8).

55 ^c These sequences are from the complementary DNA strand of the sequence of the originating fragment given in the Sequence Listing.

^d The nucleotide positions refer to the *A. fumigatus* tuf (EF-1) sequence fragment (SEQ ID NO. 404).

60 ^e The nucleotide positions refer to the *C. albicans* tuf (EF-1) sequence fragment (SEQ ID NO. 407).

Annex I: Specific and ubiquitous primers for nucleic acid amplification (tuf sequences) (continued).

			Originating DNA fragment	
5	SEQ ID NO.	Nucleotide sequence	SEQ ID NO.	Nucleotide position
10	Universal primers (fungi) (continued)			
	1982	5'-TGG ACA CYI SCA AGI G GK CYG	same as SEQ ID NO. 1981	281-301 ^a
15	1980 ^b	5'-TCR ATG GCI TCI AIR AGR GTY T	same as SEQ ID NO. 1981	488-509 ^a
	1983	5'-CYG AYT GCG CYA TIC TCA TCA	same as SEQ ID NO. 1981	143-163 ^a
20	1980 ^b	5'-TCR ATG GCI TCI AIR AGR GTY T	same as SEQ ID NO. 1981	488-509 ^a
	1984	5'-CYG AYT GYG CYA TYC TSA TCA	same as SEQ ID NO. 1981	143-163 ^a
25	1980 ^b	5'-TCR ATG GCI TCI AIR AGR GTY T	same as SEQ ID NO. 1981	488-509 ^a
Sequencing primers				
30	556	5'-CGG CGC NAT CYT SGT TGT TGC	668 ^c	306-326
	557 ^b	5'-CCM AGG CAT RAC CAT CTC GGT G	668 ^c	1047-1068
	694	5'-CGG CGC IAT CYT SGT TGT TGC	668 ^c	306-326
	557 ^b	5'-CCM AGG CAT RAC CAT CTC GGT G	668 ^c	1047-1068
35	664	5'-AAY ATG ATI ACI GGI GCI GCI CAR ATG GA	619 ^c	604-632
	652 ^b	5'-CCW AYA GTI YKI CCI CCY TCY CTI ATA	619 ^c	1482-1508
	664	5'-AAY ATG ATI ACI GGI GCI GCI CAR ATG GA	619 ^c	604-632
40	561 ^b	5'-ACI GTI CGG CCR CCC TCA CGG AT	619 ^c	1483-1505
	543	5'-ATC TTA GTA GTT TCT GCT GCT GA	607	8-30
	660 ^b	5'-GTA GAA TTG AGG ACG GTA GTT AG	607	678-700
	658	5'-GAT YTA GTC GAT GAT GAA GAA TT	621	116-138
45	659 ^b	5'-GCT TTT TGI GTT TCW GGT TTR AT	621	443-465
	658	5'-GAT YTA GTC GAT GAT GAA GAA TT	621	116-138
	661 ^b	5'-GTA GAA YTG TGG WCG ATA RTT RT	621	678-700
50	558	5'-TCI TTY AAR TAY GCI TGG GT	665 ^c	157-176
	559 ^b	5'-CCG ACR GCR AYI GTY TGI CKC AT	665 ^c	1279-1301
	813	5'-AAT CYG TYG AAA TGC AYC ACG A	665 ^c	687-708
55	559 ^b	5'-CCG ACR GCR AYI GTY TGI CKC AT	665 ^c	1279-1301

^a The nucleotide positions refer to the *A. fumigatus* tuf (EF-1) sequence fragment (SEQ ID NO. 404).

^b These sequences are from the complementary DNA strand of the sequence of the originating fragment given in the Sequence Listing.

^c Sequences from databases.

Annex I: Specific and ubiquitous primers for nucleic acid amplification (tuf s quences) (continued).

			Originating DNA fragment	
5	SEQ ID NO.	Nucleotide sequence	SEQ ID NO.	Nucleotide position
<hr/>				
10	Sequencing primers (continued)			
	558	5'-TCI TTY AAR TAY GCI TGG GT	665 ^a	157-176
	815 ^b	5'-TGG TGC ATY TCK ACR GAC TT	665 ^a	686-705
15	560	5'-GAY TTC ATY AAR AAY ATG ATY AC	665 ^a	289-311
	559 ^b	5'-CCG ACR GCR AYI GTY TGI CKC AT	665 ^a	1279-1301
	653	5'-GAY TTC ATI AAR AAY ATG AT	665 ^a	289-308
	559 ^b	5'-CCG ACR GCR AYI GTY TGI CKC AT	665 ^a	1279-1301
20	558	5'-TCI TTY AAR TAY GCI TGG GT	665 ^a	157-176
	655 ^b	5'-CCR ATA CCI CMR ATY TTG TA	665 ^a	754-773
	654	5'-TAC AAR ATY KGI GGT ATY GG	665 ^a	754-773
25	559 ^b	5'-CCG ACR GCR AYI GTY TGI CKC AT	665 ^a	1279-1301
	696	5'-ATI GGI CAY RTI GAY CAY GGI AAR AC	698 ^a	52-77
	697 ^b	5'-CCI ACI GTI CKI CCR CCY TCR CG	698 ^a	1132-1154
30	911	5'-GAC GGM KKC ATG CCG CAR AC	853	22-41
	914 ^b	5'-GAA RAG CTG CGG RCG RTA GTG	853	700-720
	912	5'-GAC GGC GKC ATG CCG CAR AC	846	20-39
	914 ^b	5'-GAA RAG CTG CGG RCG RTA GTG	846	692-712
35	913	5'-GAC GGY SYC ATG CCK CAG AC	843	251-270
	915 ^b	5'-AAA CGC CTG AGG RCG GTA GTT	843	905-925
	916	5'-GCC GAG CTG GCC GGC TTC AG	846	422-441
40	561 ^b	5'-ACI GTI CGG CCR CCC TCA CGG AT	619 ^a	1483-1505
	664	5'-AAY ATG ATI ACI GGI GCI GCI CAR ATG GA	619 ^a	604-632
	917 ^b	5'-TCG TGC TAC CCG TYG CCG CCA T	846	593-614

45

^a Sequences from databases.

^b These sequences are from the complementary DNA strand of the sequence of the originating fragment given in the Sequence Listing.

Annex I: Specific and ubiquitous primers for nucleic acid amplification (*tuf s qu nces*) (continued).

			Originating DNA fragment	
5	SEQ ID NO.	Nucleotide sequence	SEQ ID NO.	Nucleotide position
10	Sequencing primers (continued)			
	1221	5'-GAY ACI CCI GGI CAY GTI GAY TT	1230 ^a	292-314
	1226 ^b	5'-GTI RMR TAI CCR AAC ATY TC	1230 ^a	2014-2033
15	1222	5'-ATY GAY ACI CCI GGI CAY GTI GAY TT	1230 ^a	289-314
	1223 ^b	5'-AYI TCI ARR TGI ARY TCR CCC ATI CC	1230 ^a	1408-1433
	1224	5'-CCI GYI HTI YTI GAR CCI ATI ATG	1230 ^a	1858-1881
	1225 ^b	5'-TAI CCR AAC ATY TCI SMI ARI GGI AC	1230 ^a	2002-2027
20	1227	5'-GTI CCI YTI KCI GAR ATG TTY GGI TA	1230 ^a	2002-2027
	1229 ^b	5'-TCC ATY TGI GCI GCI CCI GTI ATC AT	698 ^a	4-29
	1228	5'-GTI CCI YTI KCI GAR ATG TTY GGI TAY GC	1230 ^a	2002-2030
25	1229 ^b	5'-TCC ATY TGI GCI GCI CCI GTI ATC AT	698 ^a	4-29
	1999	5'-CAT GTC AAY ATT GGT ACT ATT GGT CAT GT	498-500, 502, 505, 506, 508, 619, 2004, 2005 ^c	25-53 ^d
30	2000 ^b	5'-CCA CCY TCI CTC AMG TTG AAR CGT T	same as SEQ ID NO. 1999	1133-1157 ^d
	2001	5'-ACY ACI TTR ACI GCY GCY ATY AC	same as SEQ ID NO. 1999	67-89 ^d
35	2003 ^b	5'-CAT YTC RAI RTT GTC ACC TGG	same as SEQ ID NO. 1999	1072-1092 ^d
	2002	5'-CCI GAR GAR AGA GCI MGW GGT	same as SEQ ID NO. 1999	151-171 ^d
40	2003 ^b	5'-CAT YTC RAI RTT GTC ACC TGG	same as SEQ ID NO. 1999	1072-1092 ^d

^a Sequences from databases.

45 ^b These sequences are from the complementary DNA strand of the sequence of the originating fragment given in the Sequence Listing.

^c These sequences were aligned to derive the corresponding primer.

^d The nucleotide positions refer to the *C. albicans tuf* sequence fragment (SEQ ID NO. 2004).

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Ann x II: Specific and ubiquitous primers for nucleic acid amplification (atpD sequences).

			Originating DNA fragment	
5	SEQ ID NO.	Nucleotide sequence	SEQ ID NO.	Nucleotide position
10	<u>Bacterial species:</u> --- <i>Acinetobacter baumannii</i> ---			
	1690	5'-CAG GTC CTG TTG CGA CTG AAG AA	243	186-208
	1691 ^b	5'-CAC AGA TAA ACC TGA GTG TGC TTT C	243	394-418
15	<u>Bacterial species:</u> <i>Bacteroides fragilis</i>			
	2134	5'-CGC GTG AAG CTT CTG TG	929	184-200
	2135 ^b	5'-TCT CGC CGT TAT TCA GTT TC	929	395-414
20	<u>Bacterial species:</u> <i>Bordetella pertussis</i>			
	2180	5'-TTC GCC GGC GTG GGC	1672 ^C	544-558
	2181 ^b	5'-AGC GCC ACG CGC AGG	1672 ^C	666-680
25	<u>Bacterial species:</u> <i>Enterococcus faecium</i>			
	1698	5'-GGA ATC AAC AGA TGG TTT ACA AA	292	131-153
	1699 ^b	5'-GCA TCT TCT GGG AAA GGT GT	292	258-277
30	1700	5'-AAG ATG CGG AAA GAA GCG AA	292	271-290
	1701 ^b	5'-ATT ATG GAT CAG TTC TTG GAT CA	292	439-461
	<u>Bacterial species:</u> <i>Klebsiella pneumoniae</i>			
35	1331	5'-GCC CTT GAG GTA CAG AAT GGT AAT GAA GTT	317	88-118
	1332 ^b	5'-GAC CGC GGC GCA GAC CAT CA	317	183-203

^a These sequences were aligned to derive the corresponding primer.

40 ^b These sequences are from the complementary DNA strand of the sequence of the originating fragment given in the Sequence Listing.

^c Sequence from databases.

Annex II: Specific and ubiquitous primers for nucleic acid amplification (atpD sequences).

5			Originating DNA fragment	
	SEQ ID NO.	Nucleotide sequence	SEQ ID NO.	Nucleotide position
10	Bacterial species: <i>Streptococcus agalactiae</i>			
	627	5'-ATT GTC TAT AAA AAT GGC GAT AAG TC	379-383 ^a	42-67 ^b
	625 ^c	5'-CGT TGA AGA CAC GAC CCA AAG TAT CC	379-383 ^a	206-231 ^b
15	628	5'-AAA ATG GCG ATA AGT CAC AAA AAG TA	379-383 ^a	52-77 ^b
	625 ^c	5'-CGT TGA AGA CAC GAC CCA AAG TAT CC	379-383 ^a	206-231 ^b
	627	5'-ATT GTC TAT AAA AAT GGC GAT AAG TC	379-383 ^a	42-67 ^b
	626 ^c	5'-TAC CAC CTT TTA AGT AAG GTG CTA AT	379-383 ^a	371-396 ^b
20	628	5'-AAA ATG GCG ATA AGT CAC AAA AAG TA	379-383 ^a	52-77 ^b
	626 ^c	5'-TAC CAC CTT TTA AGT AAG GTG CTA AT	379-383 ^a	371-396 ^b
25	Bacterial group: <i>Campylobacter jejuni</i> and <i>C. coli</i>			
	2131	5'-AAG CMA TTG TTG TAA ATT TTG AAA G	1576,1600, 1849,1863,2139 ^{d,a}	7-31 ^e
	2132 ^c	5'-TCA TAT CCA TAG CAA TAG TTC TA	1576,1600, 1849,1863,2139 ^{d,a}	92-114 ^e
30	Bacterial genus: <i>Bordetella</i> sp.			
	825	5'-ATG AGC ARC GSA ACC ATC GTT CAG TG	1672 ^d	1-26
	826 ^c	5'-TCG ATC GTG CCG ACC ATG TAG AAC GC	1672 ^d	1342-1367
35	Fungal genus: <i>Candida</i> sp.			
	634	5'-AAC ACY GTC AGR RCI ATT GCY ATG GA	460-472, 474-478 ^a	101-126 ^f
40	635 ^c	5'-AAA CCR GTI ARR GCR ACT CTI GCT CT	460-472, 474-478 ^a	617-642 ^f

^a These sequences were aligned to derive the corresponding primer.

45 ^b The nucleotide positions refer to the *S. agalactiae* atpD sequence fragment (SEQ ID NO. 380).

^c These sequences are from the complementary DNA strand of the sequence of the originating fragment given in the Sequence Listing.

^d Sequence from databases.

50 ^e The nucleotide positions refer to the *C. jejuni* atpD sequence fragment (SEQ ID NO. 1576).

^f The nucleotide positions refer to the *C. albicans* atpD sequence fragment (SEQ ID NO. 460).

Annex II: Specific and ubiquitous primers for nucleic acid amplification (*atpD* sequences) (continued).

		Originating DNA fragment	
SEQ ID NO.	Nucleotide s quence	SEQ ID NO.	Nucleotide position
<hr/>			
10	<hr/> Universal primers <hr/>		
562	5'-CAR ATG RAY GAR CCI CCI GGI GYI MGI ATG	243,244,262, 264,280,284, 291,297,309, 311,315,317, 324,329,332, 334-336,339, 342,343,351, 356,357,364-366,370,375, 379,393 ^a	528-557 ^b
15			
20			
563 ^c	5'-GGY TGR TAI CCI ACI GCI GAI GGC AT	243,244,262, 264,280,284, 291,297,309, 311,315,317, 324,329,332, 334-336,339, 342,343,351, 356,357,364-366,370,375, 379,393 ^a	687-712 ^b
25			
30			
564	5'-TAY GGI CAR ATG AAY GAR CCI CCI GGI AA	243,244,262, 264,280,284, 291,297,309, 311,315,317, 324,329,332, 334-336,339, 342,343,351, 356,357,364-366,370,375, 379,393 ^a	522-550 ^b
35			
40			
565 ^c	5'-GGY TGR TAI CCI ACI GCI GAI GGD AT	243,244,262, 264,280,284, 291,297,309, 311,315,317, 324,329,332, 334-336,339, 342,343,351, 356,357,364-366,370,375, 379,393 ^a	687-712 ^b
45			
50			

^a These sequences were aligned to derive the corresponding primer.

^b The nucleotide positions refer to the *K. pneumoniae atpD* sequence fragment (SEQ ID NO. 317).

^c These sequences are from the complementary DNA strand of the sequence of the originating fragment given in the Sequence Listing.

Annex II: Specific and ubiquitous primers for nucleic acid amplification (atpD sequences) (continued).

			Originating DNA fragment	
5	SEQ ID NO.	Nucleotide sequence	SEQ ID NO.	Nucleotide position
10	Universal primers (continued)			
	640	5'-TCC ATG GTI TWY GGI CAR ATG AA	248,284,315, 317,343,357, 366,370,379,393 ^a	513-535 ^b
15	641 ^c	5'-TGA TAA CCW ACI GCI GAI GGC ATA CG	248,284,315, 317,343,357, 366,370,379,393 ^a	684-709 ^b
20	642	5'-GGC GTI GGI GAR CGI ACI CGT GA	248,284,315, 317,343,357, 366,370,379,393 ^a	438-460 ^b
	641 ^c	5'-TGA TAA CCW ACI GCI GAI GGC ATA CG	248,284,315, 317,343,357, 366,370,379,393 ^a	684-709 ^b
25	Sequencing primers			
	566	5'-TTY GGI GGI GCI GGI GTI GGI AAR AC	669 ^d	445-470
30	567 ^c	5'-TCR TCI GCI GGI ACR TAI AYI GCY TG	669 ^d	883-908
	566	5'-TTY GGI GGI GCI GGI GTI GGI AAR AC	669 ^d	445-470
	814	5'-GCI GGC ACG TAC ACI GCC TG	666 ^d	901-920
35	568	5'-RTI ATI GGI GCI GTI RTI GAY GT	669 ^d	25-47
	567 ^c	5'-TCR TCI GCI GGI ACR TAI AYI GCY TG	669 ^d	883-908
	570	5'-RTI RYI GGI CCI GTI RTI GAY GT	672 ^d	31-53
	567 ^c	5'-TCR TCI GCI GGI ACR TAI AYI GCY TG	669 ^d	883-908
40	572	5'-RTI RTI GGI SCI GTI RTI GA	669 ^d	25-44
	567 ^c	5'-TCR TCI GCI GGI ACR TAI AYI GCY TG	669 ^d	883-908
	569	5'-RTI RTI GGI SCI GTI RTI GAT AT	671 ^d	31-53
45	567 ^c	5'-TCR TCI GCI GGI ACR TAI AYI GCY TG	669 ^d	883-908
	571	5'-RTI RTI GGI CCI GTI RTI GAT GT	670 ^d	31-53
	567 ^c	5'-TCR TCI GCI GGI ACR TAI AYI GCY TG	669 ^d	883-908

50 ^a These sequences were aligned to derive the corresponding primer.

^b The nucleotide positions refer to the *K. pneumoniae* atpD sequence fragment (SEQ ID NO. 317).

^c These sequences are from the complementary DNA strand of the sequence of the originating fragment given in the Sequence Listing.

55 ^d Sequences from databases.

Annex II: Specific and ubiquitous primers for nucleic acid amplification (atpD sequences) (continued).

			Originating DNA fragment	
5	SEQ ID NO.	Nucleotide sequence	SEQ ID NO.	Nucleotide position
10	Sequencing primers (continued)			
	700	5'-TIR TIG AYG TCG ART TCC CTC ARG	669 ^a	38-61
	567 ^b	5'-TCR TCI GCI GGI ACR TAI AYI GCY TG	669 ^a	883-908
15	568	5'-RTI ATI GGI GCI GTI RTI GAY GT	669 ^a	25-47
	573 ^b	5'-CCI CCI ACC ATR TAR AAI GC	666 ^a	1465-1484
	574	5'-ATI GCI ATG GAY GGI ACI GAR GG	666 ^a	283-305
	573 ^b	5'-CCI CCI ACC ATR TAR AAI GC	666 ^a	1465-1484
20	574	5'-ATI GCI ATG GAY GGI ACI GAR GG	666 ^a	283-305
	708 ^b	5'-TCR TCC ATI CCI ARI ATI GCI ATI AT	666 ^a	1258-1283
	681	5'-GGI SSI TTY GGI ISI GGI AAR AC	685	694-716
25	682 ^b	5'-GTI ACI GGY TCY TCR AAR TTI CCI CC	686	1177-1202
	681	5'-GGI SSI TTY GGI ISI GGI AAR AC	685	694-716
	683 ^b	5'-GTI ACI GGI TCI SWI AWR TCI CCI CC	685	1180-1205
30	681	5'-GGI SSI TTY GGI ISI GGI AAR AC	685	694-716
	699	5'-GTI ACI GGY TCY TYR ARR TTI CCI CC	686	1177-1202
	681	5'-GGI SSI TTY GGI ISI GGI AAR AC	685	694-716
	812 ^b	5'-GTI ACI GGI TCY TYR ARR TTI CCI CC	685	1180-1205
35	1213	5'-AAR GGI GGI ACI GCI GCI ATH CCI GG	714 ^a	697-722
	1212 ^b	5'-CCI CCI RGI GGI GAI ACI GCW CC	714 ^a	1189-1211
	1203	5'-GGI GAR MGI GGI AAY GAR ATG	709 ^a	724-744
40	1207 ^b	5'-CCI TCI TCW CCI GGC ATY TC	709 ^a	985-1004
	1204	5'-GCI AAY AAC ITC IWM YAT GCC	709 ^a	822-842
	1206 ^b	5'-CKI SRI GTI GAR TCI GCC A	709 ^a	926-944
45	1205	5'-AAY ACI TCI AWY ATG CCI GT	709 ^a	826-845
	1207 ^b	5'-CCI TCI TCW CCI GGC ATY TC	709 ^a	985-1004
	2282	5'-AGR RGC IMA RAT GTA TGA	714 ^a	84-101
	2284 ^b	5'-TCT GWG TRA CIG GYT CKG AGA	714 ^a	1217-1237
50	2283	5'-ATI TAT GAY GGI ITT CAG AGG C	714 ^a	271-292
	2285 ^b	5'-CMC CIC CWG GTG GWG AWA C	714 ^a	1195-1213

55 ^a Sequences from databases.

^b These sequences are from the complementary DNA strand of the sequence of the originating fragment given in the Sequence Listing.

Annex III: Internal hybridization probes for specific detection of tuf sequences.

			Originating DNA fragment	
5	SEQ ID NO.	Nucleotide sequence	SEQ ID NO.	Nucleotide position
10	<u>Bacterial species:</u> <i>Abiotrophia adiacens</i>			
	2170	5'-ACG TGA CGT TGA CAA ACC A	1715	313-331
15	<u>Bacterial species:</u> <i>Chlamydia pneumoniae</i>			
	2089	5'-ATG CTG AAC TTA TTG ACC TT	20	136-155
	2090	5'-CGT TAC TGG AGT CGA AAT G	20	467-485
20	<u>Bacterial species:</u> <i>Enterococcus faecalis</i>			
	580	5'-GCT AAA CCA GCT ACA ATC ACT CCA C	62-63,607 ^a	584-608 ^b
	603	5'-GGT ATT AAA GAC GAA ACA TC	62-63,607 ^a	440-459 ^b
	1174	5'-GAA CGT GGT GAA GTT CGC	62-63,607 ^a	398-415 ^b
25	<u>Bacterial species:</u> <i>Enterococcus faecium</i>			
	602	5'-AAG TTG AAG TTG TTG GTA TT	64,608 ^a	426-445 ^c
30	<u>Bacterial species:</u> <i>Enterococcus gallinarum</i>			
	604	5'-GGT GAT GAA GTA GAA ATC GT	66,609 ^a	419-438 ^d
	<u>Bacterial species:</u> <i>Escherichia coli</i>			
35	579	5'-GAA GGC CGT GCT GGT GAG AA	78	503-522
	2168	5'-CAT CAA AGT TGG TGA AGA AGT TG	78	409-431
40	<u>Bacterial species:</u> <i>Neisseria gonorrhoeae</i>			
	2166	5'-GAC AAA CCA TTC CTG CTG	126	322-339 ^e
	<u>Fungal species:</u> <i>Candida albicans</i>			
45	577	5'-CAT GAT TGA ACC ATC CAC CA	407-411 ^a	406-425 ^f
	<u>Fungal species:</u> <i>Candida dubliniensis</i>			
50	578	5'-CAT GAT TGA AGC TTC CAC CA	412,414-415 ^a	418-437 ^g

^a These sequences were aligned to derive the corresponding primer.

^b The nucleotide positions refer to the *E. faecalis* tuf sequence fragment (SEQ ID NO. 607).

^c The nucleotide positions refer to the *E. faecium* tuf sequence fragment (SEQ ID NO. 608).

^d The nucleotide positions refer to the *E. gallinarum* tuf sequence fragment (SEQ ID NO. 609).

^e The nucleotide positions refer to the *N. gonorrhoeae* tuf sequence fragment (SEQ ID NO. 126).

^f The nucleotide positions refer to the *C. albicans* tuf(EF-1) sequence fragment (SEQ ID NO. 408).

^g The nucleotide positions refer to the *C. dubliniensis* tuf(EF-1) sequence fragment (SEQ ID NO. 414).

**Annex III: Internal hybridization probes for specific detection of
tuf sequences (continued).**

5			Originating DNA fragment	
	SEQ ID NO.	Nucleotide sequence	SEQ ID NO.	Nucleotide position
10	Bacterial species: <i>Haemophilus influenzae</i>			
	581	5'-ACA TCG GTG CAT TAT TAC GTG G	610 ^a	551-572
15	Bacterial species: <i>Mycoplasma pneumoniae</i>			
	2095	5'-CGG TCG GGT TGA ACG TGG	2097 ^a	687-704
	Bacterial species: <i>Staphylococcus aureus</i>			
20	584	5'-ACA TGA CAC ATC TAA AAC AA	176-180 ^b	369-388 ^c
	585	5'-ACC ACA TAC TGA ATT CAA AG	176-180 ^b	525-544 ^c
	586	5'-CAG AAG TAT ACG TAT TAT CA	176-180 ^b	545-564 ^c
	587	5'-CGT ATT ATC AAA AGA CGA AG	176-180 ^b	555-574 ^c
	588	5'-TCT TCT CAA ACT ATC GTC CA	176-180 ^b	593-612 ^c
25	Bacterial species: <i>Staphylococcus epidermidis</i>			
	589	5'-GCA CGA AAC TTC TAA AAC AA	185,611 ^b	445-464 ^d
	590	5'-TAT ACG TAT TAT CTA AAG AT	185,611 ^b	627-646 ^d
30	591	5'-TCC TGG TTC TAT TAC ACC AC	185,611 ^b	586-605 ^d
	592	5'-CAA AGC TGA AGT ATA CGT AT	185,611 ^b	616-635 ^d
	593	5'-TTC ACT AAC TAT CGC CCA CA	185,611 ^b	671-690 ^d
	Bacterial species: <i>Staphylococcus haemolyticus</i>			
35	594	5'-ATT GGT ATC CAT GAC ACT TC	186,188-190 ^b	437-456 ^e
	595	5'-TTA AAG CAG ACG TAT ACG TT	186,188-190 ^b	615-634 ^e
	Bacterial species: <i>Staphylococcus hominis</i>			
40	596	5'-GAA ATT ATT GGT ATC AAA GA	191,193-196 ^b	431-450 ^f
	597	5'-ATT GGT ATC AAA GAA ACT TC	191,193-196 ^b	437-456 ^f
	598	5'-AAT TAC ACC TCA CAC AAA AT	191,193-196 ^b	595-614 ^f
45	^a Sequences from databases. ^b These sequences were aligned to derive the corresponding probe. ^c The nucleotide positions refer to the <i>S. aureus</i> tuf sequence fragment (SEQ ID NO. 179). ^d The nucleotide positions refer to the <i>S. epidermidis</i> tuf sequence fragment (SEQ ID NO. 611). ^e The nucleotide positions refer to the <i>S. haemolyticus</i> tuf sequence fragment (SEQ ID NO. 186). ^f The nucleotide positions refer to the <i>S. hominis</i> tuf sequence fragment (SEQ ID NO. 191).			
55				

Annex III: Internal hybridization probes for specific detection of *tuf* sequences (continued).

			Originating DNA fragment	
5	SEQ ID NO.	Nucleotide sequence	SEQ ID NO.	Nucleotide position
10	<u>Bacterial species:</u> <i>Staphylococcus saprophyticus</i>			
	599	5'-CGG TGA AGA AAT CGA AAT CA	198-200 ^a	406-425 ^b
	600	5'-ATG CAA GAA GAA TCA AGC AA	198-200 ^a	431-450 ^b
	601	5'-GTT TCA CGT GAT GAT GTA CA	198-200 ^a	536-555 ^b
15	695	5'-GTT TCA CGT GAT GAC GTA CA	198-200 ^a	563-582 ^b
	<u>Bacterial species:</u> <i>Streptococcus agalactiae</i>			
	582 ^c	5'-TTT CAA CTT CGT CGT TGA CAC GAA CAG T	207-210 ^a	404-431 ^d
20	583 ^c	5'-CAA CTG CTT TTT GGA TAT CTT CTT TAA TAC CAA CG	207-210 ^a	433-467 ^d
	1199	5'-GTA TTA AAG AAG ATA TCC AAA AAG C	207-210 ^a	438-462 ^d
	<u>Bacterial species:</u> <i>Streptococcus pneumoniae</i>			
25	1201	5'-TCA AAG AAG AAA CTA AAA AAG CTG T	971,977, 979,986 ^a	513-537 ^e
	<u>Bacterial species:</u> <i>Streptococcus pyogenes</i>			
30	1200	5'-TCA AAG AAG AAA CTA AAA AAG CTG T	1002	473-497
	<u>Bacterial group:</u> <i>Enterococcus casseliflavus-flavescens-gallinarum</i> group			
35	620	5'-ATT GGT GCA TTG CTA CGT	58,65,66 ^a	527-544 ^f
	1122	5'-TGG TGC ATT GCT ACG TGG	58,65,66 ^a	529-546 ^f
	<u>Bacterial group:</u> <i>Enterococcus</i> sp., <i>Gemella</i> sp., <i>A. adiacens</i>			
40	2172	5'-GTG TTG AAA TGT TCC GTA AA	58-62,67-71, 87-88,607-609, 727,871 1715,1722 ^a	477-496 ^g

- 45 ^a These sequences were aligned to derive the corresponding primer.
- ^b The nucleotide positions refer to the *S. saprophyticus* *tuf* sequence fragment (SEQ ID NO. 198).
- ^c These sequences are from the complementary DNA strand of the sequence of the originating fragment given in the Sequence Listing.
- 50 ^d The nucleotide positions refer to the *S. agalactiae* *tuf* sequence fragment (SEQ ID NO. 209).
- ^e The nucleotide positions refer to the *S. pneumoniae* *tuf* sequence fragment (SEQ ID NO. 986).
- ^f The nucleotide positions refer to the *E. flavescens* *tuf* sequence fragment (SEQ ID NO. 65).
- 55 ^g The nucleotide positions refer to the *E. faecium* *tuf* sequence fragment (SEQ ID NO. 608).

Annex III: Internal hybridization probes for specific detection of tuf sequences (continued).

			Originating DNA fragment	
5	SEQ ID NO.	Nucleotide sequence	SEQ ID NO.	Nucleotide position
10	<u>Bacterial genus:</u> <i>Gemella</i>			
	2171	5'-TCG TTG GAT TAA CTG AAG AA	87,88 ^a	430-449 ^b
15	<u>Bacterial genus:</u> <i>Staphylococcus</i> sp.			
	605	5'-GAA ATG TTC CGT AAA TTA TT	176-203 ^a	403-422 ^c
	606	5'-ATT AGA CTA CGC TGA AGC TG	176-203 ^a	420-439 ^c
	1175	5'-GTT ACT GGT GTA GAA ATG TTC	176-203 ^a	391-411 ^c
	1176	5'-TAC TGG TGT AGA AAT GTT C	176-203 ^a	393-411 ^c
20	<u>Bacterial genus:</u> <i>Streptococcus</i> sp.			
	1202	5'-GTG TTG AAA TGT TCC GTA AAC A	206-231,971, 977,979,982-986 ^a	466-487 ^d
25	<u>Fungal species:</u> <i>Candida albicans</i>			
	1156	5'-GTT GAA ATG CAT CAC GAA CAA TT	407-412,624 ^a	680-702 ^e
30	<u>Fungal group:</u> <i>Candida albicans</i> and <i>C. tropicalis</i>			
	1160	5'-CGT TTC TGT TAA AGA AAT TAG AAG	407-412, 429,624 ^a	748-771 ^e
35	<u>Fungal species:</u> <i>Candida dubliniensis</i>			
	1166	5'-ACG TTA AGA ATG TTT CTG TCA A	414-415 ^a	750-771 ^f
	1168	5'-GAA CAA TTG GTT GAA GGT GT	414-415 ^a	707-726 ^f
40	<u>Fungal species:</u> <i>Candida glabrata</i>			
	1158	5'-AAG AGG TAA TGT CTG TGG T	417	781-799
	1159	5'-TGA AGG TTT GCC AGG TGA	417	718-735
45	<u>Fungal species:</u> <i>Candida krusei</i>			
	1161	5'-TCC AGG TGA TAA CGT TGG	422	720-737

50

^a These sequences were aligned to derive the corresponding primer.

^b The nucleotide positions refer to the *G. haemolysans* tuf sequence fragment (SEQ ID NO. 87).

55 ^c The nucleotide positions refer to the *S. aureus* tuf sequence fragment (SEQ ID NO. 179).

^d The nucleotide positions refer to the *S. pneumoniae* tuf sequence fragment (SEQ ID NO. 986).

^e The nucleotide positions refer to the *C. albicans* tuf(EF-1) sequence fragment (SEQ ID NO. 408).

60 ^f The nucleotide positions refer to the *C. dubliniensis* tuf(EF-1) sequence fragment (SEQ ID NO. 414).

Annex III: Internal hybridization probes for specific detection of tuf sequences (continued).

		Originating DNA fragment		
5	SEQ ID NO.	Nucleotide sequence	SEQ ID NO.	Nucleotide position
10	<u>Fungal group:</u>	<i>Candida lusitaniae</i> and <i>C. guilliermondii</i>		
	1162	5'-CAA GTC CGT GGA AAT GCA	418,424 ^a	682-699 ^b
15	<u>Fungal species:</u>	<i>Candida parapsilosis</i>		
	1157	5'-AAG AAC GTT TCA GTT AAG GAA AT	426	749-771
	<u>Fungal species:</u>	<i>Candida zeylanoides</i>		
20	1165	5'-GGT TTC AAC GTG AAG AAC	432	713-730
	<u>Fungal genus:</u>	<i>Candida</i> sp.		
25	1163	5'-GTT GGT TTC AAC GTT AAG AAC	407-412,414-415,417,418,422,429 ^a	728-748 ^c
	1164	5'-GGT TTC AAC GTC AAG AAC	413,416,420,421,424,425,426,428,431 ^a	740-757 ^b
30	1167	5'-GTT GGT TTC AAC GT	406-426, 428-432, 624 ^a	728-741 ^c

^a These sequences were aligned to derive the corresponding primer.

35 ^b The nucleotide positions refer to the *C. lusitanae* tuf(EF-1) sequence fragment (SEQ ID NO. 424).

^c The nucleotide positions refer to the *C. albicans* tuf(EF-1) sequence fragment (SEQ ID NO. 408).

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Annex IV: Strategy for the selection of amplification/sequencing primers from atpD (F-type) sequences.

		23	49	443	472	881	910 NO.:	SEQ ID	Accession #:
5		AGTgCAT CGGCGCCGCTT ATCGAGCTGG...TCTTCG CGCGTCTCTGG CGTGGGCAAG ACCG...TCCA GCGCGTGT ACCTCCCTCC GCACGACT					-	-	X78877
	B. cepacia	AGTgCAT CGGCGCCGCTG GTGGATATTC...TCTTCG CGCGGCGCGG CGTGGGCAAG ACCG...TCCA GCGCGTGT ACCTCCCTCC GCACGACT					-	-	Genome project
	B. pertussis	AAATCAT CGGCGCCGCTG ATCGAGCTGG...TCTTCG CGCGGCGCGG CGTGGGCAAG ACCG...TCCA GCGCGTGT ACCTCCCTCC GCACGACT					-	-	Genome project
10	P. aeruginosa	AGTgCAT CGGCGCCGCTG GTGGATATTC...TCTTCG CGCGGCGCGG CGTGGGCAAG ACCG...TCCA GCGCGTGT ACCTCCCTCC GCACGACT					-	-	J01594
	E. coli	AAATCAT CGGCGCCGCTG ATCGAGCTGG...TCTTCG CGCGGCGCGG CGTGGGCAAG ACCG...TCCA GCGCGTGT ACCTCCCTCC GCACGACT					-	-	Genome project
	M. gonorrhoeae	AGTgCAT CGGCGCCGCTG GTGGATATTC...TCTTCG CGCGGCGCGG CGTGGGCAAG ACCG...TCCA GCGCGTGT ACCTCCCTCC GCACGACT					-	-	U64318
	M. thermoacetica	AGTgCAT CGGCGCCGCTG ATCGAGCTGG...TCTTCG CGCGGCGCGG CGTGGGCAAG ACCG...TCCA GCGCGTGT ACCTCCCTCC GCACGACT					-	-	X76879
	S. aurantiaea	AGTgCAT CGGCGCCGCTG GTGGATATTC...TCTTCG CGCGGCGCGG CGTGGGCAAG ACCG...TCCA GCGCGTGT ACCTCCCTCC GCACGACT					-	-	273419
15	M. tuberculosis	GGGTGAC TGGGCGCCGCTG ATCGAGCTGG...TCTTCG CGCGGCGCGG CGTGGGCAAG ACCG...TCCA GCGCGTGT ACCTCCCTCC GCACGACT					-	-	M22247
	C. lytica	AAATCAT CGGCGCCGCTG GTGGATATTC...TCTTCG CGCGGCGCGG CGTGGGCAAG ACCG...TCCA GCGCGTGT ACCTCCCTCC GCACGACT					672	-	M22535
	A. woodii	AGTgCAT CGGCGCCGCTG ATCGAGCTGG...TCTTCG CGCGGCGCGG CGTGGGCAAG ACCG...TCCA GCGCGTGT ACCTCCCTCC GCACGACT					-	-	U10505
	C. acetobutylicum	AGTgCAT CGGCGCCGCTG GTGGATATTC...TCTTCG CGCGGCGCGG CGTGGGCAAG ACCG...TCCA GCGCGTGT ACCTCCCTCC GCACGACT					671	-	AF101055
20	M. pneumoniae	AGTgCAT CGGCGCCGCTG GTGGATATTC...TCTTCG CGCGGCGCGG CGTGGGCAAG ACCG...TCCA GCGCGTGT ACCTCCCTCC GCACGACT					-	-	U43738
	H. pylori	AGTgCAT CGGCGCCGCTG GTGGATATTC...TCTTCG CGCGGCGCGG CGTGGGCAAG ACCG...TCCA GCGCGTGT ACCTCCCTCC GCACGACT					670	-	AF004014
	Selected sequences for universal primers	RTIAT IGGICGICGTI RTIGAYGT							
		RTIY IGGICGICGTI RTIGAYGT							568
25		RTIY IGGICGICGTI RTIGAYGT							570
		RTIY IGGICGICGTI RTIGAYGT							572
		RTIY IGGICGICGTI RTIGAYGT							569
		RTIY IGGICGICGTI RTIGAYGT							571
		RTIY IGGICGICGTI RTIGAYGT							566
30	Selected sequence for universal primer*		TTYG GIGGICGICG IGTIGGIAAR AC						
								CA RGCIRITIT AYGTICGICG IGAYCA	567

The sequence numbering refers to the *Escherichia coli atpD* gene fragment (SEQ ID NO. 669). Nucleotides in capitals are identical to the selected sequences or match those sequences. Mismatches are indicated by lower-case letters. Dots indicate gaps in the sequences displayed.

"R" "Y" "M" "K" "W" and "S" designate nucleotide positions which are degenerated. "R" stands for A or G; "Y" stands for C or T; "M" stands for A or C; "K" stands for G or T; "W" stands for A or T; "S" stands for C or G. "I" stands for inosine which is a nucleotide analog that can bind to any of the four nucleotides A, C, G or T.

* This sequence is the reverse-complement of the selected primer.

Annex V: Strategy for the selection of universal amplification/sequencing primers from *atpD* (V-type) sequences.

5

	691	719	1177	1208	SEQ ID NO.:
<i>E. hirae</i>	CC AGGTCCGTTT	GGTCAGGGA	AGACAGT...TCTGCTGGAG	ATATCTcttGA	ACCAGTGA CT CA
<i>H. salinarum</i>	CC GGGCCCGTTC	GGGTCCGGGA	AGACGGT...CCGGCCGGG	ACTTCTcttGA	GCCGGTCACC CA
<i>T. thermophilus</i>	CC TGGGCCCTTC	GGCAGCGGA	AGACCGT...CCGGCCGGG	ACATgtctGA	GCCCGTGACC CA
Human	CC TGGGGCCCTTC	GGATGTGGCA	AGACTGT...CCGGCTGGAG	ACTTCTctAGA	tCCCGTGACG AC
<i>T. congolense</i>	CC TGGCGCGTTT	GGATCGGGNA	AGACGGT...CTGTGAGGTG	ACTTTTcttGA	cCCAGTGAGG TC
<i>P. falciparum</i>	CC TGGTGCTATT	GGTTCTGGAA	AAACTTG...CCAGGTGGTG	ATTTTCTctGA	cCCTGTAACT AC
<i>C. pneumoniae</i>	CC AGAACCTTTT	GGTTCAGGGA	AAACAGT...GCACGAGGAA	ACTTTTGAAGA	ACCAGTGA CT CA

15 Selected sequences for universal primers

20 Selected sequences
for universal primers^a

The sequence numbering refers to the *Enterococcus hirae atpD* gene fragment (SEQ ID NO. 685). Nucleotides in capitals are identical to the selected sequences or match those sequences. Mismatches for SEQ ID NOS. 681 and 682 are indicated by lower-case letters. Mismatches for SEQ ID NO. 603 are indicated by underlined nucleotides. Dots indicate gaps in the sequences displayed.

30 "R" "Y" "M" "K" "W" and "S" designate nucleotide positions which are degenerated. "R" stands for A or G; "Y" stands for C or T; "M" stands for A or C; "K" stands for G or T; "W" stands for A or T; "S" stands for C or G. "I" stands for inosine which is a nucleotide analog that can bind to any of the four nucleotides A, C, G or T.

^a These sequences are the reverse-complement of the selected primers.

Annex VI: Strategy for the selection of universal amplification/sequencing primers from tuf (M) sequences (organelle origin).

		601	635	1479	1511	SEQ IDAccession NO.: #:	
5							
	<i>C. neoformans</i> ^a	AAGAA	CATGATCACC	GGTaCctCCC	AGgctGACTG...CGCcgTCCgA	GACatGcGAC AGACCGTTGc CGT	- U81803
	<i>S. cerevisiae</i> ^a	AAGAA	CATGATTACT	GGTaCttCTC	AAGctGACTG...CGCtgTCCAg	GACatGaGAC AAAGTGTcGc TGT	665 X00779
	<i>O. volvulus</i> ^a	AAGAA	TATGATCACA	GGTaCttCTC	AGgctGACTG...TGCTgtTcGt	GATatGaGAC AAACaGTTGc GGT	- M64333
	Human ^a	AAAAA	CATGATTACA	GGGACATCTC	AGgctGACTG...TGCTgtTcGt	GATatGaGAC AGACaGTTGc TGT	- X03558
10	<i>G. max B1b</i>	AAGAA	CATGATCACC	GGCGTGCCTC	AGATGGACGG...TGCTATTAGA	GAAGGAGGCA AAAGTGTGg AGC	- Y15107
	<i>G. max B2b</i>	AAAAA	CATGATCACC	GGCGCGCCCT	AGATGGACGG...TGCTATTAGA	GAAGGAGGCA AAAGTGTGg AGC	- Y15108
	<i>E. coli</i> ^c	AAAAA	CATGATCACC	GCTGCTGCTC	AGATGGACGG...CGCaTCCgt	GAAGGCGGCC GTACCGTTGc CGC	78 -
	<i>S. aureofaciens</i> ^c	AAGAA	CATGATCACC	GGTGGCGCCC	AGATGGACGG...CGCaTCCgt	GAGGGTGGTc GTACCGTTGg CGC	- AF007125
	<i>E. tenella</i> ^b	AAAAA	TATGATTACA	GGAGCAGCAC	AAATGGATGG...TGCTATTAGA	GAAGGAGGAA AAAGTATAGg AGC	- AT755521
15	<i>T. gondii</i> ^b	AAGAA	TATGATTACT	GGAGCGGCAC	AAATGGATGG...TGCTATTAGA	GAAGGAGGTT GTACTATAGg AGC	- Y11431
	<i>S. cerevisiae</i> ^b	AAGAA	TATGATTACC	GCTGCTGCTC	AAATGGATGG...CAATcTACAg	GAGGCTGGAA GAAGTGTGg TAC	619 K00428
	<i>A. thaliana</i> ^b	AAAAA	TATGATTACT	GGAGCTGCGC	AAATGGATGG...TGCCtTAAGg	GAAGGAGGTA GAACaGTTGg AGC	- X89227
20	Selected sequence for universal primer	AA	YATGATIACI	GGIGCIGCIC	ARATGGA		664
	Selected sequences for universal primers				TATIAGR GARGGIGGIM RIACITRWG ^d ATCCGT GAGGGYGGCC GITCIGT ^d		652 561

The sequence numbering refers to the *Saccharomyces cerevisiae tuf* (M) gene (SEQ ID NO. 619). Nucleotides in capitals are identical to the selected sequences or match those sequences. Mismatches for SEQ ID NOS. 652 and 664 are indicated by lower-case letters. Mismatches for SEQ ID NO. 561 are indicated by underlined nucleotides. Dots indicate gaps in the sequences displayed.

"R" "Y" "M" "K" "W" and "S" designate nucleotide positions which are degenerated. "R" stands for A or G; "Y" stands for C or T; "M" stands for A or C; "K" stands for G or T; "W" stands for A or T; "S" stands for C or G. "I" stands for inosine which is a nucleotide analog that can bind to any of the four nucleotides A, C, G or T.

^a This sequence refers to *tuf*(EF-1) gene.

^b This sequence refers to *tuf* (M) or organelle gene.

^c This sequence refers to *tuf* gene from bacteria.

^d These sequences are the reverse-complement of the selected primers.

Annex VII: Strategy for the selection of eukaryotic sequencing primers from tuf (EF-1) sequences.

5	154	179	286	314	SEQ ID Accession NO.:
	GG TTCTTTCAAG	TACGCTTGGG	TTTT...ACAGA	TTTCATCAAG AACATGATTA	CTGG... X00779
	GG CTCCTTCAAG	TACGCGTGGG	TGCT...CGTGA	CTTCATCAAG AACATGATCA	CGGG... D64080
	GG TTCTTTCAAA	TACGCTTGGG	TTCT...ACAGA	TTTCATCAAG AATATGATCA	CTGG... M29934
10	TC TTCTTTCAAG	TACGCTTGGG	TTCT...CGAGA	CTTCATCAAG AACATGATCA	CCGG... U81803
	GG ATCATTCAAA	TATGCTTGGG	TCCT...ACAGA	TTTCATTAAG AACATGATTA	CTGG... M92073
	GG CTCCTTCAAG	TACGCGTGGG	TCCT...CGCGA	CTTCATCAAG AACATGATCA	CGGG... D14342
	AA ATCCTTCAAA	TATGCGTGGG	TCCT...CGTGA	CTTCATCAAG AACATGATCA	CTGG... U14100
	GG CTCCTTCAAG	TATGCGTGGG	TCCT...ACAGA	CTTCATCAAG AACATGATTA	CAGG... X03558
	GC CTCCTTCAAG	TACGCGTGGG	TGCT...CGCGA	CTTCATCAAG AACATGATCA	CCGG... U72244
	GG CTCCTTCAAA	TATGCTTGGG	TATT...CGTGA	TTTCATTAAG AATATGATCA	CAGG... M64333
	GG TagTTTCAAA	TATGCTTGGG	TTTT...AAACA	TTTCATTAAG AATATGATTA	CTGG... AJ224150
	GG AagTTTAAAG	TACGCGTGGG	TGTT...AAGGA	TTTCATTAAG AACATGATTA	CCGG... AJ224153
	GG TTCCTTCAAG	TACGCGTGGG	TTTT...CGTGA	TTTCATCAAG AACATGATTA	CCGG... U42189
20	TC TTCTTTCAAG	TACGCGTGGG	TCCT...CGCGA	CTTCATCAAG AACATGATCA	CCGG... L76077
	GG TTCTTTCAAG	TACGCTTGGG	TTCT...CGAGA	TTTCATCAAG AACATGATCA	CCGG... AF054510
	Selected sequences for amplification primers	TCITTYAAR TAYGCITGGG T			
25			GA YTTTCATYAAR AAYATGATYA C		558
			GA YTTTCATIAAR AAYATGAT		560
					653

30 The sequence numbering refers to the *Saccharomyces cerevisiae* tuf (EF-1) gene fragment (SEQ ID NO. 665). Nucleotides in capitals are identical to the selected sequences SEQ ID NOs. 558, 560 or 653, or match those sequences. Mismatches for SEQ ID no. 558 and 560 are indicated by lower-case letters. Mismatches for SEQ ID NO. 653 are indicated by underlined nucleotides. Dots indicate gaps in the sequences displayed.

35 "R" "Y" "M" "K" "W" and "S" designate nucleotide positions which are degenerated. "R" stands for A or G; "Y" stands for C or T; "M" stands for A or C; "K" stands for G or T; "W" stands for A or T; "S" stands for C or G. "I" stands for inosine which is a nucleotide analog that can bind to any of the four nucleotides A, C, G or T.

5

275

30 The sequence numbering refers to the *Saccharomyces cerevisiae* *tuf* (EF-1) gene fragment (SEQ ID NO. 665). Nucleotides in capitals are identical to the selected sequences or match those sequences. Mismatches are indicated by lower-case letters. "~" indicate incomplete sequence data. Dots indicate gaps in the sequences displayed.

"R" "Y" "M" "K" "W" and "S" designate nucleotide positions which are degenerated. "R" stands for A or G; "Y" stands for C or T; "M" stands for A or C; "K" stands for G or T; "W" stands for A or T; "S" stands for C or G. "I" stands for inosine which is a nucleotide analog that can bind to any of the four nucleotides A, C, G or T.

^a This sequences are the reverse-complement of the selected primers.

Annex VIII: Strategy for the selection of Streptococcus agalactiae-specific amplification primers from tuf sequences.

		305	334	517	542	SEQ ID NO.:	Accession #:
5	<i>S. agalactiae</i>	CCAGAA CGTGATAC TG ACAAACCTTT	ACTT...GGAC	AACGTTGGTG	TTCTTCTTCG TG	207	-
	<i>S. agalactiae</i>	CCAGAA CGTGATAC TG ACAAACCTTT	ACTT...GGAC	AACGTTGGTG	TTCTTCTTCG TG	208	-
	<i>S. agalactiae</i>	CCAGAA CGTGATAC TG ACAAACCTTT	ACTT...GGAC	AACGTTGGTG	TTCTTCTTCG TG	209	-
	<i>S. agalactiae</i>	CCAGAA CGTGATAC TG ACAAACCTTT	ACTT...GGAC	AACGTTGGTG	TTCTTCTTCG TG	210	-
	<i>S. anginosus</i>	CCAGAA CGTGATAC TG ACAAACCTTT	GCTT...AGAT	AACGTTGGTG	TTCTTCTTCG TG	211	-
10	<i>S. anginosus</i>	CCAGAA CGTGATAC TG ACAAACCTTT	GCTT...AGAT	AACGTTGGTG	TTCTTCTTCG TG	221	-
	<i>S. bovis</i>	CCAGAA CGTGATAC TG ACAAACCTTT	GCTT...GGAT	AACGTTGGTG	TTCTTCTTCG TG	212	-
	<i>S. gordonii</i>	CCAGAA CGTGATAC TG ACAAACCTTT	GCTT...AGAT	AACGTTGGTG	TTCTTCTTCG TG	223	-
	<i>S. mutans</i>	CCAGAA CGTGATAC TG ACAAACCTTT	GCTT...GGAT	AACGTTGGTG	TTCTTCTTCG TG	224	-
	<i>S. pneumoniae</i>	CCAGAA CGTGATAC TG ACAAACCTTT	GCTT...AGAT	AACGTTGGTG	TTCTTCTTCG TG	145 ^a	-
15	<i>S. sanguinis</i>	CCAGAA CGTGATAC TG ACAAACCTTT	GCTT...GGAC	AACGTTGGTG	TTCTTCTTCG TG	227	-
	<i>S. sobrinus</i>	CCAGAA CGTGATAC TG ACAAACCTTT	GCTT...AGAT	AACGTTGGTG	TTCTTCTTCG TG	228	-
	<i>B. cepacia</i>	CCGAG CGTGAGTGTG ACAAGCCATT	CCTG...TGAC	AACGTTGGTG	TCTTCTTCG CG	16	P33165
	<i>B. fragilis</i>	CCTCG CGTGAGTGTG ACAAGCCATT	CCTG...TGAC	AACGTTGGTG	TCTTCTTCG CG	-	299104
	<i>B. subtilis</i>	CCAGAA CGTGATAC TG ACAAACCTTT	CCTC...CGAC	AACGTTGGTG	TCTTCTTCG TG	-	-
20	<i>C. diphtheriae</i>	CCAGAG CGTGATAC TG ACAAGCCATT	CCTC...CGAC	AACGTTGGTG	TCTTCTTCG TG	662	-
	<i>C. trachomatis</i>	CCAGAA CGTGATAC TG ACAAGCCATT	CCTA...AGAG	AACGTTGGTG	TCTTCTTCG TG	22	-
	<i>E. coli</i>	CCAGAG CGTGATAC TG ACAAGCCATT	CCTG...TGAG	AACGTTGGTG	TCTTCTTCG TG	78	-
	<i>G. vaginalis</i>	CCAact CactGATcctG ACAAGCCATT	CCTG...CGAT	AACGTTGGTG	TTCTTCTTCG CG	135 ^a	-
25	<i>S. aureus</i>	CCAGAA CGTGATcctG ACAAGCCATT	CATg...TGAC	AACGTTGGTG	catTatTcCG TG	179	-

Selected sequence for species-specific primer

GAA CGTGATAC TG ACAAACCTTT A

549

Selected sequence for species-specific primer^b

C AACGTTGGTG TTCTTCTTC

550

The sequence numbering refers to the Streptococcus agalactiae tuf gene fragment (SEQ ID NO. 209). Nucleotides in capitals are identical to the selected sequences or match those sequences. Mismatches are indicated by lower-case letters. Dots indicate gaps in the sequences displayed.

"R" "Y" "M" "K" "W" and "S" designate nucleotide positions which are degenerated. "R" stands for A or G; "Y" stands for C or T; "M" stands for A or C; "K" stands for G or T; "W" stands for A or T; "S" stands for C or G. "I" stands for inosine which is a nucleotide analog that can bind to any of the four nucleotides A, C, G or T.

^a The SEQ ID NO. refers to previous patent publication WO98/20157.

^b This sequence is the reverse-complement of the selected primer.

Annex IX: Strategy for the selection of *Streptococcus agalactiae*-specific hybridization probes from tuf sequences.

		SEQ ID NO.: Accession #:
5	<i>S. acidominimus</i>	401
	<i>S. agalactiae</i>	431 433
	<i>S. agalactiae</i>	470
10	<i>S. agalactiae</i>	206
	<i>S. agalactiae</i>	209
	<i>S. agalactiae</i>	144*
	<i>S. agalactiae</i>	207
	<i>S. agalactiae</i>	210
	<i>S. agalactiae</i>	208
	<i>S. agalactiae</i>	211
	<i>S. agalactiae</i>	212
	<i>S. agalactiae</i>	213
	<i>S. agalactiae</i>	214
	<i>S. agalactiae</i>	215
	<i>S. agalactiae</i>	216
	<i>S. agalactiae</i>	217
	<i>S. agalactiae</i>	218
	<i>S. agalactiae</i>	219
	<i>S. agalactiae</i>	220
	<i>S. agalactiae</i>	222
	<i>S. agalactiae</i>	223
	<i>S. agalactiae</i>	224
	<i>S. agalactiae</i>	P33170
	<i>S. agalactiae</i>	225
	<i>S. agalactiae</i>	145*
	<i>S. agalactiae</i>	226
	<i>S. agalactiae</i>	146*
	<i>S. agalactiae</i>	227
	<i>S. agalactiae</i>	228
	<i>S. agalactiae</i>	229
	<i>S. agalactiae</i>	230
	<i>S. agalactiae</i>	231
	<i>S. agalactiae</i>	Genome project
40	<i>S. agalactiae</i>	582
	<i>S. agalactiae</i>	583

The sequence numbering refers to the *Streptococcus agalactiae* tuf gene fragment (SEQ ID NO. 209). Nucleotides in capitals are identical to the selected sequences or match those sequences. Mismatches are indicated by lower-case letters. Dots indicate gaps in the sequences displayed.

* The SEQ ID NO. refers to previous patent publication WO98/20157.
 * These sequences are the reverse-complement of the selected probes.

Ann x X: Strategy for the selection of Streptococcus agalactiae-specific amplification primers from atpD sequences.

NO.:	39	80	203	234	368	SEQ ID 399
5	TT GATTGCTAT AAAATGGCG ATAACTCACA AAAAGTAGTA..TAAGGATA	CTTTGGGTCG TGTCTTCAAC GTTC..CTT ATTACACCT TACTTAAAG	GTGGTAAAG 380			
	TT GATTGCTAT AAAATGGCG ATAACTCACA AAAAGTAGTA..TAAGGATA	CTTTGGGTCG TGTCTTCAAC GTTC..CTT ATTACACCT TACTTAAAG	GTGGTAAAG 379			
10	TT GATTGCTAT AAAATGGCG ATAACTCACA AAAAGTAGTA..TAAGGATA	CTTTGGGTCG TGTCTTCAAC GTTC..CTT ATTACACCT TACTTAAAG	GTGGTAAAG 381			
	TT GATTGCTAT AAAATGGCG ATAACTCACA AAAAGTAGTA..TAAGGATA	CTTTGGGTCG TGTCTTCAAC GTTC..CTT ATTACACCT TACTTAAAG	GTGGTAAAG 382			
	TT GATTGCTAT AAAATGGCG ATAACTCACA AAAAGTAGTA..TAAGGATA	CTTTGGGTCG TGTCTTCAAC GTTC..CTT ATTACACCT TACTTAAAG	GTGGTAAAG 383			
	TT GATTGCTAT AAAATGGCG ATAACTCACA AAAAGTAGTA..TAAGGATA	CTTTGGGTCG TGTCTTCAAC GTTC..CTT ATTACACCT TACTTAAAG	GTGGTAAAG 387			
15	TT GATTGCTAT AAAATGGCG ATAACTCACA AAAAGTAGTA..TAAGGATA	CTTTGGGTCG TGTCTTCAAC GTTC..CTT ATTACACCT TACTTAAAG	GTGGTAAAG 381			
	TT GATTGCTAT AAAATGGCG ATAACTCACA AAAAGTAGTA..TAAGGATA	CTTTGGGTCG TGTCTTCAAC GTTC..CTT ATTACACCT TACTTAAAG	GTGGTAAAG 382			
	TT GATTGCTAT AAAATGGCG ATAACTCACA AAAAGTAGTA..TAAGGATA	CTTTGGGTCG TGTCTTCAAC GTTC..CTT ATTACACCT TACTTAAAG	GTGGTAAAG 383			
	TT GATTGCTAT AAAATGGCG ATAACTCACA AAAAGTAGTA..TAAGGATA	CTTTGGGTCG TGTCTTCAAC GTTC..CTT ATTACACCT TACTTAAAG	GTGGTAAAG 387			
	TT GATTGCTAT AAAATGGCG ATAACTCACA AAAAGTAGTA..TAAGGATA	CTTTGGGTCG TGTCTTCAAC GTTC..CTT ATTACACCT TACTTAAAG	GTGGTAAAG 381			
	TT GATTGCTAT AAAATGGCG ATAACTCACA AAAAGTAGTA..TAAGGATA	CTTTGGGTCG TGTCTTCAAC GTTC..CTT ATTACACCT TACTTAAAG	GTGGTAAAG 382			
	TT GATTGCTAT AAAATGGCG ATAACTCACA AAAAGTAGTA..TAAGGATA	CTTTGGGTCG TGTCTTCAAC GTTC..CTT ATTACACCT TACTTAAAG	GTGGTAAAG 383			
	TT GATTGCTAT AAAATGGCG ATAACTCACA AAAAGTAGTA..TAAGGATA	CTTTGGGTCG TGTCTTCAAC GTTC..CTT ATTACACCT TACTTAAAG	GTGGTAAAG 387			
20	TT GATTGCTAT AAAATGGCG ATAACTCACA AAAAGTAGTA..TAAGGATA	CTTTGGGTCG TGTCTTCAAC GTTC..CTT ATTACACCT TACTTAAAG	GTGGTAAAG 381			
	TT GATTGCTAT AAAATGGCG ATAACTCACA AAAAGTAGTA..TAAGGATA	CTTTGGGTCG TGTCTTCAAC GTTC..CTT ATTACACCT TACTTAAAG	GTGGTAAAG 382			
	TT GATTGCTAT AAAATGGCG ATAACTCACA AAAAGTAGTA..TAAGGATA	CTTTGGGTCG TGTCTTCAAC GTTC..CTT ATTACACCT TACTTAAAG	GTGGTAAAG 383			
	TT GATTGCTAT AAAATGGCG ATAACTCACA AAAAGTAGTA..TAAGGATA	CTTTGGGTCG TGTCTTCAAC GTTC..CTT ATTACACCT TACTTAAAG	GTGGTAAAG 387			
	TT GATTGCTAT AAAATGGCG ATAACTCACA AAAAGTAGTA..TAAGGATA	CTTTGGGTCG TGTCTTCAAC GTTC..CTT ATTACACCT TACTTAAAG	GTGGTAAAG 381			
	TT GATTGCTAT AAAATGGCG ATAACTCACA AAAAGTAGTA..TAAGGATA	CTTTGGGTCG TGTCTTCAAC GTTC..CTT ATTACACCT TACTTAAAG	GTGGTAAAG 382			
	TT GATTGCTAT AAAATGGCG ATAACTCACA AAAAGTAGTA..TAAGGATA	CTTTGGGTCG TGTCTTCAAC GTTC..CTT ATTACACCT TACTTAAAG	GTGGTAAAG 383			
	TT GATTGCTAT AAAATGGCG ATAACTCACA AAAAGTAGTA..TAAGGATA	CTTTGGGTCG TGTCTTCAAC GTTC..CTT ATTACACCT TACTTAAAG	GTGGTAAAG 387			
25	TT GATTGCTAT AAAATGGCG ATAACTCACA AAAAGTAGTA..TAAGGATA	CTTTGGGTCG TGTCTTCAAC GTTC..CTT ATTACACCT TACTTAAAG	GTGGTAAAG 381			
	TT GATTGCTAT AAAATGGCG ATAACTCACA AAAAGTAGTA..TAAGGATA	CTTTGGGTCG TGTCTTCAAC GTTC..CTT ATTACACCT TACTTAAAG	GTGGTAAAG 382			
	TT GATTGCTAT AAAATGGCG ATAACTCACA AAAAGTAGTA..TAAGGATA	CTTTGGGTCG TGTCTTCAAC GTTC..CTT ATTACACCT TACTTAAAG	GTGGTAAAG 383			
	TT GATTGCTAT AAAATGGCG ATAACTCACA AAAAGTAGTA..TAAGGATA	CTTTGGGTCG TGTCTTCAAC GTTC..CTT ATTACACCT TACTTAAAG	GTGGTAAAG 387			
	TT GATTGCTAT AAAATGGCG ATAACTCACA AAAAGTAGTA..TAAGGATA	CTTTGGGTCG TGTCTTCAAC GTTC..CTT ATTACACCT TACTTAAAG	GTGGTAAAG 381			
	TT GATTGCTAT AAAATGGCG ATAACTCACA AAAAGTAGTA..TAAGGATA	CTTTGGGTCG TGTCTTCAAC GTTC..CTT ATTACACCT TACTTAAAG	GTGGTAAAG 382			
	TT GATTGCTAT AAAATGGCG ATAACTCACA AAAAGTAGTA..TAAGGATA	CTTTGGGTCG TGTCTTCAAC GTTC..CTT ATTACACCT TACTTAAAG	GTGGTAAAG 383			
	TT GATTGCTAT AAAATGGCG ATAACTCACA AAAAGTAGTA..TAAGGATA	CTTTGGGTCG TGTCTTCAAC GTTC..CTT ATTACACCT TACTTAAAG	GTGGTAAAG 387			
30	TT GATTGCTAT AAAATGGCG ATAACTCACA AAAAGTAGTA..TAAGGATA	CTTTGGGTCG TGTCTTCAAC GTTC..CTT ATTACACCT TACTTAAAG	GTGGTAAAG 381			
	TT GATTGCTAT AAAATGGCG ATAACTCACA AAAAGTAGTA..TAAGGATA	CTTTGGGTCG TGTCTTCAAC GTTC..CTT ATTACACCT TACTTAAAG	GTGGTAAAG 382			
	TT GATTGCTAT AAAATGGCG ATAACTCACA AAAAGTAGTA..TAAGGATA	CTTTGGGTCG TGTCTTCAAC GTTC..CTT ATTACACCT TACTTAAAG	GTGGTAAAG 383			
	TT GATTGCTAT AAAATGGCG ATAACTCACA AAAAGTAGTA..TAAGGATA	CTTTGGGTCG TGTCTTCAAC GTTC..CTT ATTACACCT TACTTAAAG	GTGGTAAAG 387			
	TT GATTGCTAT AAAATGGCG ATAACTCACA AAAAGTAGTA..TAAGGATA	CTTTGGGTCG TGTCTTCAAC GTTC..CTT ATTACACCT TACTTAAAG	GTGGTAAAG 381			
	TT GATTGCTAT AAAATGGCG ATAACTCACA AAAAGTAGTA..TAAGGATA	CTTTGGGTCG TGTCTTCAAC GTTC..CTT ATTACACCT TACTTAAAG	GTGGTAAAG 382			
	TT GATTGCTAT AAAATGGCG ATAACTCACA AAAAGTAGTA..TAAGGATA	CTTTGGGTCG TGTCTTCAAC GTTC..CTT ATTACACCT TACTTAAAG	GTGGTAAAG 383			
	TT GATTGCTAT AAAATGGCG ATAACTCACA AAAAGTAGTA..TAAGGATA	CTTTGGGTCG TGTCTTCAAC GTTC..CTT ATTACACCT TACTTAAAG	GTGGTAAAG 387			
35	TT GATTGCTAT AAAATGGCG ATAACTCACA AAAAGTAGTA..TAAGGATA	CTTTGGGTCG TGTCTTCAAC GTTC..CTT ATTACACCT TACTTAAAG	GTGGTAAAG 381			
	TT GATTGCTAT AAAATGGCG ATAACTCACA AAAAGTAGTA..TAAGGATA	CTTTGGGTCG TGTCTTCAAC GTTC..CTT ATTACACCT TACTTAAAG	GTGGTAAAG 382			
	TT GATTGCTAT AAAATGGCG ATAACTCACA AAAAGTAGTA..TAAGGATA	CTTTGGGTCG TGTCTTCAAC GTTC..CTT ATTACACCT TACTTAAAG	GTGGTAAAG 383			
	TT GATTGCTAT AAAATGGCG ATAACTCACA AAAAGTAGTA..TAAGGATA	CTTTGGGTCG TGTCTTCAAC GTTC..CTT ATTACACCT TACTTAAAG	GTGGTAAAG 387			
	TT GATTGCTAT AAAATGGCG ATAACTCACA AAAAGTAGTA..TAAGGATA	CTTTGGGTCG TGTCTTCAAC GTTC..CTT ATTACACCT TACTTAAAG	GTGGTAAAG 381			
	TT GATTGCTAT AAAATGGCG ATAACTCACA AAAAGTAGTA..TAAGGATA	CTTTGGGTCG TGTCTTCAAC GTTC..CTT ATTACACCT TACTTAAAG	GTGGTAAAG 382			
	TT GATTGCTAT AAAATGGCG ATAACTCACA AAAAGTAGTA..TAAGGATA	CTTTGGGTCG TGTCTTCAAC GTTC..CTT ATTACACCT TACTTAAAG	GTGGTAAAG 383			
	TT GATTGCTAT AAAATGGCG ATAACTCACA AAAAGTAGTA..TAAGGATA	CTTTGGGTCG TGTCTTCAAC GTTC..CTT ATTACACCT TACTTAAAG	GTGGTAAAG 387			

The sequence numbering refers to the *Streptococcus agalactiae* tuf gene fragment (SEQ ID NO. 380). Nucleotides in capitals are identical to the selected sequences or match those sequences. Mismatches are indicated by lower-case letters. Dots indicate gaps in the sequences displayed.

^{a,b,c} These sequences were obtained from Genbank and have accession #: a=AB009314, d=AF001955, e=U31170, and f=V00311.

^d These sequences were obtained from genome sequencing projects.

^e These sequences are the reverse-complement of the selected primers.

Annex XI: Strategy for the selection of *Candida albicans*/dubliniensis-specific amplification primers, *Candida albicans*-specific hybridization probe and *Candida dubliniensis*-specific hybridization probe from tuf sequences.

5	337	368	403	428	460	491	SEQ ID NO.:	Accession #:
	CGTC AAGNAGGTTG GTTACAACCC AAGACTG...CAACATGA TTGAACCATC CACCAACT...C AATCCCGGTA AGTTACTGG TAAGACCTTG T						624	-
	CGTC AAGNAGGTTG GTTACAACCC AAGACTG...CAACATGA TTGAACCATC CACCAACT...C AATCCCGGTA AGTTACTGG TAAGACCTTG T						409	-
10	CGTC AAGNAGGTTG GTTACAACCC AAGACTG...CAACATGA TTGAACCATC CACCAACT...C AATCCCGGTA AGTTACTGG TAAGACCTTG T						410	-
	CGTC AAGNAGGTTG GTTACAACCC AAGACTG...CAACATGA TTGAACCATC CACCAACT...C AATCCCGGTA AGTTACTGG TAAGACCTTG T						407	-
	CGTC AAGNAGGTTG GTTACAACCC AAGACTG...CAACATGA TTGAACCATC CACCAACT...C AATCCCGGTA AGTTACTGG TAAGACCTTG T						408	-
	CGTC AAGNAGGTTG GTTACAACCC AAGACTG...CAACATGA TTGAACCATC CACCAACT...C AATCCCGGTA AGTTACTGG TAAGACCTTG T						412	-
	CGTC AAGNAGGTTG GTTACAACCC AAGACTG...CAACATGA TTGAACCATC CACCAACT...C AATCCCGGTA AGTTACTGG TAAGACCTTG T						414	-
	CGTC AAGNAGGTTG GTTACAACCC AAGACTG...CAACATGA TTGAACCATC CACCAACT...C AATCCCGGTA AGTTACTGG TAAGACCTTG T						415	-
15	CATC AAGNAGGTTG GTTACAACCC AAGACTG...CAACATGA TTGAACCATC CACCAACT...C AATCCCGGTA AGTTACTGG TAAGACCTTG T						417	-
	CATC AAGNAGGTTG GTTACAACCC AAGACTG...CAACATGA TTGAACCATC CACCAACT...C AATCCCGGTA AGTTACTGG TAAGACCTTG T						418	-
	CATC AAGNAGGTTG GTTACAACCC AAGACTG...CAACATGA TTGAACCATC CACCAACT...C AATCCCGGTA AGTTACTGG TAAGACCTTG T						421	-
	CATC AAGNAGGTTG GTTACAACCC AAGACTG...CAACATGA TTGAACCATC CACCAACT...C AATCCCGGTA AGTTACTGG TAAGACCTTG T						422	-
20	CATC AAGNAGGTTG GTTACAACCC AAGACTG...CAACATGA TTGAACCATC CACCAACT...C AATCCCGGTA AGTTACTGG TAAGACCTTG T						424	-
	CATC AAGNAGGTTG GTTACAACCC AAGACTG...CAACATGA TTGAACCATC CACCAACT...C AATCCCGGTA AGTTACTGG TAAGACCTTG T						623	-
	CATC AAGNAGGTTG GTTACAACCC AAGACTG...CAACATGA TTGAACCATC CACCAACT...C AATCCCGGTA AGTTACTGG TAAGACCTTG T						426	-
	CATC AAGNAGGTTG GTTACAACCC AAGACTG...CAACATGA TTGAACCATC CACCAACT...C AATCCCGGTA AGTTACTGG TAAGACCTTG T						429	-
	CATC AAGNAGGTTG GTTACAACCC AAGACTG...CAACATGA TTGAACCATC CACCAACT...C AATCCCGGTA AGTTACTGG TAAGACCTTG T						404	-
25	TATC AAGNAGGTTG GTTACAACCC AAGACTG...CAACATGA TTGAACCATC CACCAACT...C AATCCCGGTA AGTTACTGG TAAGACCTTG T						447	X03558
	TATC AAGNAGGTTG GTTACAACCC AAGACTG...CAACATGA TTGAACCATC CACCAACT...C AATCCCGGTA AGTTACTGG TAAGACCTTG T						622	-
	TATC AAGNAGGTTG GTTACAACCC AAGACTG...CAACATGA TTGAACCATC CACCAACT...C AATCCCGGTA AGTTACTGG TAAGACCTTG T						-	U042189

30 Selected sequence
for species-specific
amplification primer* C AAGNAGGTTG GTTACAACCC AAGA

35 Selected sequence
for species-specific
amplification primer**

40 Selected sequences
for species-specific
hybridization probes

CATGA TTGAACCATC CACCA (*C. albicans*)
CATGA TTGAAGCTTC CACCA (*C. dubliniensis*)

577
578

45 The sequence numbering refers to the *Candida albicans* tuf gene fragment (SEQ ID NO. 408). Nucleotides in capitals are identical to the selected sequences or match those sequences. Mismatches for SEQ ID NO. 577 are indicated by lower-case letters. Mismatches for SEQ ID NO. 578 are indicated by underlined nucleotides. Dots indicate gaps in the sequences displayed. "R" "y" "M" "K" "W" and "S" designate nucleotide positions which are degenerated. "R" stands for A or G; "y" stands for C or T; "M" stands for A or C; "K" stands for G or T; "W" stands for A or T; "S" stands for C or G. "I" stands for inosine which is a nucleotide analog that can bind to any of the four nucleotides A, C, G or T.

* *C. albicans* primers have been described in a previous patent (publication WO98/20157, SEQ ID NOS. 11-12)
* This sequence is the reverse-complement of the selected primer.

Annex XII: Strategy for the selection of Staphylococcus-specific amplification primers from tuf sequences.

		310	340	652	682	SEQ ID NO.:	Accession #:
5	<i>S. aureus</i>	A CAGCCCGTGT TGAACGTGGT CAATCAAG...CACTTACCA	GAAGTACTG	AAATGGTTAT	GC	179	-
	<i>S. aureus</i>	A CAGCCCGTGT TGAACGTGGT CAATCAAG...CACTTACCA	GAAGTACTG	AAATGGTTAT	GC	176	-
	<i>S. aureus</i>	A CAGCCCGTGT TGAACGTGGT CAATCAAG...CACTTACCA	GAAGTACTG	AAATGGTTAT	GC	177	-
	<i>S. aureus</i>	A CAGCCCGTGT TGAACGTGGT CAATCAAG...CACTTACCA	GAAGTACTG	AAATGGTTAT	GC	180	-
	<i>S. aureus</i>	A CAGCCCGTGT TGAACGTGGT CAATCAAG...CACTTACCA	GAAGTACTG	AAATGGTTAT	GC	181	-
10	<i>S. capitis capitis</i>	A CAGCCCGTGT TGAACGTGGT CAATCAAG...CACTTACCA	GAAGTACTG	AAATGGTTAT	GC	182	-
	<i>M. caseolyticus</i>	A CTGACCGTGT TGAACGTGGT CAATCAAG...CACTTACCA	GAAGTACTG	AAATGGTTAT	GC	183	-
	<i>S. cohnii</i>	A CAGCCCGTGT TGAACGTGGT CAATCAAG...CACTTACCA	GAAGTACTG	AAATGGTTAT	GC	184	-
	<i>S. epidermidis</i>	A CAGCCCGTGT TGAACGTGGT CAATCAAG...CACTTACCA	GAAGTACTG	AAATGGTTAT	GC	185	-
	<i>S. epidermidis</i>	A CAGCCCGTGT TGAACGTGGT CAATCAAG...CACTTACCA	GAAGTACTG	AAATGGTTAT	GC	141*	-
15	<i>S. haemolyticus</i>	A CAGCCCGTGT TGAACGTGGT CAATCAAG...CACTTACCA	GAAGTACTG	AAATGGTTAT	GC	186	-
	<i>S. haemolyticus</i>	A CAGCCCGTGT TGAACGTGGT CAATCAAG...CACTTACCA	GAAGTACTG	AAATGGTTAT	GC	188	-
	<i>S. haemolyticus</i>	A CAGCCCGTGT TGAACGTGGT CAATCAAG...CACTTACCA	GAAGTACTG	AAATGGTTAT	GC	189	-
	<i>S. hominis hominis</i>	A CAGCCCGTGT TGAACGTGGT CAATCAAG...CACTTACCA	GAAGTACTG	AAATGGTTAT	GC	191	-
20	<i>S. hominis</i>	A CAGCCCGTGT TGAACGTGGT CAATCAAG...CACTTACCA	GAAGTACTG	AAATGGTTAT	GC	193	-
	<i>S. hominis</i>	A CAGCCCGTGT TGAACGTGGT CAATCAAG...CACTTACCA	GAAGTACTG	AAATGGTTAT	GC	194	-
	<i>S. hominis</i>	A CAGCCCGTGT TGAACGTGGT CAATCAAG...CACTTACCA	GAAGTACTG	AAATGGTTAT	GC	195	-
	<i>S. hominis</i>	A CAGCCCGTGT TGAACGTGGT CAATCAAG...CACTTACCA	GAAGTACTG	AAATGGTTAT	GC	196	-
	<i>S. hominis</i>	A CAGCCCGTGT TGAACGTGGT CAATCAAG...CACTTACCA	GAAGTACTG	AAATGGTTAT	GC	197	-
	<i>S. lugdunensis</i>	A CAGCCCGTGT TGAACGTGGT CAATCAAG...CACTTACCA	GAAGTACTG	AAATGGTTAT	GC	198	-
25	<i>S. saprophyticus</i>	A CAGCCCGTGT TGAACGTGGT CAATCAAG...CACTTACCA	GAAGTACTG	AAATGGTTAT	GC	199	-
	<i>S. saprophyticus</i>	A CAGCCCGTGT TGAACGTGGT CAATCAAG...CACTTACCA	GAAGTACTG	AAATGGTTAT	GC	200	-
	<i>S. saprophyticus</i>	A CAGCCCGTGT TGAACGTGGT CAATCAAG...CACTTACCA	GAAGTACTG	AAATGGTTAT	GC	201	-
	<i>S. sciuri sciuri</i>	A CAGCCCGTGT TGAACGTGGT CAATCAAG...CACTTACCA	GAAGTACTG	AAATGGTTAT	GC	187	-
	<i>S. warneri</i>	A CAGCCCGTGT TGAACGTGGT CAATCAAG...CACTTACCA	GAAGTACTG	AAATGGTTAT	GC	192	-
30	<i>S. warneri</i>	A CAGCCCGTGT TGAACGTGGT CAATCAAG...CACTTACCA	GAAGTACTG	AAATGGTTAT	GC	202	-
	<i>S. warneri</i>	A CAGCCCGTGT TGAACGTGGT CAATCAAG...CACTTACCA	GAAGTACTG	AAATGGTTAT	GC	-	299104
	<i>B. subtilis</i>	A CTGACCGTGT TGAACGTGGT CAATCAAG...CACTTACCA	GAAGTACTG	AAATGGTTAT	GC	78	-
	<i>E. coli</i>	A CCGTCCGTGT TGAACGTGGT CAATCAAG...CACTTACCA	GAAGTACTG	AAATGGTTAT	GC	138*	-
35	<i>L. monocytogenes</i>	A CTGACCGTGT TGAACGTGGT CAATCAAG...CACTTACCA	GAAGTACTG	AAATGGTTAT	GC	553	-
	Selected sequence for genus-specific primer	GGCCCGTGT TGAACGTGGT CAATCA					
40	Selected sequences for genus-specific primers ^b		TTACCA GAAGTACTG AAATGGTTA			575	
			TTACCA GAAGTACTG AAATGGTTA			707	

The sequence numbering refers to the *Staphylococcus aureus* tuf gene fragment (SEQ ID NO. 179). Nucleotides in capitals are identical to the selected sequences or match those sequences. Mismatches are indicated by lower-case letters. "-" indicate incomplete sequence data. Dots indicate gaps in the sequences displayed.

"R" "Y" "N" "K" "W" and "S" designate nucleotide positions which are degenerated. "R" stands for A or G; "Y" stands for C or T; "N" stands for A or C; "K" stands for G or T; "W" stands for A or T; "S" stands for C or G. "I" stands for inosine which is a nucleotide analog that can bind to any of the four nucleotides A, C, G or T.

* The SEQ ID NO. refers to previous patent publication WO98/20157.
^b These sequences are the reverse-complement of the selected primers.

Annex XIII: Strategy for the selection of the Staphylococcus-specific hybridization probe from tuf s quences.

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		400	425	SEQ ID NO.:	Accession #:
	<i>S. aureus</i>	G TTGAAATGTT CCGTAAATTA TTAGA	179	-	
10	<i>S. aureus</i>	G TTGAAATGTT CCGTAAATTA TTAGA	176	-	
	<i>S. aureus</i>	G TTGAAATGTT CCGTAAATTA TTAGA	177	-	
	<i>S. aureus</i>	G TTGAAATGTT CCGTAAATTA TTAGA	178	-	
	<i>S. aureus aureus</i>	G TTGAAATGTT CCGTAAATTA TTAGA	180	-	
	<i>S. auricularis</i>	G TAGAAATGTT CCGTAAATTA TTAGA	181	-	
15	<i>S. capitis capitis</i>	G TAGAAATGTT CCGTAAATTA TTAGA	182	-	
	<i>M. caseolyticus</i>	G TAGAAATGTT CCGTAAATTA TTAGA	183	-	
	<i>S. cohnii</i>	G TAGAAATGTT CCGTAAATTA TTAGA	184	-	
	<i>S. epidermidis</i>	G TAGAAATGTT CCGTAAATTA TTAGA	185	-	
	<i>S. haemolyticus</i>	G TAGAAATGTT CCGTAAATTA TTAGA	186	-	
20	<i>S. haemolyticus</i>	G TAGAAATGTT CCGTAAATTA TTAGA	189	-	
	<i>S. haemolyticus</i>	G TAGAAATGTT CCGTAAATTA TTAGA	190	-	
	<i>S. haemolyticus</i>	G TAGAAATGTT CCGTAAATTA TTAGA	188	-	
	<i>S. hominis</i>	G TAGAAATGTT CCGTAAATTA TTAGA	196	-	
	<i>S. hominis</i>	G TAGAAATGTT CCGTAAATTA TTAGA	194	-	
25	<i>S. hominis hominis</i>	G TAGAAATGTT CCGTAAATTA TTAGA	191	-	
	<i>S. hominis</i>	G TAGAAATGTT CCGTAAATTA TTAGA	193	-	
	<i>S. hominis</i>	G TAGAAATGTT CCGTAAATTA TTAGA	195	-	
	<i>S. lugdunensis</i>	G TAGAAATGTT CCGTAAATTA TTAGA	197	-	
	<i>S. saprophyticus</i>	G TAGAAATGTT CCGTAAATTA TTAGA	198	-	
30	<i>S. saprophyticus</i>	G TAGAAATGTT CCGTAAATTA TTAGA	200	-	
	<i>S. saprophyticus</i>	G TAGAAATGTT CCGTAAATTA TTAGA	199	-	
	<i>S. sciuri sciuri</i>	G TTGAAATGTT CCGTAAATTA TTAGA	201	-	
	<i>S. warneri</i>	G TAGAAATGTT CCGTAAgTTA TTAGA	187	-	
	<i>S. warneri</i>	G TAGAAATGTT CCGTAAgTTA TTAGA	192	-	
35	<i>S. warneri</i>	G TAGAAATGTT CCGTAAgTTA TTAGA	202	-	
	<i>S. warneri</i>	G TAGAAATGTT CCGTAAgTTA TTAGA	203	-	
	<i>B. subtilis</i>	G TTGAAATGTT CCGTAAgCTt cTTGA	-	299104	
	<i>E. coli</i>	G TTGAAATGTT CCGcAAAcTg cTGGA	78	-	
40	<i>L. monocytogenes</i>	G TAGAAATGTT CCGTAAATTA cTAGA	138 ^a	-	
	Selected sequence for genus-specific hybridization probe			605	
		GAAATGTT CCGTAAATTA TT			

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The sequence numbering refers to the *Staphylococcus aureus* tuf gene fragment (SEQ ID NO. 179). Nucleotides in capitals are identical to the selected sequence or match that sequence. Mismatches are indicated by lower-case letters.

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^a The SEQ ID NO. refers to previous patent publication W098/20157.

Annex XIV: Strategy for the selection of *Staphylococcus saprophyticus*-specific and of *Staphylococcus haemolyticus*-specific hybridization probes from *tuf* sequences.

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							SEQ ID NO.:
10		339				383	
	<i>S. aureus</i>	AG TtGGTGAAGA	AgTtGAAATC	ATcGGTtTaC	ATGACACaTC	TAA	179
	<i>S. aureus</i>	AG TtGGTGAAGA	AgTtGAAATC	ATcGGTtTaC	ATGACACaTC	TAA	176
	<i>S. aureus</i>	AG TtGGTGAAGA	AgTtGAAATC	ATcGGTtTaC	ATGACACaTC	TAA	177
	<i>S. aureus</i>	AG TtGGTGAAGA	AgTtGAAATC	ATcGGTtTaC	ATGACACaTC	TAA	178
15	<i>S. aureus aureus</i>	AG TtGGTGAAGA	AgTtGAAATC	ATcGGTtTaC	ATGACACaTC	TAA	180
	<i>S. auricularis</i>	AG TCGGTGAAGA	AgTtGAAATC	ATcGGTATga	AaGACggTTC	AAA	181
	<i>S. capitis capitis</i>	AG TtGGTGAAGA	AgTtGAAATC	ATcGGTATCC	AcGAaACTTC	TAA	182
	<i>M. caseolyticus</i>	AG TtGGTGAAGA	AgTtGAAATC	ATTGGTtTaa	cTGAagaac	AAA	183
	<i>S. cohnii</i>	AG TCGGTGAAGA	AgTtGAAATC	ATcGGTATgC	AaGAagaTTC	CAA	184
20	<i>S. epidermidis</i>	AG TtGGTGAAGA	AgTtGAAATC	ATcGGTATgC	AcGAaACTTC	TAA	185
	<i>S. haemolyticus</i>	AG TtGGTGAAGA	AgTtGAAATC	ATTGGTATCC	ATGACACTTC	TAA	186
	<i>S. haemolyticus</i>	AG TtGGTGAAGA	AgTtGAAATC	ATTGGTATCC	ATGACACTTC	TAA	189
	<i>S. haemolyticus</i>	AG TtGGTGAAGA	AgTtGAAATC	ATTGGTATCC	ATGACACTTC	TAA	190
	<i>S. haemolyticus</i>	AG TtGGTGAAGA	AgTtGAAATt	ATTGGTATCa	AaGAaACTTC	TAA	188
25	<i>S. hominis</i>	AG TtGGTGAAGA	AgTtGAAATt	ATTGGTATCa	AaGAaACTTC	TAA	194
	<i>S. hominis hominis</i>	AG TtGGTGAAGA	AgTtGAAATt	ATTGGTATCa	AaGAaACTTC	TAA	191
	<i>S. hominis</i>	AG TtGGTGAAGA	AgTtGAAATt	ATTGGTATCa	AaGAaACTTC	TAA	193
	<i>S. hominis</i>	AG TtGGTGAAGA	AgTtGAAATt	ATTGGTATCa	AaGAaACTTC	TAA	195
	<i>S. hominis</i>	AG TtGGTGAAGA	AgTtGAAATt	ATTGGTATCa	AaGAtACTTC	TAA	196
30	<i>S. lugdunensis</i>	AG TCGGTGAAGA	AgTtGAAATt	ATTGGTATCC	AcGAtACTaC	TAA	197
	<i>S. saprophyticus</i>	AG TCGGTGAAGA	AATCGAAATC	ATcGGTATgC	AaGAagaATC	CAA	198
	<i>S. saprophyticus</i>	AG TCGGTGAAGA	AATCGAAATC	ATcGGTATgC	AaGAagaATC	CAA	200
	<i>S. saprophyticus</i>	AG TCGGTGAAGA	AATCGAAATC	ATcGGTATgC	AaGAagaATC	CAA	199
	<i>S. sciuri sciuri</i>	TG TtGGTGAAGA	AgTtGAAATC	ATcGGTtTaa	cTGAagaATC	TAA	201
35	<i>S. warneri</i>	AG TtGGTGAAGA	AgTtGAAATC	ATcGGTtTaC	ATGACACTTC	TAA	187
	<i>S. warneri</i>	AG TtGGTGAAGA	AgTtGAAATC	ATcGGTtTaC	ATGACACTTC	TAA	192
	<i>S. warneri</i>	AG TtGGTGAAGA	AgTtGAAATC	ATcGGTtTaC	ATGACACTTC	TAA	202
	<i>S. warneri</i>	AG TtGGTGAAGA	AgTtGAAATC	ATcGGTtTaC	ATGACACTTC	TAA	203
	<i>B. subtilis</i>	AG TCGGTGAAGA	AgTtGAAATC	ATcGGTcTtC	AaGAagagag	AAA	- ^a
40	<i>E. coli</i>	AG TtGGTGAAGA	AgTtGAAATC	gTTGGTATCa	AaGAgACTCa	GAA	78
	<i>L. monocytogenes</i>	AG TtGGTGAcGA	AgTaGAAGtT	ATcGGTATCg	AaGAagaaag	AAA	138 ^b

Selected sequences for
species-specific

45	hybridization probes	CGGTGAAGA AATCGAAATC A (<i>S. saprophyticus</i>)	599
		(<i>S. haemolyticus</i>) ATTGGTATCC ATGACACTTC	594

50 The sequence numbering refers to the *Staphylococcus aureus tuf* gene fragment (SEQ ID NO. 179). Nucleotides in capitals are identical to the selected sequences or match those sequences. Mismatches are indicated by lower-case letters.

^a This sequence was obtained from Genbank accession #Z99104.

^b The SEQ ID NO. refers to previous patent publication WO98/20157.

Annex XV: Strategy for the selection of *Staphylococcus aureus*-specific and of *Staphylococcus epidermidis*-specific hybridization probes from tuf sequences.

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		521	547	592	617	SEQ ID NO.:
10	<i>S. aureus</i>	TACACCACA TACTGAATTC AAAGCAG...TTCTTctCa AACTATCGtC CACAATT				179
	<i>S. aureus</i>	TACACCACA TACTGAATTC AAAGCAG...TTCTTctC- - - - -				178
	<i>S. aureus</i>	TACACCACA TACTGAATTC AAAGCAG...TTCTTctCa AACTATCGtC CACAATT				176
	<i>S. aureus</i>	TACACCACA TACTGAATTC AAAGCAG...TTCTTctCa AACTATCGtC CACAATT				177
	<i>S. aureus aureus</i>	TACACCACA TACTGAATTC AAAGCAG...TTCTTctCa AACTATCGtC CACAATT				180
15	<i>S. auricularis</i>	TACACCACA cACTaAATTC ActGCAG...TTCTTctCT AACTAcCGtC CACAATT				181
	<i>S. capitis capitis</i>	CACACCACA cACTaAATTC AAAGCGG...TTCTTCagT AACTAcCGCC CACAATT				182
	<i>M. caseolyticus</i>	TACTCCACA TACTaAATTC AAAGCTG...TTCTTCACT AACTAcCGCC CtCAGTT				183
	<i>S. cohnii</i>	TACACCACA cACaaAcTTt AAAGCGG...TTCTTCagT AACTATCGCC CACAATT				184
	<i>S. epidermidis</i>	TACACCACA cACaaAATTC AAAGCTG...TTCTTCACT AACTATCGCC CACAATT				185
20	<i>S. haemolyticus</i>	CACACCTCA cACaaAATTC AAAGCAG...TTCTTCaCa AACTATCGtC CACAATT				186
	<i>S. haemolyticus</i>	CACACCTCA cACaaAATTC AAAGCAG...TTCTTCaCa AACTATCGtC CACAATT				189
	<i>S. haemolyticus</i>	CACACCTCA cACaaAATTC AAAGCAG...TTCTTCaCa AACTATCGtC CACAATT				190
	<i>S. haemolyticus</i>	TACACCTCA cACaaAATTC AAAGCAG...TTCTTCACT AACTATCGtC CACAATT				188
	<i>S. hominis</i>	CACACCTCA cACaaAATTC AAAGCAG...TTCTTCACT AACTATCGtC CACAATT				195
25	<i>S. hominis</i>	TACACCTCA cACaaAATTC AAAGCAG...TTCTTCACT AACTATCGtC CACAATT				196
	<i>S. hominis hominis</i>	TACACCTCA cACaaAATTC AAAGCAG...TTCTTctCT AACTATCGtC CACAATT				191
	<i>S. hominis</i>	TACACCTCA cACaaAATTC AAAGCAG...TTCTTctCT AACTATCGtC CACAATT				193
	<i>S. hominis</i>	TACACCTCA cACaaAATTC AAAGCAG...TTCTTctCT AACTATCGtC CACAATT				194
	<i>S. lugdunensis</i>	TACACCTCA cACTaAATTC AAAGCTG...TTCTTctCa AACTAcCGCC CACAATT				197
30	<i>S. saprophyticus</i>	TACACCACA TACaaAATTC AAAGCGG...TTCTTCACT AACTAcCGCC CACAATT				198
	<i>S. saprophyticus</i>	TACACCACA TACaaAATTC AAAGCGG...TTCTTCACT AACTAcCGCC CACAATT				199
	<i>S. saprophyticus</i>	TACACCACA TACaaAATTC AAAGCGG...TTCTTCACT AACTAcCGCC CACAATT				200
	<i>S. sciuri sciuri</i>	CACACCTCA cACTaAATTC AAAGCTG...TTCTTCaCa AACTAcCGCC CACAATT				201
	<i>S. warneri</i>	TACACCACA TACaaAATTC AAAGCGG... - - - - -				192
35	<i>S. warneri</i>	TACACCACA TACaaAATTC AAAGCGG...TTCTTCagT AACTAcCGCC CACAATT				187
	<i>S. warneri</i>	TACACCACA TACaaAATTC AAAGCGG...TTCTTCagT AACTAcCGCC CACAATT				202
	<i>S. warneri</i>	TACACCACA TACaaAATTC AAAGCGG...TTCTTCagT AACTAcCGCC CACAATT				203
	<i>B. subtilis</i>	CACtCCACA cAgcaAATTC AAAGCTG...TTCTTctCT AACTAcCGtC CtCAGTT				- ^a
	<i>E. coli</i>	CAAgCCgCA cACcaAgTTC gAatCTG...TTCTTCAaa ggCTAcCGtC CgCAGTT				78
40	<i>L. monocytogenes</i>	TACTCCACA cACTaAcTTC AAAGCTG...TTCTTCAac AACTAcCGCC CACAATT				138 ^b
Selected sequences for species-specific hybridization probes						
45		ACCACA TACTGAATTC AAAG (<i>S. aureus</i>)				585
		(<i>S. epidermidis</i>) TTCACT AACTATCGCC CACA				593

The sequence numbering refers to the *Staphylococcus aureus* tuf gene fragment (SEQ ID NO. 179). Nucleotides in capitals are identical to the selected sequences or match those sequences. Mismatches are indicated by lower-case letters. "-" indicate incomplete sequence data. Dots indicate gaps in the sequences displayed.

^a This sequence was obtained from Genbank accession #Z99104.

^b The SEQ ID NO. refers to previous patent publication WO98/20157.

Annex XVI: Strategy for the selection of the *Staphylococcus hominis*-specific hybridization probe from *tuf* s quences.

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		358	383	SEQ ID NO.:
	<i>S. aureus</i>	ATC ATcGGTtTac	AtGAcACaTC TAA	179
10	<i>S. aureus</i>	ATC ATcGGTtTac	AtGAcACaTC TAA	176
	<i>S. aureus</i>	ATC ATcGGTtTac	AtGAcACaTC TAA	177
	<i>S. aureus</i>	ATC ATcGGTtTac	AtGAcACaTC TAA	178
	<i>S. aureus aureus</i>	ATC ATcGGTtTac	AtGAcACaTC TAA	180
	<i>S. auricularis</i>	ATC ATcGGTATgA	AAGAcggTTC AAA	181
15	<i>S. capitis capitis</i>	ATC ATcGGTATCc	AcGAAACTTC TAA	182
	<i>M. caseolyticus</i>	ATC ATTGGTtTaA	ctGAAGAaAC AAA	183
	<i>S. cohnii</i>	ATC ATcGGTATgc	AAGAgaATTC CAA	184
	<i>S. epidermidis</i>	ATC ATcGGTATgc	AcGAAACTTC TAA	185
	<i>S. haemolyticus</i>	ATC ATTGGTATCc	AtGAcACTTC TAA	186
20	<i>S. haemolyticus</i>	ATC ATTGGTATCc	AtGAcACTTC TAA	189
	<i>S. haemolyticus</i>	ATC ATTGGTATCc	AtGAcACTTC TAA	190
	<i>S. haemolyticus</i>	ATT ATTGGTATCA	AAGAACTTC TAA	188
	<i>S. hominis</i>	ATT ATTGGTATCA	AAGAtACTTC TAA	196
	<i>S. hominis</i>	ATT ATTGGTATCA	AAGAACTTC TAA	194
25	<i>S. hominis hominis</i>	ATT ATTGGTATCA	AAGAACTTC TAA	191
	<i>S. hominis</i>	ATT ATTGGTATCA	AAGAACTTC TAA	193
	<i>S. hominis</i>	ATT ATTGGTATCA	AAGAACTTC TAA	195
	<i>S. lugdunensis</i>	ATT ATTGGTATCc	AcGAtACTaC TAA	197
	<i>S. saprophyticus</i>	ATC ATcGGTATgc	AAGAgaATC CAA	198
30	<i>S. saprophyticus</i>	ATC ATcGGTATgc	AAGAgaATC CAA	200
	<i>S. saprophyticus</i>	ATC ATcGGTATgc	AAGAgaATC CAA	199
	<i>S. sciuri sciuri</i>	ATC ATcGGTtTaA	ctGAAGAaATC TAA	201
	<i>S. warneri</i>	ATC ATcGGTtTac	AtGAcACTTC TAA	187
	<i>S. warneri</i>	ATC ATcGGTtTac	AtGAcACTTC TAA	192
35	<i>S. warneri</i>	ATC ATcGGTtTac	AtGAcACTTC TAA	202
	<i>S. warneri</i>	ATC ATcGGTtTac	AtGAcACTTC TAA	203
	<i>B. subtilis</i>	ATC ATcGGTcTtc	AAGAagagag AAA	- ^a
	<i>E. coli</i>	ATC gTTGGTATCA	AAGagACTca GAA	78
	<i>L. monocytogenes</i>	GTT ATcGGTATCg	AAGAagaag AAA	138 ^b

40

Selected sequence for
species-specific
hybridization probe

ATTGGTATCA AAGAACTTC

597

45

The sequence numbering refers to the *Staphylococcus aureus tuf* gene fragment (SEQ ID NO. 179). Nucleotides in capitals are identical to the selected sequences or match those sequences. Mismatches are indicated by lower-case letters. Dots indicate gaps in the sequences displayed.

50

^a This sequence was obtained from Genbank accession #Z99104.

^b The SEQ ID NO. refers to previous patent publication WO98/20157.

Annex XVII: Strategy for the selection of the *Enterococcus*-specific primers from tuf sequences.

amplification

		270	298	556	582	SEQ ID NO.:	Accession #:
5	<i>E. avium</i>	TGAATTAAT	GGCTGCTGTT	GACGAATAT...TGAA	GATATCCAAC	GTGGACAAAGT	ATT
	<i>E. casseliflavus</i>	TGGAATTAAT	GGCTGCAAGT	GACGAATAT...TGAA	GACATCCAAC	GTGGACAAAGT	ATT
	<i>E. cecorum</i>	TGAATTAAT	GGCTGCAAGT	GACGAATAT...TGAA	GATATCCAAC	GTGGACAAAGT	ATT
	<i>E. dispar</i>	TGAATTAAT	GGCTGCAAGT	GACGAATAT...TGAA	GATATCCAAC	GTGGACAAAGT	ATT
	<i>E. durans</i>	TGAATTAAT	GGCTGCAAGT	GACGAATAT...TGAA	GATATCCAAC	GTGGACAAAGT	ATT
10	<i>E. flavescens</i>	TGGAATTAAT	GGCTGCAAGT	GACGAATAT...TGAA	GATATCCAAC	GTGGACAAAGT	ATT
	<i>E. faecium</i>	TGAATTAAT	GGCTGCAAGT	GACGAATAT...TGAA	GATATCCAAC	GTGGACAAAGT	ATT
	<i>E. faecalis</i>	TGAATTAAT	GGCTGCAAGT	GACGAATAT...TGAA	GATATCCAAC	GTGGACAAAGT	ATT
	<i>E. gallinarum</i>	TGAATTAAT	GGCTGCAAGT	GACGAATAT...TGAA	GATATCCAAC	GTGGACAAAGT	ATT
	<i>E. hirae</i>	TGAATTAAT	GGCTGCAAGT	GACGAATAT...TGAA	GATATCCAAC	GTGGACAAAGT	ATT
15	<i>E. mundtii</i>	TGAATTAAT	GGCTGCAAGT	GACGAATAT...TGAA	GATATCCAAC	GTGGACAAAGT	ATT
	<i>E. pseudosavium</i>	TGAATTAAT	GGCTGCAAGT	GACGAATAT...TGAA	GATATCCAAC	GTGGACAAAGT	ATT
	<i>E. raffinosus</i>	TGAATTAAT	GGCTGCAAGT	GACGAATAT...TGAA	GATATCCAAC	GTGGACAAAGT	ATT
	<i>E. saccharolyticus</i>	TGAATTAAT	GGCTGCAAGT	GACGAATAT...TGAA	GATATCCAAC	GTGGACAAAGT	ATT
	<i>E. solitarius</i>	TGAATTAAT	GGCTGCAAGT	GACGAATAT...TGAA	GATATCCAAC	GTGGACAAAGT	ATT
20	<i>E. coli</i>	TGAATTAAT	GGCTGCAAGT	GACGAATAT...TGAA	GATATCCAAC	GTGGACAAAGT	ATT
	<i>B. cepacia</i>	TGAATTAAT	GGCTGCAAGT	GACGAATAT...TGAA	GATATCCAAC	GTGGACAAAGT	ATT
	<i>B. fragilis</i>	TGAATTAAT	GGCTGCAAGT	GACGAATAT...TGAA	GATATCCAAC	GTGGACAAAGT	ATT
	<i>B. subtilis</i>	TGAATTAAT	GGCTGCAAGT	GACGAATAT...TGAA	GATATCCAAC	GTGGACAAAGT	ATT
	<i>C. diphtheriae</i>	TGAATTAAT	GGCTGCAAGT	GACGAATAT...TGAA	GATATCCAAC	GTGGACAAAGT	ATT
25	<i>C. trachomatis</i>	TGAATTAAT	GGCTGCAAGT	GACGAATAT...TGAA	GATATCCAAC	GTGGACAAAGT	ATT
	<i>S. aureus</i>	TGAATTAAT	GGCTGCAAGT	GACGAATAT...TGAA	GATATCCAAC	GTGGACAAAGT	ATT
	<i>S. pneumoniae</i>	TGAATTAAT	GGCTGCAAGT	GACGAATAT...TGAA	GATATCCAAC	GTGGACAAAGT	ATT
	<i>A. adiacens</i>	TGAATTAAT	GGCTGCAAGT	GACGAATAT...TGAA	GATATCCAAC	GTGGACAAAGT	ATT
30	<i>G. haemolysans</i>	TGAATTAAT	GGCTGCAAGT	GACGAATAT...TGAA	GATATCCAAC	GTGGACAAAGT	ATT
	<i>G. morbillorum</i>	TGAATTAAT	GGCTGCAAGT	GACGAATAT...TGAA	GATATCCAAC	GTGGACAAAGT	ATT

Selected sequence for amplification primer

AAATTAAT GGCTGCTGTT GATGAA

1137

Selected sequence for amplification primer^b

A GATATCCAAC GTGGACAAAGT

1136

The sequence numbering refers to the *Enterococcus* *durans* tuf gene fragment (SEQ ID NO. 61). Nucleotides in capitals are identical to the selected sequences or match those sequences. Mismatches are indicated by lower-case letters. Dots indicate gaps in the sequences displayed. "y", "w", and "s" designate nucleotide positions which are degenerated. "y" stands for C or T; "w" stands for A or T; "s" stands for C or G. "I" stands for inosine which is a nucleotide analog that can bind to any of the four nucleotides A, C, G or T.

^a The SEQ ID NO. refers to previous patent publication WO98/20157.

^b This sequence is the reverse-complement of the selected primer.

Annex XVIII: Strategy for the selection of the *Enterococcus faecalis*-specific hybridization probe, of the *Enterococcus faecium*-specific hybridization probe and of the *Enterococcus casseliflavus-flavescens-gallinarum* group-specific hybridization probe from tuf sequences.

5

		448...526	549	SEQ ID NO.:	Accession #:
395	<i>E. avium</i>	GTGGA ACCTGGACAA GTTCGCGTTG GTGACGAAAGT TGAATCGTGA GGTATCGCT...CATC GGTGCTTTGT TACGTGGTGT	131 ^a		-
	<i>E. casseliflavus</i>	GTGGA ACCTGGACAA GTTCGCGTTG GTGACGAAAGT TGAATCGTGA GGTATCGCT...CATC GGTGCTTTGT TACGTGGTGT	58		-
10	<i>E. cecorum</i>	GTGGA ACCTGGACAA GTTCGCGTTG GTGACGAAAGT TGAATCGTGA GGTATCGCT...CATC GGTGCTTTGT TACGTGGTGT	59		-
	<i>E. dispar</i>	GTGGA ACCTGGACAA GTTCGCGTTG GTGACGAAAGT TGAATCGTGA GGTATCGCT...CATC GGTGCTTTGT TACGTGGTGT	60		-
	<i>E. durans</i>	GTGGA ACCTGGACAA GTTCGCGTTG GTGACGAAAGT TGAATCGTGA GGTATCGCT...CATC GGTGCTTTGT TACGTGGTGT	61		-
	<i>E. faecalis</i>	GTGGA ACCTGGACAA GTTCGCGTTG GTGACGAAAGT TGAATCGTGA GGTATCGCT...CATC GGTGCTTTGT TACGTGGTGT	62		-
	<i>E. faecium</i>	GTGGA ACCTGGACAA GTTCGCGTTG GTGACGAAAGT TGAATCGTGA GGTATCGCT...CATC GGTGCTTTGT TACGTGGTGT	608		-
15	<i>E. flavescens</i>	GTGGA ACCTGGACAA GTTCGCGTTG GTGACGAAAGT TGAATCGTGA GGTATCGCT...CATC GGTGCTTTGT TACGTGGTGT	65		-
	<i>E. gallinarum</i>	GTGGA ACCTGGACAA GTTCGCGTTG GTGACGAAAGT TGAATCGTGA GGTATCGCT...CATC GGTGCTTTGT TACGTGGTGT	609		-
	<i>E. hirae</i>	GTGGA ACCTGGACAA GTTCGCGTTG GTGACGAAAGT TGAATCGTGA GGTATCGCT...CATC GGTGCTTTGT TACGTGGTGT	67		-
	<i>E. mundtii</i>	GTGGA ACCTGGACAA GTTCGCGTTG GTGACGAAAGT TGAATCGTGA GGTATCGCT...CATC GGTGCTTTGT TACGTGGTGT	68		-
20	<i>E. pseudovarium</i>	GTGGA ACCTGGACAA GTTCGCGTTG GTGACGAAAGT TGAATCGTGA GGTATCGCT...CATC GGTGCTTTGT TACGTGGTGT	69		-
20	<i>E. raffinosus</i>	GTGGA ACCTGGACAA GTTCGCGTTG GTGACGAAAGT TGAATCGTGA GGTATCGCT...CATC GGTGCTTTGT TACGTGGTGT	70		-
20	<i>E. saccharolyticus</i>	GTGGA ACCTGGACAA GTTCGCGTTG GTGACGAAAGT TGAATCGTGA GGTATCGCT...CATC GGTGCTTTGT TACGTGGTGT	71		-
20	<i>E. solitarius</i>	GTGGA ACCTGGACAA GTTCGCGTTG GTGACGAAAGT TGAATCGTGA GGTATCGCT...CATC GGTGCTTTGT TACGTGGTGT	72		-
20	<i>C. diphtheriae</i>	GTGGA ACCTGGACAA GTTCGCGTTG GTGACGAAAGT TGAATCGTGA GGTATCGCT...CATC GGTGCTTTGT TACGTGGTGT	662		-
25	<i>G. vaginalis</i>	GTGGA ACCTGGACAA GTTCGCGTTG GTGACGAAAGT TGAATCGTGA GGTATCGCT...CATC GGTGCTTTGT TACGTGGTGT	135 ^a		-
25	<i>B. cepacia</i>	GTGGA ACCTGGACAA GTTCGCGTTG GTGACGAAAGT TGAATCGTGA GGTATCGCT...CATC GGTGCTTTGT TACGTGGTGT	16		-
25	<i>S. aureus</i>	GTGGA ACCTGGACAA GTTCGCGTTG GTGACGAAAGT TGAATCGTGA GGTATCGCT...CATC GGTGCTTTGT TACGTGGTGT	179		-
30	<i>B. subtilis</i>	GTGGA ACCTGGACAA GTTCGCGTTG GTGACGAAAGT TGAATCGTGA GGTATCGCT...CATC GGTGCTTTGT TACGTGGTGT	-		299104
30	<i>S. pneumoniae</i>	GTGGA ACCTGGACAA GTTCGCGTTG GTGACGAAAGT TGAATCGTGA GGTATCGCT...CATC GGTGCTTTGT TACGTGGTGT	145 ^a		-
30	<i>E. coli</i>	GTGGA ACCTGGACAA GTTCGCGTTG GTGACGAAAGT TGAATCGTGA GGTATCGCT...CATC GGTGCTTTGT TACGTGGTGT	78		-
30	<i>B. fragilis</i>	GTGGA ACCTGGACAA GTTCGCGTTG GTGACGAAAGT TGAATCGTGA GGTATCGCT...CATC GGTGCTTTGT TACGTGGTGT	-		M22247
30	<i>C. trachomatis</i>	GTGGA ACCTGGACAA GTTCGCGTTG GTGACGAAAGT TGAATCGTGA GGTATCGCT...CATC GGTGCTTTGT TACGTGGTGT	22		-
35	Selected sequences for species-specific or group-specific hybridization probes	GA ACCTGGTGA GTTCGC (<i>E. faecalis</i>) AAGT TGAATGTTGT GGTATT (<i>E. faecium</i>) T GGTGCATTGC TACGTGG	1174 602 1122		

The sequence numbering refers to the *Enterococcus faecium* tuf gene fragments (SEQ ID NO. 608). Nucleotides in capitals are identical to the selected sequences or match those sequences. Mismatches are indicated by lower-case letters. Dots indicate gaps in the sequences displayed.

^a The SEQ ID NO. refers to previous patent publication WO98/20157.

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Annex XIX: Strategy for the selection of primers for the identification of platelets contaminants from tuf sequences.

		467	495	689	717	SEQ ID NO.:	Accession #:
5	<i>B. cereus</i>	GTA ACTGGTGTAG AGATGTTCCG TAAACT...C AGTTCTACTT	CGGTACAACT	GACGTAAAC	7	-	-
	<i>B. subtilis</i>	GTT ACAGGTGTTG AAATGTTCCG TAAAGT...C AGTTCTACTT	CCGTACAACT	GACGTAAAC	-	299104	-
	<i>E. cloacae</i>	TGT ACTGGCGTTG AAATGTTCCG CAAACT...C AGTTCTACTT	CCGTACAACT	GACGTGAC	54	-	-
10	<i>E. coli</i>	TGT ACTGGCGTTG AAATGTTCCG CAAACT...C AGTTCTACTT	CCGTACAACT	GACGTGAC	78	-	-
	<i>K. oxytoca</i>	TGT ACTGGCGTTG AAATGTTCCG CAAACT...C AGTTCTACTT	CCGTACAACT	GACGTGAC	100	-	-
	<i>K. pneumoniae</i>	TGT ACTGGCGTTG AAATGTTCCG CAAACT...C AGTTCTACTT	CCGTACAACT	GACGTGAC	103	-	-
	<i>P. aeruginosa</i>	TGC ACCGGCGTTG AAATGTTCCG CAAAGT...C AGTTCTACTT	CCGTACCACT	GACGTGAC	153	-	-
	<i>S. agalactiae</i>	GTT ACTGGTGTG AAATGTTCCG TAAACA...C AATTCTACTT	CCGTACAACT	GACGTAAAC	209	-	-
15	<i>S. aureus</i>	GTT ACAGGTGTTG AAATGTTCCG TAAAT...C AATTCTACTT	CCGTACAACT	GACGTAAAC	140 ^a	-	-
	<i>S. choleraesuis</i>	TGT ACTGGCGTTG AAATGTTCCG CAAACT...C AGTTCTACTT	CCGTACAACT	GACGTGAC	159	-	U040453
	<i>S. epidermidis</i>	GTT ACTGGTGTG AAATGTTCCG TAAAT...C AATTCTACTT	CCGTACAACT	GACGTAAAC	611	-	-
	<i>S. marcescens</i>	TGT ACTGGCGTTG AAATGTTCCG CAAACT...C AGTTCTACTT	CCGTACCACT	GACGTGAC	168	-	-
	<i>S. mutans</i>	GTT ACTGGTGTG AAATGTTCCG TAAACA...C AATTCTACTT	CCGTACAACT	GACGTAAAC	224	-	-
20	<i>S. pyogenes</i>	GTT ACTGGTGTG AAATGTTCCG TAAACA...C AATTCTACTT	CCGTACAACT	GACGTAAAC	-	-	-
	<i>S. salivarius</i>	GTT ACTGGTGTG AAATGTTCCG TAAACA...C AGTTCTACTT	CCGTACAACT	GACGTAAAC	146 ^a	-	-
	<i>S. sanguinis</i>	GTT ACTGGTGTG AAATGTTCCG TAAACA...C AGTTCTACTT	CCGTACAACT	GACGTAAAC	227	-	-
	<i>Y. enterocolitica</i>	TGT ACTGGCGTTG AAATGTTCCG CAAACT...C AGTTCTACTT	CCGTACAACT	GACGTAAAC	235	-	-
25	Selected sequence for amplification primer	ACTGGTGTG AAATGTTCCG YAA			636		
30	Selected sequence for amplification primer ^b		TTCCTAATTC	CCGTACAACT	637		

The sequence numbering refers to the *E. coli* tuf gene fragment (SEQ ID NO. 78). Nucleotides in capitals are identical to the selected sequences or match those sequences. Mismatches are indicated by lower-case letters. Dots indicate gaps in the sequences displayed.

"R" "Y" "M" "K" "W" and "S" designate nucleotide positions which are degenerated. "R" stands for A or G; "Y" stands for C or T; "M" stands for A or C; "K" stands for G or T; "W" stands for A or T; "S" stands for C or G. "I" stands for inosine which is a nucleotide analog that can bind to any of the four nucleotides A, C, G or T.

^a The SEQ ID NO. refers to previous patent publication WO98/20157.

^b This sequence is the reverse-complement of the selected primer.

Annex XX: Strategy for the selection of the universal amplification primers from *atpD* sequences.

		616	657	781	812	SEQ ID NO.:	Accession #:
5	<i>C. glutamicum</i>	GTGTTGGGTC AGATGATGA GGCACAGGA GTCCGTATG CGC...CGTATG	CGC...CGTATG	CCTTCGCGCG TGGGTACCA	GCCAAC	-	X76875
	<i>M. tuberculosis</i>	GTATTGGGAC AGATGACGA GCGCGGGGC ACCGTATG CGT...CGGATG	CGT...CGGATG	CCGTCGGCGG TGGGTACCA	GCCAC	291	273419
	<i>E. faecalis</i>	GTGTTGGGAC AGATGACGA ACCACAGGT GCTCGATG CGG...CGTATG	CGG...CGTATG	CCTTCGCGCG TGGGTACCA	ACCAAC	380	-
	<i>S. agalactiae</i>	GTCTTTGGTC AAATGAATGA ACCACAGGA GCACGTATG CGT...CGTATG	CGT...CGTATG	CCTTCAGCGG TGGGTATCA	ACCAAC	-	228592
10	<i>B. subtilis</i>	GTATTGGGTC AAATGAATGA GCGCGGGGC GCACGTATG CGT...CGTATG	CGT...CGTATG	CCTTCAGCGG TGGGTATCA	ACCAAC	324	-
	<i>L. monocytogenes</i>	GTATTGGGTC AAATGAATGA GCGCGGGGC GCACGTATG CGT...CGTATG	CGT...CGTATG	CCATCTGCGG TGGGTATCA	ACCAAC	366	-
	<i>S. aureus</i>	GTATTGGGTC AAATGAATGA GCGCGGGGC GCACGTATG CGT...CGTATG	CGT...CGTATG	CCTTCGCGG TGGGTATCA	ACCAAC	243	-
	<i>A. baumannii</i>	GTCTACGGTC AGATGAACGA GCCACAGGT AACCGTATG CGC...CGTATG	CGC...CGTATG	CCATCTGCGG TGGGTATCA	ACCTAC	264	-
	<i>N. gonorrhoeae</i>	GTCTATGGCC AGATGAACGA GCCACAGGT AACCGTATG CGC...CGTATG	CGC...CGTATG	CCTTCGCGG TGGGTATCA	ACCGAC	284	-
15	<i>C. freundii</i>	GTCTATGGCC AGATGAACGA GCCACAGGT AACCGTATG CGC...CGTATG	CGC...CGTATG	CCATCTGCGG TGGGTATCA	ACCGAC	669	-
	<i>E. cloacae</i>	GTCTATGGCC AGATGAACGA GCCACAGGT AACCGTATG CGC...CGTATG	CGC...CGTATG	CCTTCGCGG TGGGTATCA	ACCGAC	351	V00267
	<i>E. coli</i>	GTCTATGGCC AGATGAACGA GCCACAGGT AACCGTATG CGC...CGTATG	CGC...CGTATG	CCTTCGCGG TGGGTATCA	ACCGAC	317	-
	<i>S. typhimurium</i>	GTCTATGGCC AGATGAACGA GCCACAGGT AACCGTATG CGC...CGTATG	CGC...CGTATG	CCATCTGCGG TGGGTATCA	ACCGAC	357	-
	<i>K. pneumoniae</i>	GTCTATGGCC AGATGAACGA GCCACAGGT AACCGTATG CGC...CGTATG	CGC...CGTATG	CCATCTGCGG TGGGTATCA	ACCGAC	393	-
20	<i>S. marcescens</i>	GTCTATGGCC AGATGAACGA GCCACAGGT AACCGTATG CGC...CGTATG	CGC...CGTATG	CCATCTGCGG TGGGTATCA	ACCGAC	-	X76877
	<i>Y. enterocolitica</i>	GTCTATGGCC AGATGAACGA GCCACAGGT AACCGTATG CGC...CGTATG	CGC...CGTATG	CCATCTGCGG TGGGTATCA	ACCGAC	-	U32730
	<i>B. cepacia</i>	GTCTATGGCC AGATGAACGA GCCACAGGT AACCGTATG CGC...CGTATG	CGC...CGTATG	CCATCTGCGG TGGGTATCA	ACCGAC	-	U43738
	<i>H. influenzae</i>	GTCTATGGCC AGATGAACGA GCCACAGGT AACCGTATG CGC...CGTATG	CGC...CGTATG	CCATCTGCGG TGGGTATCA	ACCGAC	670	V00267
	<i>M. pneumoniae</i>	GTCTATGGCC AGATGAACGA GCCACAGGT AACCGTATG CGC...CGTATG	CGC...CGTATG	CCATCTGCGG TGGGTATCA	ACCGAC	-	M22247
25	<i>H. pylori</i>	GTCTATGGCC AGATGAACGA GCCACAGGT AACCGTATG CGC...CGTATG	CGC...CGTATG	CCATCTGCGG TGGGTATCA	ACCGAC	-	-
	<i>B. fragilis</i>	GTCTATGGCC AGATGAACGA GCCACAGGT AACCGTATG CGC...CGTATG	CGC...CGTATG	CCATCTGCGG TGGGTATCA	ACCGAC	-	-
30	Selected sequences for universal primers	C ARATGATGATG ACCACAGGT AACCGTATG TATGGGTC AGATGAATGA ACCACAGGT AACCGTATG					
	Selected sequences for universal primers*	ATH CCITCIGGTC TGGGTATCA RCC ATG CCITCIGGTC TGGGTATCA RCC					

35 The sequence numbering refers to the *Escherichia coli atpD* gene fragment (SEQ ID NO. 669). Nucleotides in capitals are identical to the selected sequences or match those sequences. Mismatches for SEQ ID NOS. 562 and 565 are indicated by lower-case letters. Mismatches for SEQ ID NOS. 564 and 563 are indicated by underlined nucleotides. Dots indicate gaps in the sequences displayed.

40 "R" "Y" "M" "K" "W" and "S" letters designate nucleotide positions which are degenerated. "R" stands for A or G; "Y" stands for C or T; "M" stands for A or C; "K" stands for G or T; "W" stands for A or T; "H" stands for A, C or T; "S" stands for C or G. "I" stands for inosine which is a nucleotide analog that can bind to any of the four nucleotides A, C, G or T.
 * These sequences are the reverse-complement of the selected primers.

Annex XXI: Specific and ubiquitous primers for nucleic acid amplification (rca sequences).

		Originating DNA fragment	
SEQ ID NO.	Nucleotide sequence	SEQ ID NO.	Nucleotide position
<hr/>			
10	Universal primers (recA)		
919	5'-GGI CCI GAR TCI TMI GGI AAR AC	918 ^a	437-459
920 ^b	5'-TCI CCV ATI TCI CCI TCI AIY TC	918 ^a	701-723
15			
921	5'-TIY RTI GAY GCI GAR CAI GC	918 ^a	515-534
922 ^b	5'-TAR AAY TTI ARI GCI YKI CCI CC	918 ^a	872-894
Sequencing primers (recA)			
20			
1605	5'-ATY ATY GAA RTI TAY GCI CC	1704 ^a	220-239
1606	5'-CCR AAC ATI AYI CCI ACT TTT TC	1704 ^a	628-650
Universal primers (rad51)			
25			
935	5'-GGI AAR WSI CAR YTI TGY CAY AC	939 ^a	568-590
936 ^b	5'-TCI SIY TCI GGI ARR CAI GG	939 ^a	1126-1145
Universal primers (dmc1)			
30			
937	5'-ATI ACI GAR GYI TTY GGI GAR TT	940 ^a	1038-1060
938 ^b	5'-CYI GTI GYI SWI GCR TGI GC	940 ^a	1554-1573

^a Sequences from databases.

^b These sequences are from the complementary DNA strand of the sequence of the originating fragment given in the Sequence Listing.

Annex XXII: Specific and ubiquitous primers for nucleic acid amplification (*speA* sequences).

5			Originating DNA fragment	
	SEQ ID NO.	Nucleotide sequence	SEQ ID NO.	Nucleotide position
10	<u>Bacterial species: <i>Streptococcus pyogenes</i></u>			
	994	5'-TGG ACT AAC AAT CTC GCA AGA GG	993 ^a	60-82
15	995 ^b	5'-ACA TTC TCG TGA GTA ACA GGG T	993 ^a	173-194
	996	5'-ACA AAT CAT GAA GGG AAT CAT TTA G	993 ^a	400-424
	997 ^b	5'-CTA ATT CTT GAG CAG TTA CCA TT	993 ^a	504-526
	998	5'-GGA GGG GTA ACA AAT CAT GAA GG	993 ^a	391-413
20	997 ^b	5'-CTA ATT CTT GAG CAG TTA CCA TT	993 ^a	504-526

^a Sequence from databases.

^b These sequences are from the complementary DNA strand of the sequence of the originating fragment given in the Sequence Listing.

Annex XXIII: First strategy for the selection of *Streptococcus pyogenes*-specific amplification primers from *speA* sequences.

Accession #	57	85	170	197	SEQ ID NO.:
5	speA X61573	CCATT GGCTTAACAA CCTCAAGA AGTAT...GTGACCCCT.GT	ggtTCACGAG AATGTAAA	-	-
	speA AF029051	----- GGCTTAACAA CCTCAAGA AGTAT...GTGACCCCT.GT	ggtTCACGAG AATGTAAA	-	-
	speA X61571	TCATT GGACTTAACAA TCTCGAAGA GGTAT...GTGACCCCT.GT	TACTCAGAG AATGTGAA	-	-
	speA X61570	TCATT GGACTTAACAA TCTCGAAGA GGTAT...GTGACCCCT.GT	TACTCAGAG AATGTGAA	-	-
	speA X61568	TCATT GGACTTAACAA TCTCGAAGA GGTAT...GTGACCCCT.GT	TACTCAGAG AATGTGAA	-	-
10	speA X61569	TCATT GGACTTAACAA TCTCGAAGA GGTAT...GTGACCCCT.GT	TACTCAGAG AATGTGAA	-	-
	speA X61572	TCATT GGACTTAACAA TCTCGAAGA GGTAT...GTGACCCCT.GT	TACTCAGAG AATGTGAA	-	-
	speA X61560	TCATT GGACTTAACAA TCTCGAAGA GGTAT...GTGACCCCT.GT	TACTCAGAG AATGTGAA	-	-
	speA U40453	TCATT GGACTTAACAA TCTCGAAGA GGTAT...GTGACCCCT.GT	TACTCAGAG AATGTGAA	-	-
	speA X61554	TCATT GGACTTAACAA TCTCGAAGA GGTAT...GTGACCCCT.GT	TACTCAGAG AATGTGAA	-	-
15	speA X61557	TCATT GGACTTAACAA TCTCGAAGA GGTAT...GTGACCCCT.GT	TACTCAGAG AATGTGAA	-	-
	speA X61559	TCATT GGACTTAACAA TCTCGAAGA GGTAT...GTGACCCCT.GT	TACTCAGAG AATGTGAA	-	-
	speA X61558	TCATT GGACTTAACAA TCTCGAAGA GGTAT...GTGACCCCT.GT	TACTCAGAG AATGTGAA	-	-
	speA X61556	TCATT GGACTTAACAA TCTCGAAGA GGTAT...GTGACCCCT.GT	TACTCAGAG AATGTGAA	-	-
	speA X61555	TCATT GGACTTAACAA TCTCGAAGA GGTAT...GTGACCCCT.GT	TACTCAGAG AATGTGAA	-	-
20	speA X61560	TCATT GGACTTAACAA TCTCGAAGA GGTAT...GTGACCCCT.GT	TACTCAGAG AATGTGAA	-	-
	speA X61561	TCATT GGACTTAACAA TCTCGAAGA GGTAT...GTGACCCCT.GT	TACTCAGAG AATGTGAA	-	-
	speA X61566	TCATT GGACTTAACAA TCTCGAAGA GGTAT...GTGACCCCT.GT	TACTCAGAG AATGTGAA	-	-
	speA X61567	TCATT GGACTTAACAA TCTCGAAGA GGTAT...GTGACCCCT.GT	TACTCAGAG AATGTGAA	-	-
	speA X61562	TCATT GGACTTAACAA TCTCGAAGA GGTAT...GTGACCCCT.GT	TACTCAGAG AATGTGAA	-	-
25	speA X61563	TCATT GGACTTAACAA TCTCGAAGA GGTAT...GTGACCCCT.GT	TACTCAGAG AATGTGAA	-	-
	speA X61564	TCATT GGACTTAACAA TCTCGAAGA GGTAT...GTGACCCCT.GT	TACTCAGAG AATGTGAA	-	-
	speA X61565	TCATT GGACTTAACAA TCTCGAAGA GGTAT...GTGACCCCT.GT	TACTCAGAG AATGTGAA	-	-
	speA AF055698	----- GGACTTAACAA TCTCGAAGA GGTAT...GTGACCCCT.GT	TACTCAGAG AATGTGAA	-	-
	speA X03929 ^a	TCATT GGACTTAACAA TCTCGAAGA AGGTA...GTGACCCCTGGT	TACTCAGAG AATGTGAA	-	-
30	Selected sequence for species-specific primer	T GGACTTAACAA TCTCGAAGA GG			994
35	Selected sequence for species-specific primer ^b	ACCCT.GT TACTCAGAG AATGT			995

The sequence numbering refers to the *Streptococcus pyogenes speA* gene fragment (SEQ ID NO. 993). Nucleotides in capitals are identical to the selected sequences or match those sequences. Mismatches are indicated by lower-case letters. "-" indicate incomplete sequence data. Dots indicate gaps in the sequences displayed.

^a The extra G nucleotide introducing a gap in the sequence is probably a sequencing error.

^b This sequence is the reverse-complement of the selected primer.

Annex XXIV: Second strategy for the selection of *Streptococcus pyogenes*-sp cific amplification primers from *speA* sequences.

Accession #	388	427	501	529	SEQ ID NO.:
5	<i>speA</i> X61573	TA TGGAGGGGTA ACAAAATCATG AAGGGATCA TTAGAAA...AAAAATGGT	TTAGAAA...AAAAATGGT	AACTGCTCAA GAATTAGACT	-
	<i>speA</i> AF029051	TA TGGAGGGGTA ACAAAATCATG AAGGGATCA TTAGAAA...AAAAATGGT	TTAGAAA...AAAAATGGT	AACTGCTCAA GAATTAGACT	-
	<i>speA</i> X61571	TA CGGAGGGGTA ACAAAATCATG AAGGGATCA TTAGAAA...AAAAATGGT	TTAGAAA...AAAAATGGT	AACTGCTCAA GAATTAGACT	-
	<i>speA</i> X61570	TA CGGAGGGGTA ACAAAATCATG AAGGGATCA TTAGAAA...AAAAATGGT	TTAGAAA...AAAAATGGT	AACTGCTCAA GAATTAGACT	-
	<i>speA</i> X61568	TA CGGAGGGGTA ACAAAATCATG AAGGGATCA TTAGAAA...AAAAATGGT	TTAGAAA...AAAAATGGT	AACTGCTCAA GAATTAGACT	-
10	<i>speA</i> X61569	TA CGGAGGGGTA ACAAAATCATG AAGGGATCA TTAGAAA...AAAAATGGT	TTAGAAA...AAAAATGGT	AACTGCTCAA GAATTAGACT	-
	<i>speA</i> X61572	TA CGGAGGGGTA ACAAAATCATG AAGGGATCA TTAGAAA...AAAAATGGT	TTAGAAA...AAAAATGGT	AACTGCTCAA GAATTAGACT	-
	<i>speA</i> X61560	TA CGGAGGGGTA ACAAAATCATG AAGGGATCA TTAGAAA...AAAAATGGT	TTAGAAA...AAAAATGGT	AACTGCTCAA GAATTAGACT	-
	<i>speA</i> U40453	TA CGGAGGGGTA ACAAAATCATG AAGGGATCA TTAGAAA...AAAAATGGT	TTAGAAA...AAAAATGGT	AACTGCTCAA GAATTAGACT	-
	<i>speA</i> X61554	TA CGGAGGGGTA ACAAAATCATG AAGGGATCA TTAGAAA...AAAAATGGT	TTAGAAA...AAAAATGGT	AACTGCTCAA GAATTAGACT	993
15	<i>speA</i> X61557	TA CGGAGGGGTA ACAAAATCATG AAGGGATCA TTAGAAA...AAAAATGGT	TTAGAAA...AAAAATGGT	AACTGCTCAA GAATTAGACT	-
	<i>speA</i> X61559	TA CGGAGGGGTA ACAAAATCATG AAGGGATCA TTAGAAA...AAAAATGGT	TTAGAAA...AAAAATGGT	AACTGCTCAA GAATTAGACT	-
	<i>speA</i> X61558	TA CGGAGGGGTA ACAAAATCATG AAGGGATCA TTAGAAA...AAAAATGGT	TTAGAAA...AAAAATGGT	AACTGCTCAA GAATTAGACT	-
	<i>speA</i> X61556	TA CGGAGGGGTA ACAAAATCATG AAGGGATCA TTAGAAA...AAAAATGGT	TTAGAAA...AAAAATGGT	AACTGCTCAA GAATTAGACT	-
	<i>speA</i> X61555	TA CGGAGGGGTA ACAAAATCATG AAGGGATCA TTAGAAA...AAAAATGGT	TTAGAAA...AAAAATGGT	AACTGCTCAA GAATTAGACT	-
20	<i>speA</i> X61560	TA CGGAGGGGTA ACAAAATCATG AAGGGATCA TTAGAAA...AAAAATGGT	TTAGAAA...AAAAATGGT	AACTGCTCAA GAATTAGACT	-
	<i>speA</i> X61561	TA CGGAGGGGTA ACAAAATCATG AAGGGATCA TTAGAAA...AAAAATGGT	TTAGAAA...AAAAATGGT	AACTGCTCAA GAATTAGACT	-
	<i>speA</i> X61566	TA CGGAGGGGTA ACAAAATCATG AAGGGATCA TTAGAAA...AAAAATGGT	TTAGAAA...AAAAATGGT	AACTGCTCAA GAATTAGACT	-
	<i>speA</i> X61567	TA CGGAGGGGTA ACAAAATCATG AAGGGATCA TTAGAAA...AAAAATGGT	TTAGAAA...AAAAATGGT	AACTGCTCAA GAATTAGACT	-
	<i>speA</i> X61562	TA CGGAGGGGTA ACAAAATCATG AAGGGATCA TTAGAAA...AAAAATGGT	TTAGAAA...AAAAATGGT	AACTGCTCAA GAATTAGACT	-
25	<i>speA</i> X61563	TA CGGAGGGGTA ACAAAATCATG AAGGGATCA TTAGAAA...AAAAATGGT	TTAGAAA...AAAAATGGT	AACTGCTCAA GAATTAGACT	-
	<i>speA</i> X61564	TA CGGAGGGGTA ACAAAATCATG AAGGGATCA TTAGAAA...AAAAATGGT	TTAGAAA...AAAAATGGT	AACTGCTCAA GAATTAGACT	-
	<i>speA</i> X61565	TA CGGAGGGGTA ACAAAATCATG AAGGGATCA TTAGAAA...AAAAATGGT	TTAGAAA...AAAAATGGT	AACTGCTCAA GAATTAGACT	-
	<i>speA</i> AF055698	TA CGGAGGGGTA ACAAAATCATG AAGGGATCA TTAGAAA...AAAAATGGT	TTAGAAA...AAAAATGGT	AACTGCTCAA GAATTAGACT	-
30	<i>speA</i> X03929	TA CGGAGGGGTA ACAAAATCATG AAGGGATCA TTAGAAA...AAAAATGGT	TTAGAAA...AAAAATGGT	AACTGCTCAA GAATTAGACT	-
Selected sequences for species-specific primers					998
					996
Selected sequence for species-specific primer*					997

The sequence numbering refers to the *Streptococcus pyogenes speA* gene fragment (SEQ ID NO. 993). Dots indicate gaps in the sequences displayed.

* This sequence is the reverse-complement of the selected primer.

Annex XXVII: Strategy for the selection of *stx*-specific amplification primers and hybridization probe.

5	stx1	M19473	543	570	614	641	684	708	SEQ ID NO.:				
	stx1	M16625	AGCGa	TgtTAcGgTt	TgtTAcTgTg	ACA...CAAC	ACTGgATgAT	ctcAgTgBgC	gtTcTtTA...A	AGgTgAgTA	gCgTcTgCC	tGAC	-
	stx1	M17358	AGCGa	TgtTAcGgTt	TgtTAcTgTg	ACA...CAAC	ACTGgATgAT	ctcAgTgBgC	gtTcTtTA...A	AGgTgAgTA	gCgTcTgCC	tGAC	-
	stx1	Z36900	AGCGa	TgtTAcGgTt	TgtTAcTgTg	ACA...CAAC	ACTGgATgAT	ctcAgTgBgC	gtTcTtTA...A	AGgTgAgTA	gCgTcTgCC	tGAT	-
	stx1	L04539	AGCGa	TgtTAcGgTt	TgtTAcTgTg	ACA...CAAC	ACTGgATgAT	ctcAgTgBgC	gtTcTtTA...A	AGgTgAgTA	gCgTcTgCC	tGAT	-
10	stx1	M19437	AGCGa	TgtTAcGgTt	TgtTAcTgTg	ACA...CAAC	ACTGgATgAT	ctcAgTgBgC	gtTcTtTA...A	AGgTgAgTA	gCgTcTgCC	tGAC	-
	stx1	M24352	AGCGa	TgtTAcGgTt	TgtTAcTgTg	ACA...CAAC	ACTGgATgAT	ctcAgTgBgC	gtTcTtTA...A	AGgTgAgTA	gCgTcTgCC	tGAC	-
	stx1	X07903	AGCGa	TgtTAcGgTt	TgtTAcTgTg	ACA...CAAC	ACTGgATgAT	ctcAgTgBgC	gtTcTtTA...A	AGgTgAgTA	gCgTcTgCC	tGAC	-
	stx1	Z36899	AGCGa	TgtTAcGgTt	TgtTAcTgTg	ACA...CAAC	ACTGgATgAT	ctcAgTgBgC	gtTcTtTA...A	AGgTgAgTA	gCgTcTgCC	tGAC	-
	stx1	Z36901	AGCGa	TgtTAcGgTt	TgtTAcTgTg	ACA...CAAC	ACTGgATgAT	ctcAgTgBgC	gtTcTtTA...A	AGgTgAgTA	gCgTcTgCC	tGAC	-
15	stx2	X61283	AGCAG	TtCTGCGTtT	TgtTAcTgTg	ACA...AGGC	ACTGtCTGtA	..AACTGCTC	CTGtGTtA...G	CGAATCAGCA	ATGtGCTTCC	GGAG	1076
	stx2	L11079	AGCAG	TtCTGCGTtT	TgtTAcTgTg	ACA...AGGC	ACTGtCTGtA	..AACTGCTC	CTGtGTtA...G	CGAATCAGCA	ATGtGCTTCC	GGAG	-
	stx2	M21534	AGCAG	TtCTGCGTtT	TgtTAcTgTg	ACA...TGGC	ACTGtCTGtA	..AACTGCTC	CTGtGTtA...G	CGAATCAGCA	ATGtGCTTCC	GGAG	-
	stx2	M36727	AGCAG	TtCTGCGTtT	TgtTAcTgTg	ACA...TGGC	ACTGtCTGtA	..AACTGCTC	CTGtGTtA...G	CGAATCAGCA	ATGtGCTTCC	GGAG	-
20	stx2	U72191	AGCAG	TtCTGCGTtT	TgtTAcTgTg	ACA...TGGC	ACTGtCTGtA	..AACTGCTC	CTGtGTtA...G	CGAATCAGCA	ATGtGCTTCC	GGAG	-
	stx2	X81415	AGCAG	TtCTGCGTtT	TgtTAcTgTg	ACA...TGGC	ACTGtCTGtA	..AACTGCTC	CTGtGTtA...G	CGAATCAGCA	ATGtGCTTCC	GGAG	-
	stx2	X81416	AGCAG	TtCTGCGTtT	TgtTAcTgTg	ACA...TGGC	ACTGtCTGtA	..AACTGCTC	CTGtGTtA...G	CGAATCAGCA	ATGtGCTTCC	GGAG	-
	stx2	X81417	AGCAG	TtCTGCGTtT	TgtTAcTgTg	ACA...TGGC	ACTGtCTGtA	..AACTGCTC	CTGtGTtA...G	CGAATCAGCA	ATGtGCTTCC	GGAG	-
25	stx2	X81418	AGCAG	TtCTGCGTtT	TgtTAcTgTg	ACA...TGGC	ACTGtCTGtA	..AACTGCTC	CTGtGTtA...G	CGAATCAGCA	ATGtGCTTCC	GGAG	-
	stx2	E03962	AGCAG	TtCTGCGTtT	TgtTAcTgTg	ACA...AGGC	ACTGtCTGtA	..AACTGCTC	CTGtGTtA...G	CGAATCAGCA	ATGtGCTTCC	GGAG	-
	stx2	E03959	AGCAG	TtCTGCGTtT	TgtTAcTgTg	ACA...AGGC	ACTGtCTGtA	..AACTGCTC	CTGtGTtA...G	CGAATCAGCA	ATGtGCTTCC	GGAG	-
	stx2	X07865	AGCAG	TtCTGCGTtT	TgtTAcTgTg	ACA...AGGC	ACTGtCTGtA	..AACTGCTC	CTGtGTtA...G	CGAATCAGCA	ATGtGCTTCC	GGAG	-
	stx2	Y10775	AGCAG	TtCTGCGTtT	TgtTAcTgTg	ACA...AGGC	ACTGtCTGtA	..AACTGCTC	CTGtGTtA...G	CGAATCAGCA	ATGtGCTTCC	GGAG	-
30	stx2	Z37725	AGCAG	TtCTGCGTtT	TgtTAcTgTg	ACA...AGGC	ACTGtCTGtA	..AACTGCTC	CTGtGTtA...G	CGAATCAGCA	ATGtGCTTCC	GGAG	1077
	stx2	Z50754	AGCAG	TtCTGCGTtT	TgtTAcTgTg	ACA...AGGC	ACTGtCTGtA	..AACTGCTC	CTGtGTtA...G	CGAATCAGCA	ATGtGCTTCC	GGAG	-
	stx2	X67514	AGCAG	TtCTGCGTtT	TgtTAcTgTg	ACA...AGGC	ACTGtCTGtA	..AACTGCTC	CTGtGTtA...G	CGAATCAGCA	ATGtGCTTCC	GGAG	-
	stx2	L11078	AGCAG	TtCTGCGTtT	TgtTAcTgTg	ACA...AGGC	ACTGtCTGtA	..AACTGCTC	CTGtGTtA...G	CGAATCAGCA	ATGtGCTTCC	GGAG	-
	stx2	X65949	AGCAG	TtCTGCGTtT	TgtTAcTgTg	ACA...AGGC	ACTGtCTGtA	..AACTGCTC	CTGtGTtA...G	CGAATCAGCA	ATGtGCTTCC	GGAG	-
35	stx2	AF043627	AGCAG	TtCTGCGTtT	TgtTAcTgTg	ACA...TGGC	ACTGtCTGtA	..AACTGCTC	CTGtGTtA...G	CGAATCAGCA	ATGtGCTTCC	GGAG	-
	Selected sequence for amplification primer												
	AG	TtCTGCGTtT	TgtTAcTgTg										1078
40	Selected sequence for hybridization probe												
	C	ACTGtCTGtA	..AACTGCTC	CTGt									1085
	Selected sequence for amplification primer												
	AAATCAGCA	ATGtGCTTCC	G										1079

The sequence numbering refers to the *Escherichia coli stx* gene fragment (SEQ ID NO. 1077). Nucleotides in capitals are identical to the selected sequences or match those sequences. Mismatches are indicated by lower-case letters. Dots indicate gaps in the sequences displayed. This sequence is the reverse-complement of the selected primer.

Annex XXVIII: Strategy for the selection of vanA-specific amplification primers from van sequences.

	Accession #	926	952	1230	1255	SEQ ID NO.:
5	vanA X56895	GTCAT AGCGCGGACG AATTGGACTA C...GT AGAGGTCTAG CCCGTGTGGA TATG				1139
	vanA M97297	GTCAT AGCGCGGACG AATTGGACTA C...GT AGAGGTCTAG CCCGTGTGGA TATG				1141
	-	GTCAT AGCGCGGACG AATTGGACTA C...GT AGAGGTCTAG CCCGTGTGGA TATG				1051
	-	GTCAT AGCGCGGACG AATTGGACTA C...GT AGAGGTCTAG CCCGTGTGGA TATG				1052
	-	GTCAT AGCGCGGACG AATTGGACTA C...GT AGAGGTCTAG CCCGTGTGGA TATG				1053
10	vanA -	GTCAT AGCGCGGACG AATTGGACTA C...GT AGAGGTCTAG CCCGTGTGGA TATG				1054
	-	GTCAT AGCGCGGACG AATTGGACTA C...GT AGAGGTCTAG CCCGTGTGGA TATG				1055
	-	GTCAT AGCGCGGACG AATTGGACTA C...GT AGAGGTCTAG CCCGTGTGGA TATG				1056
	-	GTCAT AGCGCGGACG AATTGGACTA C...GT AGAGGTCTAG CCCGTGTGGA TATG				1057
15	vanA -	GTCAT AGCGCGGACG AATTGGACTA C...GT AGAGGTCTAG CCCGTGTGGA TATG				1049
	-	GTCAT AGCGCGGACG AATTGGACTA C...GT AGAGGTCTAG CCCGTGTGGA TATG				1050
	-	GTCAT AGCGCGGACG AATTGGACTA C...GT AGAGGTCTAG CCCGTGTGGA TATG				1117
	vanB U94526	GTAAC gGtaCGGAAG AActTaaACGC T...GC AGAGGgCTtG CCCGTGTGGA TCtt				-
	vanB U94527	GTAAC gGtaCGGAAG AActTaaACGC T...GC AGAGGgCTtG CCCGTGTGGA TCtt				-
	vanB U94528	GTAAC gGtaCGGAAG AActTaaACGC T...GC AGAGGgCTtG CCCGTGTGGA TCtt				-
	vanB U94529	GTAAC gGtaCGGAAG AActTaaACGC T...GC AGAGGgCTtG CCCGTGTGGA TCtt				-
	vanB U94530	GTAAC gGtaCGGAAG AActTaaACGC T...GC AGAGGgCTtG CCCGTGTGGA TCtt				-
20	vanB Z83305	GTAAC gGtaCGGAAG AActTaaACGC T...GC AGAGGgCTtG CCCGTGTGGA TCtt				-
	vanB U81452	GTAAC gGtaCGGAAG AActTaaACGC T...GC AGAGGgCTtG CCCGTGTGGA TCtt				-
	vanB U35369	GTAAC gGtaCGGAAG AActTaaACGC T...GC AGAGGgCTtG CCCGTGTGGA TCtt				-
	vanB U72704	GTAAC gGtaCGGAAG AActTaaACGC T...GC AGAGGgCTtG CCCGTGTGGA TCtt				-
25	vanB L06138	GTAAC gGtaCGGAAG AActTaaACGC T...GC AGAGGgCTtG CCCGTGTGGA TCtt				-
	vanB L15304	GTAAC gGtaCGGAAG AActTaaACGC T...GC AGAGGgCTtG CCCGTGTGGA TCtt				-
	vanB U00456	GTAAC gGtaCGGAAG AActTaaACGC T...GC AGAGGgCTtG CCCGTGTGGA TCtt				-
	vanD AF130997	GTAatc AagGCaGaaG AActGcAgGC A...GC AGAGGgCTtG CCCGaatGGA cCTG				-
30	vanE AF136925	GTAga caaaaaagtG AtTtatAtAA A...GC AaAGGatTAG CgaGaaTcGA cTTT				-
	Selected sequence for amplification primer	AAT AGCGCGGACG AATTGGAC				1090
35	Selected sequence for amplification primer ^a	GAGGTCTAG CCCGTGTGGA T				1089

The sequence numbering refers to the *Enterococcus faecium* vanA gene fragment (SEQ ID NO. 1139). Nucleotides in capitals are identical to the selected sequences or match those sequences. Mismatches are indicated by lower-case letters. Dots indicate gaps in the sequences displayed.

^a This sequence is the reverse-complement of the above selected primer.

Annex XXIX: Strategy for the selection of vanB-specific amplification primers from van sequences.

	Accession #	470	495	608	633	SEQ ID NO.:			
5	vanA	X56895	A CGCaATTGAA	tCGGCAAGAC	AAATAT...ACG	GaATCTTTCCG	tATtCATCAG	GAA	1139
	vanA	M97297	A CGCaATTGAA	tCGGCAAGAC	AAATAT...ACG	GaATCTTTCCG	tATtCATCAG	GAA	1141
	vanA	-	A CGCaATTGAA	tCGGCAAGAC	AAATAT...ACG	GaATCTTTCCG	tATtCATCAG	GAA	1051
	vanA	-	A CGCaATTGAA	tCGGCAAGAC	AAATAT...ACG	GaATCTTTCCG	tATtCATCAG	GAA	1052
10	vanA	-	A CGCaATTGAA	tCGGCAAGAC	AAATAT...ACG	GaATCTTTCCG	tATtCATCAG	GAA	1053
	vanA	-	A CGCaATTGAA	tCGGCAAGAC	AAATAT...ACG	GaATCTTTCCG	tATtCATCAG	GAA	1054
	vanA	-	A CGCaATTGAA	tCGGCAAGAC	AAATAT...ACG	GaATCTTTCCG	tATtCATCAG	GAA	1055
	vanA	-	A CGCaATTGAA	tCGGCAAGAC	AAATAT...ACG	GaATCTTTCCG	tATtCATCAG	GAA	1056
15	vanA	-	A CGCaATTGAA	tCGGCAAGAC	AAATAT...ACG	GaATCTTTCCG	tATtCATCAG	GAA	1057
	vanA	-	A CGCaATTGAA	tCGGCAAGAC	AAATAT...ACG	GaATCTTTCCG	tATtCATCAG	GAA	1049
	vanA	-	A CGCaATTGAA	tCGGCAAGAC	AAATAT...ACG	GaATCTTTCCG	tATtCATCAG	GAA	1050
	vanB	U94526	C TCGGATAGAA	GCgGCAGGAC	AAATAT...ACG	GTATCTTTCCG	CATCCATCAG	GAA	1117
20	vanB	U94527	C TCGGATAGAA	GCgGCAGGAC	AAATAT...ACG	GTATCTTTCCG	CATCCATCAG	GAA	-
	vanB	U94528	C TCGGATAGAA	GCgGCAGGAC	AAATAT...ACG	GTATCTTTCCG	CATCCATCAG	GAA	-
	vanB	U94529	C TCGGATAGAA	GCgGCAGGAC	AAATAT...ACG	GTATCTTTCCG	CATCCATCAG	GAA	-
	vanB	U94530	C TCGGATAGAA	GCgGCAGGAC	AAATAT...ACG	GTATCTTTCCG	CATCCATCAG	GAA	-
25	vanB	Z83305	C TCGGATAGAA	GCgGCAGGAC	AAATAT...ACG	GTATCTTTCCG	CATCCATCAG	GAA	-
	vanB	U81452	C TCGGATAGAA	GCgGCAGGAC	AAATAT...ACG	GTATCTTTCCG	CATCCATCAG	GAA	-
	vanB	U35369	C TCGGATAGAA	GCAGCAGGAC	AAATAT...ACG	GTATCTTTCCG	CATCCATCAG	GAA	-
	vanB	U72704	C TCGGATAGAA	GCgGCAGGAC	AAATAT...ATG	GTATCTTTCCG	CATCCATCAG	GAA	-
30	vanB	L06138	C TCGGATAGAA	GCAGCAGGAC	AAATAT...ACG	GTATCTTTCCG	CATCCATCAG	GAA	-
	vanB	L15304	C TCGGATAGAA	GCgGCAGGAC	AAATAT...ACG	GTATCTTTCCG	CATCCATCAG	GAA	-
	vanB	U00456	C TCGGATAGAA	GCAGCAGGAC	AAATAT...ACG	GTATCTTTCCG	CATCCATCAG	GAA	-
	vanD	AF130997	C AGCaATcGAA	GaAGCAAGAA	AAATAT...ACG	GctTtTtTtaa	gATtCATCAG	GAA	-
30	vanE	AF136925	A AGCaATAGAC	GaAGCtttcaa	AAATAT...ATG	GctTtTtTtCGa	CtatgAagAG	AAA	-
	Selected sequence for amplification primer		CGATAGAA	GCAGCAGGAC	AA				1095
35	Selected sequence for amplification primer ^a					GTATCTTTCCG	CATCCATCAG		1096

The sequence numbering refers to the *Enterococcus faecium* vanB gene fragment (SEQ ID NO. 1117). Nucleotides in capitals are identical to the selected sequences or match those sequences. Mismatches are indicated by lower-case letters. Dots indicate gaps in the sequences displayed.

^a This sequence is the reverse-complement of the above vanB sequence.

Annex XXX: Strategy for the selection of vanC-specific amplification primers from vanC sequences.

	Accession #	929	957	1064	1092	SEQ ID NO.:
5	vanC1	-	GT CGACGGTTTT	AAGAGAA...ACGGGTC	TGGCTCGAAT CGATTTTTTC	1058
	vanC1	-	GT CGACGGTTTT	AAGAGAA...ACGGGTC	TGGCTCGAAT CGATTTTTTC	1059
	vanC1	M75132	GT CGACGGTTTT	AAGAGAA...ACGGGTC	TGGCTCGAAT CGATTTTTTC	1138
	vanC2	-	GT AGACGGCITT	AAAGAAA...AAAGGTC	TGCTCGCAT CGACTTTTTT	1060
	vanC2	-	GT AGACGGCITT	AAAGAAA...AAAGGTC	TGCTCGCAT CGACTTTTTT	1061
10	vanC2	-	GT AGACGGCITT	AAAGAAA...AAAGGTC	TGCTCGCAT CGACTTTTTT	1062
	vanC2	-	GT AGACGGCITT	AAAGAAA...AAAGGTC	TGCTCGCAT CGACTTTTTT	1063
	vanC2	L29638	GT AGACGGCITT	AAAGAAA...AAAGGTC	TGCTCGCAT CGACTTTTTT	-
	vanC2	L29638	GT AGACGGCITT	AAAGAAA...AAAGGTC	TGCTCGCAT CGACTTTTTT	-
	vanC3	-	GT AGACGGCITT	AAAGAAA...AAAGGTC	TGCTCGCAT CGACTTTTTT	1064
15	vanC3	-	GT AGACGGCITT	AAAGAAA...AAAGGTC	TGCTCGCAT CGACTTTTTT	1065
	vanC3	-	GT AGACGGCITT	AAAGAAA...AAAGGTC	TGCTCGCAT CGACTTTTTT	1066
	vanC3	L29639	GT AGACGGCITT	AAAGAAA...AAAGGTC	TGCTCGCAT CGACTTTTTT	-
20	Selected sequence for r	sistance primer	GACGGYTTT	TTTGATTTTG	AAGA	1101
	Selected sequence for resistance primer ^a		GGTC	TKGCTCGMAT	CGAYTTTTT	1102

25 The sequence numbering refers to the vanC1 gene fragment (SEQ ID NO. 1138). Nucleotides in capitals are identical to the selected sequences or match those sequences. Mismatches are indicated by lower-case letters. Dots indicate gaps in the sequence displayed.

30 "R" "Y" "M" "K" "W" and "S" designate nucleotide positions which are degenerated. "R" stands for A or G; "Y" stands for C or T; "M" stands for A or C; "K" stands for G or T; "W" stands for A or T; "S" stands for C or G. "I" stands for inosine which is a nucleotide analog that can bind to any of the four nucleotides A, C, G or T.

^a This sequence is the reverse-complement of the selected sequence.

Annex XXXI: Strategy for the selection of *Streptococcus pneumoniae*-specific amplification primers and hybridization probes from *pbp1a* sequences.

[illegible]

The sequence numbering refers to the *Streptococcus pneumoniae pbp1a* gene fragment (SEQ ID NO. 1004). Nucleotides in capitals are identical to the selected sequences or match those sequences. Mismatches are indicated by lower-case letters. Dots indicate gaps in the sequences displayed.

"R" "Y" "N" "K" "W" and "S" designate nucleotide positions which are degenerated. "R" stands for A or G; "Y" stands for C or T; "N" stands for A or C; "K" stands for G or T; "W" stands for A or T; "H" stands for A, C or T; "S" stands for C or G. "I" stands for inosine which is a nucleotide analog that can bind to any of the four nucleotides A, C, G or T.

Annex XXI: Strategy for the selection of *Streptococcus pneumoniae*-specific amplification primers and hybridization probes from *pbpla* sequences (continued).

Accession #	756	783	813	840	SEQ ID NO.:
5	<i>pbpla</i> M90528	...GCTGGTAA	ACTGGGTACT	TCTAACTATA...A ATACGGGTTA	TGTAGCTCCG GATGAAA
	<i>pbpla</i> X67873	...GCTGGTAA	ACACGGGACC	TCTAACTATA...A CCTCTCAAT	TGTAGCTCCG GATGAAAC
	<i>pbpla</i> AB006868	...GCTGGTAA	ACACGGGACC	TCTAACTATA...A CCTCTCAAT	TGTAGCTCCG GATGAAAC
	<i>pbpla</i> AF046234	...GCAGGTAA	ACACGGGTACT	TCTAACTATA...A ACCTCTGGTTA	CGTAGCTCCA GATGAAA
10	<i>pbpla</i> AB006873	...GCAGGTAA	ACACGGGTACT	TCTAACTATA...A ACCTCTGGTTA	CGTAGCTCCA GATGAAA
	<i>pbpla</i> AF139883	...GCTGGTAA	ACACGGGACC	TCTAACTATA...A ACCTCTGGTTA	CGTAGCTCCA GATGAAA
	<i>pbpla</i> X67873	...GCTGGTAA	ACACGGGACC	TCTAACTATA...A ACCTCTGGTTA	CGTAGCTCCA GATGAAA
	<i>pbpla</i> X67873	...GCTGGTAA	ACACGGGACC	TCTAACTATA...A ACCTCTGGTTA	CGTAGCTCCA GATGAAA
15	<i>pbpla</i> X67873	...GCTGGTAA	ACACGGGACC	TCTAACTATA...A ACCTCTGGTTA	CGTAGCTCCA GATGAAA
	<i>pbpla</i> X67873	...GCTGGTAA	ACACGGGACC	TCTAACTATA...A ACCTCTGGTTA	CGTAGCTCCA GATGAAA
	<i>pbpla</i> X67873	...GCTGGTAA	ACACGGGACC	TCTAACTATA...A ACCTCTGGTTA	CGTAGCTCCA GATGAAA
20	<i>pbpla</i> X67873	...GCTGGTAA	ACACGGGACC	TCTAACTATA...A ACCTCTGGTTA	CGTAGCTCCA GATGAAA
	<i>pbpla</i> X67873	...GCTGGTAA	ACACGGGACC	TCTAACTATA...A ACCTCTGGTTA	CGTAGCTCCA GATGAAA
	<i>pbpla</i> X67873	...GCTGGTAA	ACACGGGACC	TCTAACTATA...A ACCTCTGGTTA	CGTAGCTCCA GATGAAA
25	<i>pbpla</i> X67873	...GCTGGTAA	ACACGGGACC	TCTAACTATA...A ACCTCTGGTTA	CGTAGCTCCA GATGAAA
	<i>pbpla</i> X67873	...GCTGGTAA	ACACGGGACC	TCTAACTATA...A ACCTCTGGTTA	CGTAGCTCCA GATGAAA
	<i>pbpla</i> X67873	...GCTGGTAA	ACACGGGACC	TCTAACTATA...A ACCTCTGGTTA	CGTAGCTCCA GATGAAA
30	<i>pbpla</i> X67873	...GCTGGTAA	ACACGGGACC	TCTAACTATA...A ACCTCTGGTTA	CGTAGCTCCA GATGAAA
	<i>pbpla</i> X67873	...GCTGGTAA	ACACGGGACC	TCTAACTATA...A ACCTCTGGTTA	CGTAGCTCCA GATGAAA
	<i>pbpla</i> X67873	...GCTGGTAA	ACACGGGACC	TCTAACTATA...A ACCTCTGGTTA	CGTAGCTCCA GATGAAA
35	<i>pbpla</i> X67873	...GCTGGTAA	ACACGGGACC	TCTAACTATA...A ACCTCTGGTTA	CGTAGCTCCA GATGAAA
	<i>pbpla</i> X67873	...GCTGGTAA	ACACGGGACC	TCTAACTATA...A ACCTCTGGTTA	CGTAGCTCCA GATGAAA
	<i>pbpla</i> X67873	...GCTGGTAA	ACACGGGACC	TCTAACTATA...A ACCTCTGGTTA	CGTAGCTCCA GATGAAA
40	<i>pbpla</i> X67873	...GCTGGTAA	ACACGGGACC	TCTAACTATA...A ACCTCTGGTTA	CGTAGCTCCA GATGAAA
	<i>pbpla</i> X67873	...GCTGGTAA	ACACGGGACC	TCTAACTATA...A ACCTCTGGTTA	CGTAGCTCCA GATGAAA
	<i>pbpla</i> X67873	...GCTGGTAA	ACACGGGACC	TCTAACTATA...A ACCTCTGGTTA	CGTAGCTCCA GATGAAA
45	<i>pbpla</i> X67873	...GCTGGTAA	ACACGGGACC	TCTAACTATA...A ACCTCTGGTTA	CGTAGCTCCA GATGAAA
	<i>pbpla</i> X67873	...GCTGGTAA	ACACGGGACC	TCTAACTATA...A ACCTCTGGTTA	CGTAGCTCCA GATGAAA
	<i>pbpla</i> X67873	...GCTGGTAA	ACACGGGACC	TCTAACTATA...A ACCTCTGGTTA	CGTAGCTCCA GATGAAA

ACTGGGTAA YGTAGCTCCA GATG

The sequence numbering refers to the *Streptococcus pneumoniae pbpla* gene fragment (SEQ ID NO. 1004). Nucleotides in capitals are identical to the selected sequences or match those sequences. Mismatches are indicated by lower case letters. Dots indicate gaps in the sequences displayed. "R" indicates incomplete sequence data. "R", "Y", "W" and "S" designate nucleotide positions which are degenerated. "R" stands for A or G; "Y" stands for C or T; "W" stands for A or T; "S" stands for C or G. "I" stands for inosine which is a nucleotide analog that can bind to any of the four nucleotides A, C, G or T. This sequence is the reverse-complement of the selected primer.

Annex XXXII: Specific and ubiquitous primers for nucleic acid amplification (toxin sequences).

5	SEQ ID NO.	Nucleotide sequence	Originating DNA fragment	
			SEQ ID NO.	Nucleotide position
10	<u>Toxin gene:</u>	<i>cdtA</i>		
	2123	5'-TCT ACC ACT GAA GCA TTA C	2129 ^a	442-460
	2124 ^b	5'-TAG GTA CTG TAG GTT TAT TG	2129 ^a	580-599
15	<u>Toxin gene:</u>	<i>cdtB</i>		
	2126	5'-ATA TCA GAG ACT GAT GAG	2130 ^a	2665-2682
	2127 ^b	5'-TAG CAT ATT CAG ACA ATA TTG T	2130 ^a	2746-2767
20	<u>Toxin gene:</u>	<i>stx₁</i>		
	1081	5'-ATG TCA GAG GGA TAG ATC CA	1076 ^a	233-252
	1080 ^b	5'-TAT AGC TAC TGT CAC CAG ACA ATG T	1076 ^a	394-418
25	<u>Toxin gene:</u>	<i>stx₂</i>		
	1078	5'-AGT TCT GCG TTT TGT CAC TGT C	1077 ^a	546-567
	1079 ^b	5'-CGG AAG CAC ATT GCT GAT T	1077 ^a	687-705
30	<u>Toxin genes:</u>	<i>stx₁</i> and <i>stx₂</i>		
	1082	5'-TTG ARC RAA ATA ATT TAT ATG TG	1076 ^a	278-300
	1083 ^b	5'-TGA TGA TGR CAA TTC AGT AT	1076 ^a	781-800
35				

^a Sequences from databases.

^b These sequences are from the complementary DNA strand of the sequence of the originating fragment given in the Sequence Listing.

Annex XXXIII: Molecular beacon internal hybridization probes for specific detection of toxin sequences.

		Originating DNA fragment	
SEQ ID NO.	Nucleotide sequence ^a	SEQ ID NO.	Nucleotide position
<hr/>			
<u>Toxin gene:</u> <i>cdtA</i>			
2125 ^b	5'-CAC GCG GAT TTT GAA TCT CTT CCT CTA GTA GCG CGT G	2129 ^c	462-488
<u>Toxin gene:</u> <i>cdtB</i>			
2128	5'-CAA CGC TGG AGA ATC TAT ATT TGT AGA AAC TGC GTT G	2130 ^c	2714-2740
<u>Toxin gene:</u> <i>stx₁</i>			
1084	5'-CCA CGC CGC TTT GCT GAT TTT TCA CAT GTT ACC GCG TGG	1076 ^c	337-363
2012 ^d	5'-CCG CGG ATT ATT AAA CCG CCC TTC CGC GG-MR-HEG-ATG TCA GAG GGA TAG ATC CA	1076 ^c	248-264
<u>Toxin gene:</u> <i>stx₂</i>			
1085	5'-CCA CGC CAC TGT CTG AAA CTG CTC CTG TG CGT GG	1077 ^c	617-638

^a Underlined nucleotides indicate the molecular beacon's stem.

^b These sequences are from the complementary DNA strand of the sequence of the originating fragment given in the Sequence Listing.

^c Sequences from databases.

^d Scorpion primer.

Annex XXXIV: Specific and ubiquitous primers for nucleic acid amplification (van sequences).

5			Originating DNA fragment	
	SEQ ID NO.	Nucleotide sequence	SEQ ID NO.	Nucleotide position
10	<u>Resistance gene:</u> vanA			
	1086	5'-CTA CTC CCG CCT TTT GGG TT	1049-1057 ^a	513-532 ^b
	1087 ^c	5'-CTC ACA GCC CGA AAC AGC CT	1049-1057 ^a	699-718 ^b
15	1086	5'-CTA CTC CCG CCT TTT GGG TT	1049-1057 ^a	513-532 ^b
	1088 ^c	5'-TGC CGT TTC CTG TAT CCG TC	1049-1057 ^a	885-904 ^b
20	1086	5'-CTA CTC CCG CCT TTT GGG TT	1049-1057 ^a	513-532 ^b
	1089 ^c	5'-ATC CAC ACG GGC TAG ACC TC	1049-1057 ^a	933-952 ^b
	1090	5'-AAT AGC GCG GAC GAA TTG GAC	1049-1057 ^a	629-649 ^b
	1091 ^c	5'-AAC GCG GCA CTG TTT CCC AA	1049-1057 ^a	734-753 ^b
25	1090	5'-AAT AGC GCG GAC GAA TTG GAC	1049-1057 ^a	629-649 ^b
	1089 ^c	5'-ATC CAC ACG GGC TAG ACC TC	1049-1057 ^a	933-952 ^b
	1092	5'-TCG GCA AGA CAA TAT GAC AGC	1049-1057 ^a	662-682 ^b
	1088 ^c	5'-TGC CGT TTC CTG TAT CCG TC	1049-1057 ^a	885-904 ^b
30	<u>Resistance gene:</u> vanB			
	1095	5'-CGA TAG AAG CAG CAG GAC AA	1117 ^d	473-492
	1096 ^c	5'-CTG ATG GAT GCG GAA GAT AC	1117 ^d	611-630
35	<u>Resistance genes:</u> vanA, vanB			
	1112	5'-GGC TGY GAT ATT CAA AGC TC	1049-1057,1117 ^a	437-456 ^b
	1113 ^c	5'-ACC GAC CTC ACA GCC CGA AA	1049-1057,1117 ^a	705-724 ^b
40	1112	5'-GGC TGY GAT ATT CAA AGC TC	1049-1057,1117 ^a	437-456 ^b
	1114 ^c	5'-TCW GAG CCT TTT TCC GGC TCG	1049-1057,1117 ^a	817-837 ^b
5	1115	5'-TTT CGG GCT GTG AGG TCG GBT GHG CG	1049-1057,1117 ^a	705-730 ^b
	1114 ^c	5'-TCW GAG CCT TTT TCC GGC TCG	1049-1057,1117 ^a	817-837 ^b
	1116	5'-TTT CGG GCT GTG AGG TCG GBT GHG CGG	1049-1057,1117 ^a	705-731 ^b
	1114 ^c	5'-TCW GAG CCT TTT TCC GGC TCG	1049-1057,1117 ^a	817-837 ^b
10	1112	5'-GGC TGY GAT ATT CAA AGC TC	1049-1057,1117 ^a	437-456 ^b
	1118 ^c	5'-TTT TCW GAG CCT TTT TCC GGC TCG	1049-1057,1117 ^a	817-840 ^b

^a These sequences were aligned to derive the corresponding primer.

^b The nucleotide positions refer to the vanA sequence fragment (SEQ ID NO. 1051).

^c These sequences are from the complementary DNA strand of the sequence of the originating fragment given in the Sequence Listing.

^d Sequences from databases.

Annex XXXIV: Specific and ubiquitous primers for nucleic acid amplification (van sequence s) (continued).

5			Originating DNA fragment	
	SEQ ID NO.	Nucleotide sequence	SEQ ID NO.	Nucleotide position
10	Resistance genes: vanA, vanB (continued)			
	1115	5'-TTT CGG GCT GTG AGG TCG GBT GHG CG	1049-1057,1117 ^a	705-730 ^b
	1118 ^c	5'-TTT TCW GAG CCT TTT TCC GGC TCG	1049-1057,1117 ^a	817-840 ^b
15	1116	5'-TTT CGG GCT GTG AGG TCG GBT GHG CGG	1049-1057,1117 ^a	705-731 ^b
	1118 ^c	5'-TTT TCW GAG CCT TTT TCC GGC TCG	1049-1057,1117 ^a	817-840 ^b
	1119	5'-TTT CGG GCT GTG AGG TCG GBT GHG C	1049-1057,1117 ^a	705-729 ^b
20	1118 ^c	5'-TTT TCW GAG CCT TTT TCC GGC TCG	1049-1057,1117 ^a	817-840 ^b
	1120	5'-TTT CGG GCT GTG AGG TCG GBT GHG	1049-1057,1117 ^a	705-728 ^b
	1118 ^c	5'-TTT TCW GAG CCT TTT TCC GGC TCG	1049-1057,1117 ^a	817-840 ^b
	1121	5'-TGT TTG WAT TGT CYG GYA TCC C	1049-1057,1117 ^a	408-429 ^b
25	1111 ^c	5'-CTT TTT CCG GCT CGW YTT CCT GAT G	1049-1057,1117 ^a	806-830 ^b
	1112	5'-GGC TGY GAT ATT CAA AGC TC	1049-1057,1117 ^a	437-456 ^b
	1111 ^c	5'-CTT TTT CCG GCT CGW YTT CCT GAT G	1049-1057,1117 ^a	806-830 ^b
30	1123	5'-TTT CGG GCT GTG AGG TCG GBT G	1049-1057,1117 ^a	705-726 ^b
	1111 ^c	5'-CTT TTT CCG GCT CGW YTT CCT GAT G	1049-1057,1117 ^a	806-830 ^b
	1112	5'-GGC TGY GAT ATT CAA AGC TC	1049-1057,1117 ^a	437-456 ^b
35	1124 ^c	5'-GAT TTG RTC CAC YTC GCC RAC A	1049-1057,1117 ^a	757-778 ^b
	Resistance gene: vanC1			
	1103	5'-ATC CCG CTA TGA AAA CGA TC	1058-1059 ^a	519-538 ^d
40	1104 ^c	5'-GGA TCA ACA CAG TAG AAC CG	1058-1059 ^a	678-697 ^d
	Resistance genes: vanC1, vanC2, vanC3			
	1097	5'-TCY TCA AAA GGG ATC ACW AAA GTM AC	1058-1066 ^a	607-632 ^d
45	1098 ^c	5'-TCT TCA AAA TCG AAA AAG CCG TC	1058-1066 ^a	787-809 ^d
	1099	5'-TCA AAA GGG ATC ACW AAA GTM AC	1058-1066 ^a	610-632 ^d
	1100 ^c	5'-GTA AAK CCC GGC ATR GTR TTG ATT TC	1058-1066 ^a	976-1001 ^d
	1101	5'-GAC GGY TTT TTY GAT TTT GAA GA	1058-1066 ^a	787-809 ^d
50	1102 ^c	5'-AAA AAR TCG ATK CGA GCM AGA CC	1058-1066 ^a	922-944 ^d
	Resistance genes: vanC2, vanC3			
	1105	5'-CTC CTA CGA TTC TCT TGA YAA ATC A	1060-1066,1140 ^a	487-511 ^e
55	1106 ^c	5'-CAA CCG ATC TCA ACA CCG GCA AT	1060-1066,1140 ^a	690-712 ^e

^a These sequences were aligned to derive the corresponding primer.

^b The nucleotide positions refer to the vanA sequence fragment (SEQ ID NO. 1051).

60 ^c These sequences are from the complementary DNA strand of the sequence of the originating fragment given in the Sequence Listing.

^d The nucleotide positions refer to the vanC1 sequence fragment (SEQ ID NO. 1058).

^e The nucleotide positions refer to the vanC2 sequence fragment (SEQ ID NO. 1140).

Annex XXXIV: Specific and ubiquitous primers for nucleic acid amplification (van sequences) (continued).

5			Originating DNA fragment	
	SEQ ID NO.	Nucleotide sequence	SEQ ID NO.	Nucleotide position
10	Resistance gene: <i>vanD</i>			
	1591	5'-ATG AGG TAA TAG AAC GGA TT	1594	797-837
	1592 ^b	5'-CAG TAT TTC AGT AAG CGT AAA	1594	979-999
15	Resistance gene: <i>vanE</i>			
	1595	5'-AAA TAA TGC TCC ATC AAT TTG CTG A	1599 ^a	74-98
	1596 ^b	5'-ATA GTC GAA AAA GCC ATC CAC AAG	1599 ^a	394-417
20	1597	5'-GAT GAA TTT GCG AAA ATA CAT GGA	1599 ^a	163-186
	1598 ^b	5'-CAG CCA ATT TCT ACC CCT TTC AC	1599 ^a	319-341
	Sequencing primers (<i>vanAB</i>)			
25	1112	5'-GGC TGY GAT ATT CAA AGC TC	1139 ^a	737-756
	1111 ^b	5'-CTT TTT CCG GCT CGW YTT CCT GAT G	1139 ^a	1106-1130
	Sequencing primers (<i>vanA</i>, <i>vanX</i>, <i>vanY</i>)			
30	1150	5'-TGA TAA TCA CAC CGC ATA CG	1141 ^a	860-879
	1151 ^b	5'-TGC TGT CAT ATT GTC TTG CC	1141 ^a	1549-1568
	1152	5'-ATA AAG ATG ATA GGC CGG TG	1141 ^a	1422-1441
	1153 ^b	5'-CTC GTA TGT CCC TAC AAT GC	1141 ^a	2114-2133
35	1154	5'-GTT TGA AGC ATA TAG CCT CG	1141 ^a	2520-2539
	1155 ^b	5'-CAG TGC TTC ATT AAC GTA GTC	1141 ^a	3089-3109
40				

^a Sequences from databases.

^b These sequences are from the complementary DNA strand of the sequence of the originating fragment given in the Sequence Listing.

Annex XXXIV: Specific and ubiquitous primers for nucleic acid amplification (van sequences) (continued).

5			Originating DNA fragment	
	SEQ ID NO.	Nucleotide sequence SEQ ID	Nucleotide NO.	position
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10	Sequencing primers (vanC1)			
	1110	5'-ACG AGA AAG ACA ACA GGA AGA CC	1138 ^a	122-144
	1109 ^b	5'-ACA TCG TGA TCG CTA AAA GGA GC	1138 ^a	1315-1337
15	Sequencing primers (vanC2, vanC3)			
	1108	5'-GTA AGA ATC GGA AAA GCG GAA GG	1140 ^a	1-23
	1107 ^b	5'-CTC ATT TGA CTT CCT CCT TTG CT	1140 ^a	1064-1086

20

^a Sequences from databases.

^b These sequences are from the complementary DNA strand of the sequence of the originating fragment given in the Sequence Listing.

Annex XXXV: Internal hybridization probes for specific detection of van sequences.

5			Originating DNA fragment	
	SEQ ID NO.	Nucleotide sequence	SEQ ID NO.	Nucleotide position
10	Resistance gene: <i>vanA</i>			
	1170	5'-ACG AAT TGG ACT ACG CAA TT	1049-1057 ^a	639-658 ^b
	2292	5'-GAA TCG GCA AGA CAA TAT G	2293 ^c	583-601
15	Resistance gene: <i>vanB</i>			
	1171	5'-ACG AGG ATG ATT TGA TTG TC	1117 ^c	560-579
	2294	5'-AAA CGA GGA TGA TTT GAT TG	2296 ^a	660-679
20	2295	5'-TTG AGC AAG CGA TTT CGG	2296 ^a	614-631
	Resistance gene: <i>vanD</i>			
25	2297	5'-TTC AGG AGG GGG ATC GC	1594 ^c	458-474

^a These sequences were aligned to derive the corresponding primer.

^b The nucleotide positions refer to the *vanA* sequence fragment (SEQ ID NO. 1051).

^c Sequences from databases.

Annex XXXVI: Specific and ubiquitous primers for nucleic acid amplification (pbp sequences).

			Originating DNA fragment	
5	SEQ ID NO.	Nucleotide sequence	SEQ ID NO.	Nucleotide position
10	<u>Resistance gene:</u> <i>pbp1a</i>			
	1129	5'-ATG ATG ACH GAM ATG ATG AAA AC	1004-1018 ^a	681-703 ^b
	1131 ^c	5'-CAT CTG GAG CTA CRT ARC CAG T	1004-1018 ^a	816-837 ^b
15	1130	5'-GAC TAT CCA AGC ATG CAT TAT G	1004-1018 ^a	456-477 ^b
	1131	5'-CAT CTG GAG CTA CRT ARC CAG T	1004-1018 ^a	816-837 ^b
	2015	5'-CCA AGA AGC TCA AAA ACA TCT G	2047 ^d	909-930
20	2016 ^c	5'-TAD CCT GTC CAW ACA GCC AT	2047 ^d	1777-1796
	Sequencing primers (<i>pbp1a</i>)			
	1125	5'-ACT CAC AAC TGG GAT GGA TG	1169 ^d	873-892
25	1126 ^c	5'-TTA TGG TTG TGC TGG TTG AGG	1169 ^d	2140-2160
	1125	5'-ACT CAC AAC TGG GAT GGA TG	1169 ^d	873-892
	1128 ^c	5'-GAC GAC YTT ATK GAT ATA CA	1169 ^d	1499-1518
30	1127	5'-KCA AAY GCC ATT TCA AGT AA	1169 ^d	1384-1403
	1126 ^c	5'-TTA TGG TTG TGC TGG TTG AGG	1169 ^d	2140-2160
	Sequencing primers (<i>pbp2b</i>)			
35	1142	5'-GAT CCT CTA AAT GAT TCT CAG GTG G	1172 ^d	1-25
	1143 ^c	5'-CAA TTA GCT TAG CAA TAG GTG TTG G	1172 ^d	1481-1505
	1142	5'-GAT CCT CTA AAT GAT TCT CAG GTG G	1172 ^d	1-25
	1145 ^c	5'-AAC ATA TTK GGT TGA TAG GT	1172 ^d	793-812
40	1144	5'-TGT YTT CCA AGG TTC AGC TC	1172 ^d	657-676
	1143 ^c	5'-CAA TTA GCT TAG CAA TAG GTG TTG G	1172 ^d	1481-1505
	Sequencing primers (<i>pbp2x</i>)			
45	1146	5'-GGG ATT ACC TAT GCC AAT ATG AT	1173 ^d	219-241
	1147 ^c	5'-AGC TGT GTT AGC VCG AAC ATC TTG	1173 ^d	1938-1961
50	1146	5'-GGG ATT ACC TAT GCC AAT ATG AT	1173 ^d	219-241
	1149 ^c	5'-TCC YAC WAT TTC TTT TTG WG	1173 ^d	1231-1250
	1148	5'-GAC TTT GTT TGG CGT GAT AT	1173 ^d	711-730
	1147 ^c	5'-AGC TGT GTT AGC VCG AAC ATC TTG	1173 ^d	1938-1961

55

^a These sequences were aligned to derive the corresponding primer.

^b The nucleotide positions refer to the *pbp1a* sequence fragment (SEQ ID NO. 1004).

^c These sequences are from the complementary DNA strand of the sequence of the originating fragment given in the Sequence Listing.

50

^d Sequences from databases.

Annex XXXVII: Internal hybridization probes for specific detection of pbp sequences.

5			Originating DNA fragment	
	SEQ ID NO.	Nucleotide sequence	SEQ ID NO.	Nucleotide position
10	Resistance gene: <i>pbplA</i>			
15	1132	5'-AGT GAA AAR ATG GCT GCT GC	1004-1018 ^a	531-550 ^b
	1133	5'-CAT CAA GAA CAC TGG CTA YGT AG	1004-1018 ^a	806-828 ^b
	1134	5'-CTA GAT AGA GCT AAA ACC TTC CT	1004-1018 ^a	417-439 ^b
	1135	5'-CAT TAT GCA AAC GCC ATT TCA AG	1004-1018 ^a	471-493 ^b
	1192	5'-GGT AAA ACA GGA ACC TCT AAC T	1004-1018 ^a	759-780 ^b
20	1193	5'-GGT AAG ACA GGT ACT TCT AAC T	1004-1018 ^a	759-780 ^b
	1194	5'-CAT TTC AAG TAA TAC AAC AGA ATC	1004-1018 ^a	485-508 ^b
	1195	5'-CAT TTC AAG TAA CAC AAC TGA ATC	1004-1018 ^a	485-508 ^b
	1196	5'-GCC ATT TCA AGT AAT ACA ACA GAA	1004-1018 ^a	483-506 ^b
	1197	5'-CAA ACG CCA TTT CAA GTA ATA CAA C	1004-1018 ^a	478-502 ^b
25	1094	5'-GGT AAA ACA GGT ACT TCT AAC TA	1004-1018 ^a	759-781 ^b
	1214	5'-GGT AAA ACA GGT ACC TCT AAC TA	1004-1018 ^a	759-781 ^b
	1216	5'-GGT AAG ACT GGT ACA TCA AAC TA	1004-1018 ^a	759-781 ^b
	1217	5'-CAA ATG CCA TTT CAA GTA ACA CAA C	1004-1018 ^a	478-502 ^b
	1218	5'-CAA ACG CCA TTT CAA GTA ACA CAA C	1004-1018 ^a	478-502 ^b
30	1219	5'-CAA ATG CTA TTT CAA GTA ATA CAA C	1004-1018 ^a	478-502 ^b
	1220	5'-CAA ACG CCA TTT CAA GTA ATA CGA C	1004-1018 ^a	478-502 ^b
	2017	5'-ACT TTG AAT AAG GTC GGT CTA G	2047 ^c	1306-1327
	2018	5'-ACA CTA AAC AAG GTT GGT TTA G	2063	354-375
	2019	5'-ACA CTA AAC AAG GTC GGT CTA G	2064	346-367
35	2020	5'-GTA GCT CCA GAT GAA ATG TTT G	2140 ^c	1732-1753
	2021	5'-GTA GCT CCA GAC GAA ATG TTT G	2057	831-852
	2022	5'-GTA GCT CCA GAT GAA ACG TTT G	2053 ^c	805-826
	2023	5'-GTA ACT CCA GAT GAA ATG TTT G	2056	819-840
	2024	5'-AGT GAA AAG ATG GCT GCT GC	2048 ^c	1438-1457
40	2025	5'-AGT GAG AAA ATG GCT GCT GC	2047 ^c	1438-1457
	2026	5'-TCC AAG CAT GCA TTA TGC AAA CG	2047 ^c	1368-1390
	2027	5'-TCG GTC TAG ATA GAG CTA AAA CG	2047 ^c	1319-1341
	2028	5'-TAT GCT CTT CAA CAA TCA CG	2047 ^c	1267-1286
	2029	5'-AGC CGT TGA GAC TTT GAA TAA G	2047 ^c	1296-1317
45	2030	5'-CTT AAT GGT CTT GGT ATC G	2047 ^c	1345-1366
	2031	5'-CGT GAC TGG GGT TCT GCT ATG A	2049 ^c	1096-1117
	2032	5'-CGT GAC TGG GGA TCA TCA ATG A	2047 ^c	1096-1117
	2033	5'-CGT GAC TGG GGT TCT GCC ATG A	2057	195-216
	2034	5'-ATC AAG AAC ACT GGC TAT GTA G	2050 ^c	787-808

50 ^a These sequences were aligned to derive the corresponding primer.

^b The nucleotide positions refer to the *pbplA* sequence fragment (SEQ ID NO. 1004).

^c Sequence from databases.

Annex XXXVII: Internal hybridization probes for specific detection of *pbp* sequences (continued).

5			Originating DNA fragment	
	SEQ ID NO.	Nucleotide sequence	SEQ ID NO.	Nucleotide position
10	<u>Resistance gene:</u> <i>pbp1a</i> (continued)			
	2035	5'-ATC AAG AAC ACT GGC TAC GTA G	2051 ^C	787-808
	2036	5'-ATC AAG AAC ACT GGT TAC GTA G	2047	1714-1735
15	2037	5'-ATC AAA AAT ACT GGT TAT GTA G	2057	813-834
	2038	5'-ATC AAG AAT ACT GGC TAC GTA G	2052 ^C	757-778
	2039	5'-ATC AAA AAC ACT GGC TAT GTA G	2053 ^C	787-808

Annex XXXVIII: Strategy for *vana*- and *vanB*- specific hybridization probes from *van* sequences (continued).

	Accession #		SEQ ID NO.:
5	<i>vana</i> X56895	GAACAggt GccGcgtT 1038	1133
	<i>vana</i> M97297	GAACAggt GccGcgtT'ag TTGtGGC...ATT CATCAGGAAG TCGAGCCGGA AAAAGGCT	1139
		GAACAggt GccGcgtT'ag TTGtGGC...ATT CATCAGGAAG TCGAGCCGGA AAAAGGCT	1141
10	<i>vana</i>	GAACAggt GccGcgtT'ag TTGtGGC...ATT CATCAGGAAG TCGAGCCGGA AAAAGGCT	1051
	<i>vana</i>	GAACAggt GccGcgtT'ag TTGtGGC...ATT CATCAGGAAG TCGAGCCGGA AAAAGGCT	1052
	<i>vana</i>	GAACAggt GccGcgtT'ag TTGtGGC...ATT CATCAGGAAG TCGAGCCGGA AAAAGGCT	1053
	<i>vana</i>	GAACAggt GccGcgtT'ag TTGtGGC...ATT CATCAGGAAG TCGAGCCGGA AAAAGGCT	1054
	<i>vana</i>	GAACAggt GccGcgtT'ag TTGtGGC...ATT CATCAGGAAG TCGAGCCGGA AAAAGGCT	1055
15	<i>vana</i>	GAACAggt GccGcgtT'ag TTGtGGC...ATT CATCAGGAAG TCGAGCCGGA AAAAGGCT	1056
	<i>vana</i>	GAACAggt GccGcgtT'ag TTGtGGC...ATT CATCAGGAAG TCGAGCCGGA AAAAGGCT	1057
	<i>vana</i>	GAACAggt GccGcgtT'ag TTGtGGC...ATT CATCAGGAAG TCGAGCCGGA AAAAGGCT	1049
20	<i>vanB</i> U94526	GCAACGAG GATGATT'ag TTGtGGC...ATT CATCAGGAAG TCGAGCCGGA AAAAGGCT	1050
	<i>vanB</i> U94527	GCAACGAG GATGATT'ag TTGtGGC...ATT CATCAGGAAG TCGAGCCGGA AAAAGGCT	1117
	<i>vanB</i> U94528	GGAACGAG GATGATT'GA TTGtGGC...ATC CATCAGGAAG TCGAGCCGGA AAAAGGCT	-
	<i>vanB</i> U94529	GGAACGAG GATGATT'GA TTGtGGC...ATC CATCAGGAAG TCGAGCCGGA AAAAGGCT	-
	<i>vanB</i> U94530	GGAACGAG GATGATT'GA TTGtGGC...ATC CATCAGGAAG TCGAGCCGGA AAAAGGCT	-
	<i>vanB</i> Z83305	GGAACGAG GATGATT'GA TTGtGGC...ATC CATCAGGAAG TCGAGCCGGA AAAAGGCT	-
	<i>vanB</i> U81452	GGAACGAG GATGATT'GA TTGtGGC...ATC CATCAGGAAG TCGAGCCGGA AAAAGGCT	-
25	<i>vanB</i> U35369	GGAACGAG GATGATT'GA TTGtGGC...ATC CATCAGGAAG TCGAGCCGGA AAAAGGCT	-
	<i>vanB</i> U72704	GGAACGAG GATGATT'GA TTGtGGC...ATC CATCAGGAAG TCGAGCCGGA AAAAGGCT	-
	<i>vanB</i> L06138	GGAACGAG GATGATT'GA TTGtGGC...ATC CATCAGGAAG TCGAGCCGGA AAAAGGCT	-
	<i>vanB</i> L15304	GGAACGAG GATGATT'GA TTGtGGC...ATC CATCAGGAAG TCGAGCCGGA AAAAGGCT	-
	<i>vanB</i> U00456	GGAACGAG GATGATT'GA TTGtGGC...ATC CATCAGGAAG TCGAGCCGGA AAAAGGCT	-
30	<i>vand</i> AF130997	GGAACGAG GATGATT'GA TTGtGGC...ATC CATCAGGAAG TCGAGCCGGA AAAAGGCT	-
	<i>vane</i> AF136925	GGAA...t GAACGATT'ca TgGtGGC...ATT CATCAGGAAG TCGAGCCGGA AAAAGGCT	-
		GG TgGtGGC...TAT GAAGGAGAAAT ACA... ..TT	-
35	Selected sequence for hybridization probe	ACGAG GATGATT'GA TTGtGGC (<i>vane</i>)	1171
40	Selected sequence for amplification primer ^a	CATCAGGAAG TCGAGCCGGA AAAAG	1111

The sequence numbering refers to the Enter to the selected sequences or match those of *Seuococcus faecium vana* gene fragment (SEQ ID NO. 1139). Nucleotides in capitals are identical displayed. Mismatches are indicated by lower-case letters. Dots indicate gaps in the sequences "R" and "W" designate nucleotide positions which are degenerated. "R" stands for A or G; "W" stands for A or T of the above selected primer.

**Annex XXXIX: Internal hybridization probe for specific
detection of *mecA*.**

5			Originating DNA fragment	
	SEQ ID NO.	Nucleotide sequence	SEQ ID NO.	Nucleotide position
10	<u>Resistance gene: <i>mecA</i></u>			
	1177	5'-GCT CAA CAA GTT CCA GAT TA	1178 ^a	1313-1332

15

^a Sequence from databases.

Annex XL: Specific and ubiquitous primers for nucleic acid amplification (*hexA* sequences).

5			Originating DNA fragment	
	SEQ ID NO.	Nucleotide sequence	SEQ ID NO.	Nucleotide position
10	<hr/>			
	<u>Bacterial species:</u>		<i>Streptococcus pneumoniae</i>	
	1179	5'-ATT TGG TGA CGG GTG ACT TT	1183 ^a	431-450
	1181 ^b	5'-AGC AGC TTA CTA GAT GCC GT	1183-1191 ^c	652-671 ^d
15				
	Sequencing primers			
	1179	5'-ATT TGG TGA CGG GTG ACT TT	1183 ^a	431-450
	1182 ^b	5'-AAC TGC AAG AGA TCC TTT GG	1183 ^a	1045-1064
20				

^a Sequences from databases.

^b These sequences are from the complementary DNA strand of the sequence of the originating fragment given in the Sequence Listing.

^c These sequences were aligned to derive the corresponding primer.

^d The nucleotide positions refer to the *hexA* sequence fragment (SEQ ID NO. 1183).

Annex XLI: Internal hybridization probe for specific detection of hexA sequences.

5			Originating DNA fragment	
	SEQ ID NO.	Nucleotide sequence	SEQ ID NO.	Nucleotide position
10	<hr/>			
	<u>Bacterial species:</u>	<i>Streptococcus pneumoniae</i>		
	1180 ^a	5'-TCC ACC GTT GCC AAT CGC A	1183-1191 ^b	629-647 ^c

^a This sequence is from the complementary DNA strand of the sequence of the originating fragment given in the Sequence Listing.

^b These sequences were aligned to derive the corresponding primer.

^c The nucleotide positions refer to the hexA sequence fragment (SEQ ID NO. 1183).

5

316

35

^a This sequence is the reverse-complement of the

Ann x XLIII: Specific and ubiquitous primers for nucleic acid amplification (pcp sequence).

		Originating DNA fragment	
SEQ ID NO.	Nucleotide sequence	SEQ ID NO.	Nucleotide position
<hr/>			
<u>Bacterial species:</u>		<i>Streptococcus pyogenes</i>	
1211	5'-ATT CTT GTA ACA GGC TTT GAT CCC	1215 ^a	291-314
1210 ^b	5'-ACC AGC TTG CCC AAT ACA AAG G	1215 ^a	473-494

^a Sequences from databases.

^b These sequences are from the complementary DNA strand of the sequence of the originating fragment given in the Sequence Listing.

Annex XLIV: Specific and ubiquitous primers for nucleic acid amplification of *S. saprophyticus* sequences of unknown coding potential.

		Originating DNA fragment	
SEQ ID NO.	Nucleotide sequence	SEQ ID NO.	Nucleotide position
Bacterial species: <i>Staphylococcus saprophyticus</i>			
1208	5'-TCA AAA AGT TTT CTA AAA AAT TTA C	74,1093, 1198 ^b	169-193 ^c
1209 ^a	5'-ACG GGC GTC CAC AAA ATC AAT AGG A	74,1093, 1198 ^b	355-379 ^c

^a This sequence is from the complementary DNA strand of the sequence of the originating fragment given in the Sequence Listing.

^b These sequences were aligned to derive the corresponding primer.

^c The nucleotide positions refer to the *S. saprophyticus* unknown gene sequence fragment (SEQ ID NO. 1198).

Annex XLV: Molecular beacon internal hybridization probes for specific detection of antimicrobial agents resistance gene sequences.

		Originating DNA fragment	
SEQ ID NO.	Nucleotide sequence ^a	SEQ ID NO.	Nucleotide position
Resistance gene: <i>gyrA</i>			
2250	5'- <u>CCG TCG</u> GAT GGT GTC GTA TAC CGC GGA GTC GCC <u>GAC GG</u>	1954 ^b	218-243
2251	5'- <u>CCG AGC</u> CGT TCT CGC TGC GTT ACA TGC TGG TGG <u>CTC CG</u>	1954 ^b	259-286
Resistance gene: <i>mecA</i>			
1231	5'- <u>GCG AGC</u> CCG AAG ATA AAA AAG AAC CTC TGC TGC <u>TCG C</u>	1178 ^b	1291-1315
Resistance gene: <i>parC</i>			
1938 ^b	5'- <u>CCG CGC</u> ACC ATT GCT TCG TAC ACT GAG GAG TCT CCG <u>CGC GG</u>	1321 ^c	232-260
1939	5'- <u>CGA CCC</u> GGA TGG TAG TAT CGA TAA TGA TCC GCC AGC GGC <u>CGG GTC G</u>	1321 ^c	317-346
1955 ^b	5'- <u>CGC GCA</u> ACC ATT GCT TCG TAC ACT GAG GAG TCT <u>GCG CG</u>	1321 ^c	235-260
Resistance gene: <i>vanA</i>			
1239	5'- <u>GCG AGC</u> GCA GAC CTT TCA GCA GAG GAG <u>GCT</u> <u>CGC</u>	1051	860-880
1240	5'- <u>GCG AGC</u> CGG CAA GAC AAT ATG ACA GCA AAA TCG <u>CTC GC</u>	1051	663-688
Resistance gene: <i>vanB</i>			
1241	5'- <u>GCG AGC</u> GGG GAA CGA GGA TGA TTT GAT TGG <u>CTC GC</u>	1117	555-577
Resistance gene: <i>vanD</i>			
1593	5'- <u>CCG AGC</u> GAT TTA CCG GAT ACT TGG CTG <u>ICG</u> <u>CTC GG</u>	1594	835-845

^a Underlined nucleotides indicate the molecular beacon's stem.

^b This sequence is from the complementary DNA strand of the sequence of the originating fragment given in the Sequence Listing.

^c Sequence from databases.

Annex XLVI: Molecular beacon internal hybridization probe for specific detection of *S. aureus* gene sequences of unknown coding potential.

		Originating DNA fragment	
SEQ ID NO.	Nucleotide sequence ^a	SEQ ID NO.	Nucleotide position

Bacterial species: *S. aureus*

1232	5'- <u>GGA</u> <u>GCC</u> <u>GCG</u> <u>CGA</u> TTT TAT AAA TGA ATG TTG	1244	53-80
	ATA ACC <u>GGC</u> <u>TCC</u>		

^a Underlined nucleotides indicate the molecular beacon's stem.

Annex XLVII: Molecular beacon internal hybridization probes for specific detection of tuf s quences.

		Originating DNA fragment	
SEQ ID NO.	Nucleotide sequence ^a	SEQ ID NO.	Nucleotide position
<hr/>			
Bacterial species: <i>Chlamydia pneumoniae</i>			
2091	5'-CGC GAC TTG AGA TGG AAC TTA GTG AGC TTC TTG GTC GCG	20	157-183
2092	5'-CGC GAC GAA AGA ACT TCC TGA AGG TCG TGC AGG TCC AG	20	491-516
Bacterial species: <i>Chlamydia trachomatis</i>			
2213	5'-CGT GCC ATT GAC ATG ATT TCC GAA GAA GAC GCT GAA GGC ACG	1739 ^b	412-441
Bacterial species: <i>Enterococcus faecalis</i>			
1236	5'-GCG AGC CGT GGT GAA GTT CGC GTT GGT GGC TCG C	883	370-391
Bacterial species: <i>Enterococcus faecium</i>			
1235	5'-GCG AGC CGA AGT TGA AGT TGT TGG TAT TGC TGG CTC GC	64	412-437
Bacterial species: <i>Legionella pneumophila</i>			
2084 ^c	5'-CAC GCG TCA ACA CCC GTA CAA GTC GTC TTT TGC GCG TG	112	461-486
Bacterial species: <i>Mycoplasma pneumoniae</i>			
2096 ^c	5'-CGC GAC CGG TAC CAC GGC CAG TAA TCG TGT CGC G	2097 ^b	658-679
Bacterial species: <i>Neisseria gonorrhoeae</i>			
2177	5'-GGC ACG GAC AAA CCA TTC CTG CTG CCT ATC GAA ACG TGT TCC CGT GCC	126	323-357
2178	5'-GGC ACG ACA AAC CAT TCC TGC TGC CTA TCG AAC GTG CC	126	323-348
2179	5'-GGC AGC TCT ACT TCC GTA CCA CTG ACG TAA CCG GCT GCC	126	692-718

^a Underlined nucleotides indicate the molecular beacon's stem.

^b Sequence from databases.

^c This sequence is from the complementary DNA strand of the sequence of the originating fragment given in the Sequence Listing.

Annex XLVII: Molecular beacon internal hybridization probes for specific detection of tuf sequences (continued).

SEQ ID NO. Nucleotide sequence ^a		Originating DNA fragment	
SEQ ID NO.	Nucleotide sequence ^a	SEQ ID NO.	Nucleotide position
Bacterial species: <i>Pseudomonas aeruginosa</i>			
2122	5'- <u>CCG</u> <u>AGC</u> GAA TGT AGG AGT CCA GGG TCT CTG CTC GG	153,880,2138 ^{b,c}	280-302 ^d
Bacterial species: <i>Staphylococcus aureus</i>			
2186	5'- <u>ACG</u> <u>CGC</u> TCA AAG CAG AAG TAT ACG TAT TAT CAA AAG ACG <u>CGC</u> GT	1728	615-646
Bacterial group: <i>Staphylococcus</i> sp. other than <i>S. aureus</i>			
1233	5'- <u>GCG</u> <u>AGC</u> GTT ACT GGT GTA GAA ATG TTC CGG CTC GC	878	372-394
Fungal species: <i>Candida albicans</i>			
2073	5'- <u>CCG</u> <u>AGC</u> AAC ATG ATT GAA CCA TCC ACC AAC TGG CTC GG	408	404-429
Fungal species: <i>Candida dubliniensis</i>			
2074	5'- <u>CCG</u> <u>AGC</u> AAC ATG ATT GAA GCT TCC ACC AAC TGG CTC GG	414	416-441
Fungal species: <i>Candida glabrata</i>			
2110 ^b	5'- <u>GCG</u> <u>GGC</u> CCT TAA CGA TTT CAG CGA ATC TGG ATT CAG CCC GC	417	307-335
2111	5'-GCG GGC ATG TTG AAG CCA CCA CCA ACG CTT CCT GGC CCG C	417	419-447
Fungal species: <i>Candida krusei</i>			
2112 ^b	5'- <u>GCG</u> <u>GGC</u> TTG ATG AAG TTT GGG TTT CCT TGA CAA TTG CCC GC	422	318-347
2113	5'- <u>GCG</u> <u>GGC</u> ACA AGG GTT GGA CTA AGG AAA CCA AGG CAG CCC GC	422	419-447
2114	5'- <u>GCG</u> <u>GGC</u> ATC GAT GCT ATT GAA CCA CCT GTC AGA CCG CCC GC	422	505-533

^a Underlined nucleotides indicate the molecular beacon's stem.

^b Sequence from databases.

^c These sequences were aligned to derive the corresponding primer.

^d The nucleotide positions refer to the *P. aeruginosa* tuf sequence fragment (SEQ ID NO. 153).

Annex XLVII: Molecular beacon internal hybridization probes for specific detection of tuf sequences (continued).

		Originating DNA fragment	
SEQ ID NO.	Nucleotide sequence ^a	SEQ ID NO.	Nucleotide position
<hr/>			
<u>Fungal species:</u> <i>Candida lusitanae</i>			
2115 ^b	5'-GCG GGC GGT AAG TCC ACC GGT AAG ACC TTG TTG GCC CGC	424	304-330
2116	5'-GCG GGC GTA AGT CAC CGG TAA GAC CTT GTT GGC CCG C	424	476-502
2117	5'-GCG GGC GAC GCC ATT GAG CCA CCT TCG AGA GCC CGC	424	512-535
<u>Fungal species:</u> <i>Candida parapsilosis</i>			
2118 ^b	5'-GCG GGC TCC TTG ACA ATT TCT TCG TAT CTG TTC TTG GCC CGC	426	301-330
<u>Fungal species:</u> <i>Candida tropicalis</i>			
2119	5'-GCG GGC TTA CAA CCC TAA GGC TGT TCC ATT CGT TGC CCG C	429	357-384
2120	5'-GCG GGC AGA AAC CAA GGC TGG TAA GGT TAC CGG AGC CCG C	429	459-487
<u>Fungal species:</u> <i>Cryptococcus neoformans</i>			
2106	5'-GCG AGC AGA GCA CGC CCT CCT CGC CGC TCG C	623,1985,1986 ^c	226-244 ^d
2107	5'-GCG AGC TCC CCA TCT CTG GTT GGC AGC CTC GC	623,1985,1986 ^c	390-408 ^d
<u>Bacterial genus:</u> <i>Legionella</i> sp.			
2083	5'-CCG CCG ATG TTC CGT AAA TTA CTT GAI GAA GGT CGA GCC GGC GG	111-112 ^a	488-519 ^e

^a Underlined nucleotides indicate the molecular beacon's stem.

^b This sequence is from the complementary DNA strand of the sequence of the originating fragment given in the Sequence Listing.

^c These sequences were aligned to derive the corresponding primer.

^d The nucleotide positions refer to the *C. neoformans* tuf (EF-1) sequence fragment (SEQ ID NO. 623).

^e The nucleotide positions refer to the *L. pneumophila* tuf (EF-1) sequence fragment (SEQ ID NO. 112).

Annex XLVII: Molecular beacon internal hybridization probes for specific detection of *tuf* sequences (continued).

		Originating DNA fragment	
SEQ ID NO.	Nucleotide sequence ^a	SEQ ID NO.	Nucleotide position
<u>Fungal genus:</u> <i>Candida sp.</i>			
2108	5'- <u>GCG</u> <u>GGC</u> AAC TTC RTC AAG AAG GTT GGT TAC AAC CCG <u>CCC</u> <u>GC</u>	414,417, 422,424,, 426,429,624 ^b	52-80 ^c
2109	5'- <u>GCG</u> <u>GGC</u> CCA ATC TCT GGT TGG AAY GGT GAC AAG <u>CCC</u> <u>GC</u>	Same as SEQ ID NO. 2108	100-125 ^c
<u>Bacterial group:</u> <i>Pseudomonads</i>			
2121	5'- <u>CGA</u> <u>CCG</u> CIA GCC GCA CAC CAA GTT <u>CCG</u> <u>GTC</u> <u>G</u>	153-155, 205,880,2137 ^d , 2138 ^{d,b}	598-616 ^e

^a Underlined nucleotides indicate the molecular beacon's stem.

^b These sequences were aligned to derive the corresponding primer.

^c The nucleotide positions refer to the *C. albicans tuf* (EF-1) sequence fragment (SEQ ID NO. 624).

^d Sequence from databases.

^e The nucleotide positions refer to the *P. aeruginosa tuf* sequence fragment (SEQ ID NO. 153).

Annex XLVIII: Molecular beacon internal hybridization probes for specific detection of *ddl* and *mtl* gene sequences.

SEQ ID NO. Nucleotide sequence ^a		Originating DNA fragment	
		SEQ ID NO.	Nucleotide position
<u>Bacterial species:</u> <i>E. faecium (ddl)</i>			
1237	5'- <u>GCG AGC</u> CGC GAA ATC GAA GTT GCT GTA TTA GGG <u>CTC GC</u>	1242 ^b	334-359
<u>Bacterial species:</u> <i>E. faecalis (mtl)</i>			
1238	5'- <u>GCG AGC</u> GGC GTT AAT TTT GGC ACC GAA GAA GAG <u>CTC GC</u>	1243 ^b	631-656

^a Underlined nucleotides indicate the molecular beacon's stem.

^b Sequence from databases.

**Annex XLIX: Internal hybridization probe for specific detection
of *S. aureus* sequences of unknown coding potential.**

		Originating DNA fragment	
SEQ ID NO.	Nucleotide sequence	SEQ ID NO.	Nucleotide position
<u>Bacterial species:</u> <i>Staphylococcus aureus</i>			
1234	5'-ACT AAA TAA ACG CTC ATT-CG	1244	35-54

Annex L: Specific and ubiquitous primers for nucleic acid amplification (antimicrobial agents resistance genes).

		Originating DNA fragment	
SEQ ID NO.	Nucleotide sequence	SEQ ID NO.	Nucleotide position
Resistance gene: <i>aac(2')-Ia</i>			
1344	5'-AGC AGC AAC GAT GTT ACG CAG CAG	1348 ^a	163-186
1345 ^b	5'-CCC GCC GAG CAT TTC AAC TAT TG	1348 ^a	392-414
1346	5'-GAT GTT ACG CAG CAG GGC AGT C	1348 ^a	172-193
1347 ^b	5'-ACC AAG CAG GTT CGC AGT CAA GTA	1348 ^a	467-490
Resistance gene: <i>aac(3')-Ib</i>			
1349	5'-CAG CCG ACC AAT GAG TAT CTT GCC	1351 ^a	178-201
1350 ^b	5'-TAA TCA GGG CAG TTG CGA CTC CTA	1351 ^a	356-379
Resistance gene: <i>aac(3')-IIb</i>			
1352	5'-CCA CGC TGA CAG AGC CGC ACC G	1356 ^a	383-404
1353 ^b	5'-GGC CAG CTC CCA TCG GAC CCT G	1356 ^a	585-606
1354	5'-CAC GCT GAC AGA GCC GCA CCG	1356 ^a	384-404
1355 ^b	5'-ATG CCG TTG CTG TCG AAA TCC TCG	1356 ^a	606-629
Resistance gene: <i>aac(3')-IVa</i>			
1357	5'-GCC CAT CCA TTT GCC TTT GC	1361 ^a	295-314
1358 ^b	5'-GCG TAC CAA CTT GCC ATC CTG AAG	1361 ^a	517-540
1359	5'-TGC CCC TGC CAC CTC ACT C	1361 ^a	356-374
1360 ^b	5'-CGT ACC AAC TTG CCA TCC TGA AGA	1361 ^a	516-539
Resistance gene: <i>aac(3')-VIa</i>			
1362	5'-CGC CGC CAT CGC CCA AAG CTG G	1366 ^a	285-306
1363 ^b	5'-CGG CAT AAT GGA GCG CGG TGA CTG	1366 ^a	551-574
1364	5'-TTT CTC GCC CAC GCA GGA AAA ATC	1366 ^a	502-525
1365 ^b	5'-CAT CCT CGA CGA ATA TGC CGC G	1366 ^a	681-702
Resistance gene: <i>aac(6')-Ia</i>			
1367	5'-CAA ATA TAC TAA CAG AAG CGT TCA	1371 ^a	56-79
1368 ^b	5'-AGG ATC TTG CCA ATA CCT TTA T	1371 ^a	269-290
1379	5'-AAA CCT TTG TTT CGG TCT GCT AAT	1371 ^a	153-176
1380 ^b	5'-AAG CGA TTC CAA TAA TAC CTT GCT	1371 ^a	320-343

^a Sequence from databases.

^b These sequences are from the complementary DNA strand of the sequence of the originating fragment given in the Sequence Listing.

Annex L: Specific and ubiquitous primers for nucleic acid amplification (antimicrobial agents resistance genes sequences) (continued).

		Originating DNA fragment	
SEQ ID NO.	Nucleotide sequence	SEQ ID NO.	Nucleotide position
<hr/>			
<u>Resistance gene:</u> <i>aac(6')-Ic</i>			
1372	5'-GCT TTC GTT GCC TTT GCC GAG GTC	1376 ^a	157-180
1373 ^b	5'-CAC CCC TGT TGC TTC GCC CAC TC	1376 ^a	304-326
1374	5'-AGA TAT TGG CTT CGC CGC ACC ACA	1376 ^a	104-127
1375 ^b	5'-CCC TGT TGC TTC GCC CAC TCC TG	1376 ^a	301-323
<u>Resistance gene:</u> <i>ant(3')-Ia</i>			
1377	5'-GCC GTG GGT CGA TGT TTG ATG TTA	1381 ^a	100-123
1378 ^b	5'-GCT CGA TGA CGC CAA CTA CCT CTG	1381 ^a	221-244
1379	5'-AGC AGC AAC GAT GTT ACG CAG CAG	1381 ^a	127-150
1380 ^b	5'-CGC TCG ATG ACG CCA ACT ACC TCT	1381 ^a	222-245
<u>Resistance gene:</u> <i>ant(4')-Ia</i>			
1382	5'-TAG ATA TGA TAG GCG GTA AAA AGC	1386 ^a	149-172
1383 ^b	5'-CCC AAA TTC GAG TAA GAG GTA TT	1386 ^a	386-408
1384	5'-GAT ATG ATA GGC GGT AAA AAG C	1386 ^a	151-172
1385 ^b	5'-TCC CAA ATT CGA GTA AGA GGT A	1386 ^a	388-409
<u>Resistance gene:</u> <i>aph(3')-Ia</i>			
1387	5'-TTA TGC CTC TTC CGA CCA TCA AGC	1391 ^a	233-256
1338 ^b	5'-TAC GCT CGT CAT CAA AAT CAC TCG	1391 ^a	488-511
1389	5'-GAA TAA CGG TTT GGT TGA TGC GAG	1391 ^a	468-491
1390 ^b	5'-ATG GCA AGA TCC TGG TAT CGG TCT	1391 ^a	669-692
<u>Resistance gene:</u> <i>aph(3')-IIa</i>			
1392	5'-TGG GTG GAG AGG CTA TTC GGC TAT	1396 ^a	43-66
1393 ^b	5'-CAG TCC CTT CCC GCT TCA GTG AC	1396 ^a	250-272
1394	5'-GAC GTT GTC ACT GAA GCG GGA AGG	1396 ^a	244-267
1395 ^b	5'-CTT GGT GGT CGA ATG GGC AGG TAG	1396 ^a	386-409

^a Sequence from databases.

^b These sequences are from the complementary DNA strand of the sequence of the originating fragment given in the Sequence Listing.

Annex L: Specific and ubiquitous primers for nucleic acid amplification (antimicrobial agents resistance genes sequences) (continued).

		Originating DNA fragment	
SEQ ID NO.	Nucleotide sequence	SEQ ID NO.	Nucleotide position
<hr/>			
<u>Resistance gene:</u> <i>aph(3')-IIIa</i>			
1397	5'-GTG GGA GAA AAT GAA AAC CTA T	1401 ^a	103-124
1398 ^b	5'-ATG GAG TGA AAG AGC CTG AT	1401 ^a	355-374
1399	5'-ACC TAT GAT GTG GAA CGG GAA AAG	1401 ^a	160-183
1400 ^b	5'-CGA TGG AGT GAA AGA GCC TGA TG	1401 ^a	354-376
<u>Resistance gene:</u> <i>aph(3')-VIIa</i>			
1402	5'-TAT TCA ACA ATT TAT CGG AAA CAG	1406 ^a	18-41
1403 ^b	5'-TCA GAG AGC CAA CTC AAC ATT TT	1406 ^a	175-197
1404	5'-AAA CAG CGT TTT AGA GCC AAA TAA	1406 ^a	36-59
1405 ^b	5'-TTC TCA GAG AGC CAA CTC AAC ATT	1406 ^a	177-200
<u>Resistance gene:</u> <i>blaCARB</i>			
1407	5'-CCC TGT AAT AGA AAA GCA AGT AGG	1411 ^a	351-374
1408 ^b	5'-TTG TCG TAT CCC TCA AAT CAC C	1411 ^a	556-577
1409	5'-TGG GAT TAC AAT GGC AAT CAG CG	1411 ^a	205-227
1410 ^b	5'-GGG GAA TAG GTC ACA AGA TCT GCT T	1411 ^a	329-353
<u>Resistance gene:</u> <i>blaCMY-2</i>			
1412	5'-GAG AAA ACG CTC CAG CAG GGC	1416 ^a	793-813
1413 ^b	5'-CAT GAG GCT TTC ACT GCG GGG	1416 ^a	975-995
1414	5'-TAT CGT TAA TCG CAC CAT CAC	1416 ^a	90-110
1415 ^b	5'-ATG CAG TAA TGC GGC TTT ATC	1416 ^a	439-459
<u>Resistance genes:</u> <i>blaCTX-M-1, blaCTX-M-2</i>			
1417	5'-TGG TTA ACT AYA ATC CSA TTG CGG A	1423 ^a	314-338
1418 ^b	5'-ATG CTT TAC CCA GCG TCA GAT T	1423 ^a	583-604
<u>Resistance gene:</u> <i>blaCTX-M-1</i>			
1419	5'-CGA TGA ATA AGC TGA TTT CTC ACG	1423 ^a	410-433
1420 ^b	5'-TGC TTT ACC CAG CGT CAG ATT ACG	1423 ^a	580-603
1421	5'-AAT TAG AGC GGC AGT CGG GAG GAA	1423 ^a	116-139
1422 ^b	5'-GAA ATC AGC TTA TTC ATC GCC ACG	1423 ^a	405-428

^a Sequence from databases.

^b These sequences are from the complementary DNA strand of the sequence of the originating fragment given in the Sequence Listing.

Annex L: Specific and ubiquitous primers for nucleic acid amplification (antimicrobial agents resistance genes sequences) (continued).

		Originating DNA fragment	
SEQ-ID NO.	Nucleotide sequence	SEQ ID NO.	Nucleotide position
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<u>Resistance gene:</u> <i>blaCTX-M-2</i>			
1424	5'-GTT AAC GGT GAT GGC GAC GCT AC	1428 ^a	30-52
1425 ^b	5'-GAA TTA TCG GCG GTG TTA ATC AGC	1428 ^a	153-176
1426	5'-CAC GCT CAA TAC CGC CAT TCC A	1428 ^a	510-531
1427 ^b	5'-TTA TCG CCC ACT ACC CAT GAT TTC	1428 ^a	687-710
<u>Resistance gene:</u> <i>blaIMP</i>			
1429	5'-TTT ACG GCT AAA GAT ACT GAA AAG T	1433 ^a	205-229
1430 ^b	5'-GTT TAA TAA AAC AAC CAC CGA ATA AT	1433 ^a	513-538
1431	5'-TAA TTG ACA CTC CAT TTA CGG CTA A	1433 ^a	191-215
1432 ^b	5'-ACC GAA TAA TAT TTT CCT TTC AGG CA	1433 ^a	497-522
<u>Resistance gene:</u> <i>blaOXA2</i>			
1434	5'-CAC AAT CAA GAC CAA GAT TTG CGA T	1438 ^a	319-343
1435 ^b	5'-GAA AGG GCA GCT CGT TAC GAT AGA G	1438 ^a	532-556
<u>Resistance gene:</u> <i>blaOXA10</i>			
1436	5'-CAG CAT CAA CAT TTA AGA TCC CCA	1439 ^a	194-217
1437 ^b	5'-CTC CAC TTG ATT AAC TGC GGA AAT TC	1439 ^a	479-504
<u>Resistance gene:</u> <i>blaPER-1</i>			
1440	5'-AGA CCG TTA TCG TAA ACA GGG CTA AG	1442 ^a	281-306
1441 ^b	5'-TTT TTT GCT CAA ACT TTT TCA GGA TC	1442 ^a	579-604
<u>Resistance gene:</u> <i>blaPER-2</i>			
1443	5'-CTT CTG CTC TGC TGA TGC TTG GC	1445 ^a	32-54
1444 ^b	5'-GGC GAC CAG GTA TTT TGT AAT ACT GC	1445 ^a	304-329
<u>Resistance genes:</u> <i>blaPER-1, blaPER-2</i>			
1446	5'-GGC CTG YGA TTT GTT ATT TGA ACT GGT	1442 ^a	414-440
1447 ^b	5'-CGC TST GGT CCT GTG GTG GTT TC	1442 ^a	652-674
1448	5'-GAT CAG GTG CAR TAT CAA AAC TGG AC	1442 ^a	532-557
1449 ^b	5'-AGC WGG TAA CAA YCC TTT TAA CCG CT	1442 ^a	671-696

^a Sequence from databases.

^b These sequences are from the complementary DNA strand of the sequence of the originating fragment given in the Sequence Listing.

Annex L: Specific and ubiquitous primers for nucleic acid amplification (antimicrobial agents resistance genes) (continued).

		Originating DNA fragment	
SEQ ID NO.	Nucleotide sequence	SEQ ID NO.	Nucleotide position
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<u>Resistance gene:</u> <i>blaSHV</i>			
1883	5'-AGC CGC TTG AGC AAA TTA AAC TA	1900 ^a	71-93
1884 ^b	5'-GTA TCC CGC AGA TAA ATC ACC AC	1900 ^a	763-785
1885	5'-AGC GAA AAA CAC CTT GCC GAC	1900 ^a	313-333
1884 ^b	5'-GTA TCC CGC AGA TAA ATC ACC AC	1900 ^a	763-785
<u>Resistance gene:</u> <i>blaTEM</i>			
1906	5'-CCT TAT TCC CTT TTT TGC GG	1927 ^a	27-46
1907 ^b	5'-CAC CTA TCT CAG CGA TCT GTC T	1927 ^a	817-838
1908	5'-AAC AGC GGT AAG ATC CTT GAG AG	1927 ^a	148-170
1907 ^b	5'-CAC CTA TCT CAG CGA TCT GTC T	1927 ^a	817-838
<u>Resistance gene:</u> <i>catI</i>			
2145	5'-GCA AGA TGT GGC GTG TTA CGG T	2147 ^a	363-384
2146 ^b	5'-GGG GCG AAG AAG TTG TCC ATA TT	2147 ^a	484-506
<u>Resistance gene:</u> <i>catII</i>			
2148	5'-CAG ATT AAA TGC GGA TTC AGC C	2150 ^a	67-88
2149 ^b	5'-ATC AGG TAA ATC ATC AGC GGA TA	2150 ^a	151-173
<u>Resistance gene:</u> <i>catIII</i>			
2151	5'-ATA TTT CAG CAT TAC CTT GGG TT	2153 ^a	419-441
2152 ^b	5'-TAC ACA ACT CTT GTA GCC GAT TA	2153 ^a	603-625
<u>Resistance gene:</u> <i>catP</i>			
2154	5'-CGC CAT TCA GAG TTT AGG AC	2156 ^a	178-197
2155 ^b	5'-TTC CAT ACC GTT GCG TAT CAC TT	2156 ^a	339-361
<u>Resistance gene:</u> <i>cat</i>			
2157	5'-CCA CAG AAA TTG ATA TTA GTG TTT TAT	2159 ^a	89-115
2158 ^b	5'-TCG CTA TTG TAA CCA GTT CTA	2159 ^a	201-221
2160	5'-TTT TGA ACA CTA TTT TAA CCA GC	2162 ^a	48-70
2161 ^b	5'-GAT TTA ACT TAT CCC AAT AAC CT	2162 ^a	231-253

^a Sequence from databases.

^b These sequences are from the complementary DNA strand of the sequence of the originating fragment given in the Sequence Listing.

Annex L: Specific and ubiquitous primers for nucleic acid amplification (antimicrobial agents resistance genes sequences) (continued).

		Originating DNA fragment	
SEQ ID NO.	Nucleotide sequence	SEQ ID NO.	Nucleotide position
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<u>Resistance gene:</u> <i>dfra</i>			
1450	5'-ACC ACT GGG AAT ACA CTT GTA ATG GC	1452 ^a	106-131
1451 ^b	5'-ATC TAC CTG GTC AAT CAT TGC TTC GT	1452 ^a	296-321
<u>Resistance gene:</u> <i>dhfrIa</i>			
1457	5'-CAA AGG TGA ACA GCT CCT GTT T	1461 ^a	75-96
1458 ^b	5'-TCC GTT ATT TTC TTT AGG TTG GTT AAA	1461 ^a	249-275
1459	5'-AAG GTG AAC AGC TCC TGT TT	1461 ^a	77-96
1560 ^b	5'-GAT CAC TAC GTT CTC ATT GTC A	1461 ^a	207-228
<u>Resistance genes:</u> <i>dhfrIa</i> , <i>dhfrXV</i>			
1453	5'-ATC GAA GAA TGG AGT TAT CGG RAA TG	1461 ^a	27-52
1454 ^b	5'-CCT AAA AYT RCT GGG GAT TTC WGG A	1461 ^a	384-408
1455	5'-CAG GTG GTG GGG AGA TAT ACA AAA	1461 ^a	290-313
1456 ^b	5'-TAT GTT AGA SRC GAA GTC TTG GKT AA	1461 ^a	416-441
<u>Resistance gene:</u> <i>dhfrIb</i>			
1466	5'-AAG CAT TGA CCT ACA ATC AGT GT	1470 ^a	98-120
1467 ^b	5'-AAT ACA ACT ACA TTG TCA TCA TTT GAT	1470 ^a	204-230
1468	5'-CGT TAC CCG CTC AGG TTG GAC ATC AA	1470 ^a	183-208
1469 ^b	5'-CAT CCC CCT CTG GCT CGA TGT CG	1470 ^a	354-376
<u>Resistance gene:</u> <i>dhfrV</i>			
1471	5'-GAT AAT GAC AAC GTA ATA GTA TTC CC	1475 ^a	208-233
1472 ^b	5'-GCT CAA TAT CAA TCG TCG ATA TA	1475 ^a	342-364
1473	5'-TTA AAG CCT TGA CGT ACA ACC AGT GG	1475 ^a	95-120
1474 ^b	5'-TGG GCA ATG TTT CTC TGT AAA TCT CC	1475 ^a	300-325
<u>Resistance genes:</u> <i>dhfrIb</i> , <i>dhfrV</i>			
1462	5'-GCA CTC CCY AAT AGG AAA TAC GC	1470 ^a	157-179
1463 ^b	5'-AGT GTT GCT CAA AAA CAA CTT CG	1470 ^a	405-427
1464	5'-ACG TTY GAA TCT ATG GGM GCA CT	1470 ^a	139-161
1465 ^b	5'-GTC GAT AAG TGG AGC GTA GAG GC	1470 ^a	328-350

^a Sequence from databases.

^b These sequences are from the complementary DNA strand of the sequence of the originating fragment given in the Sequence Listing.

Annex L: Specific and ubiquitous primers for nucleic acid amplification (antimicrobial agents resistance genes) (continued).

		Originating DNA fragment	
SEQ ID NO.	Nucleotide sequence	SEQ ID NO.	Nucleotide position
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<u>Resistance gene:</u> <i>dhfrVI</i>			
1476	5'-GGC GAG CAG CTC CTA TTC AAA G	1480 ^a	79-100
1477 ^b	5'-TAG GTA AGC TAA TGC CGA TTC AAC A	1480 ^a	237-261
1478	5'-GAG AAT GGA GTA ATT GGC TCT GGA TT	1480 ^a	31-56
1479 ^b	5'-GCG AAA TAC ACA ACA TCA GGG TCA T	1480 ^a	209-233
<u>Resistance gene:</u> <i>dhfrVII</i>			
1485	5'-AAA ATG GCG TAA TCG GTA ATG GC	1489 ^a	32-54
1486 ^b	5'-CAT TTG AGC TTG AAA TTC CTT TCC TC	1489 ^a	189-214
1487	5'-AAT CGA AAA TAT GCA GTA GTG TCG AG	1489 ^a	166-191
1488 ^b	5'-AGA CTA TTG TAG ATT TGA CCG CCA	1489 ^a	294-317
<u>Resistance genes:</u> <i>dhfrVII, dhfrXVII</i>			
1481	5'-RTT ACA GAT CAT KTA TAT GTC TCT	1489 ^a	268-291
1482 ^b	5'-TAA TTT ATA TTA GAC AWA AAA AAC TG	1489 ^a	421-446
1483	5'-CAR YGT CAG AAA ATG GCG TAA TC	1489 ^a	23-45
1484 ^b	5'-TKC AAA GCR WTT TCT ATT GAA GGA AA	1489 ^a	229-254
<u>Resistance gene:</u> <i>dhfrVIII</i>			
1490	5'-GAC CTA TGA GAG CTT GCC CGT CAA A	1494 ^a	144-168
1491 ^b	5'-TCG CCT TCG TAC AGT CGC TTA ACA AA	1494 ^a	376-401
1492	5'-CAT TTT AGC TGC CAC CGC CAA TGG TT	1494 ^a	18-43
1493 ^b	5'-GCG TCG CTG ACG TTG TTC ACG AAG A	1494 ^a	245-269
<u>Resistance gene:</u> <i>dhfrIX</i>			
1495	5'-TCT CTA AAC ATG ATT GTC GCT GTC	1499 ^a	7-30
1496 ^b	5'-CAG TGA GGC AAA AGT TTT TCT ACC	1499 ^a	133-156
1497	5'-CGG ACG ACT TCA TGT GGT AGT CAG T	1499 ^a	171-195
1498 ^b	5'-TTT GTT TTC AGT AAT GGT CGG GAC CT	1499 ^a	446-471

^a Sequence from databases.

^b These sequences are from the complementary DNA strand of the sequence of the originating fragment given in the Sequence Listing.

Annex L: Specific and ubiquitous primers for nucleic acid amplification (antimicrobial agents resistance genes sequences) (continued).

		Originating DNA fragment	
SEQ ID NO.	Nucleotide sequence	SEQ ID NO.	Nucleotide position
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<u>Resistance gene:</u> <i>dhfrXII</i>			
1500	5'-ATC GGG TTA TTG GCA ATG GTC CTA	1504 ^a	50-73
1501 ^b	5'-GCG GTA GTT AGC TTG GCG TGA GAT T	1504 ^a	201-225
1502	5'-GCG GGC GGA GCT GAG ATA TAC A	1504 ^a	304-325
1503 ^b	5'-AAC GGA GTG GGT GTA CCG AAT TAC AG	1504 ^a	452-477
<u>Resistance gene:</u> <i>dhfrXIII</i>			
1505	5'-ATT TTT CGC AGG CTC ACC GAG AGC	1507 ^a	106-129
1506 ^b	5'-CGG ATG AGA CAA CCT CGA ATT CTG CTG	1507 ^a	413-439
<u>Resistance gene:</u> <i>dhfrXV</i>			
1508	5'-AGA ATG TAT TGG TAT TTC CAT CTA TCG	1512 ^a	215-241
1509 ^b	5'-CAA TGT CGA TTG TTG AAA TAT GTA AA	1512 ^a	336-361
1510	5'-TGG AGT GCC AAA GGG GAA CAA T	1512 ^a	67-88
1511 ^b	5'-CAG ACA CAA TCA CAT GAT CCG TTA TCG	1512 ^a	266-292
<u>Resistance gene:</u> <i>dhfrXVII</i>			
1513	5'-TTC AAG CTC AAA TGA AAA CGT CC	1517 ^a	201-223
1514 ^b	5'-GAA ATT CTC AGG CAT TAT AGG GAA T	1517 ^a	381-405
1515	5'-GTG GTC AGT AAA AGG TGA GCA AC	1517 ^a	66-88
1516 ^b	5'-TCT TTC AAA GCA TTT TCT ATT GAA GG	1517 ^a	232-257
<u>Resistance gene:</u> <i>emhA</i>			
2102	5'-CAC CTT CAC CCT GAC CGA CG	2105 ^a	822-841
2103 ^b	5'-CGA ACC AGC GGA AAT AGT TGG AC	2105 ^a	948-970
<u>Resistance genes:</u> <i>ereA, ereA2</i>			
1528	5'-AAC TTG AGC GAT TTT CGG ATA CCC TG	1530 ^a	80-105
1529 ^b	5'-TTG CCG ATG AAA TAA CCG CCG ACT	1530 ^a	317-340

^a Sequence from databases.

^b These sequences are from the complementary DNA strand of the sequence of the originating fragment given in the Sequence Listing.

Annex L: Specific and ubiquitous primers for nucleic acid amplification (antimicrobial agents resistance genes sequences) (continued).

		Originating DNA fragment	
SEQ ID NO.	Nucleotide sequence	SEQ ID NO.	Nucleotide position
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<u>Resistance gene:</u> ereB			
1531	5'-TCT TTT TGT TAC GAC ATA CGC TTT T	1535 ^a	152-176
1532 ^b	5'-AGT GCT TCT TTA TCC GCT GTT CTA	1535 ^a	456-479
1533	5'-CAG CGG ATA AAG AAG CAC TAC ACA TT	1535 ^a	461-486
1534 ^b	5'-CCT CCT GAA ATA AAG CCC GAC AT	1535 ^a	727-749
<u>Resistance gene:</u> gyrA			
1340	5'-GAA CAA GGT ATG ACA CCG GAT AAA T	1299 ^a	163-188
1341 ^b	5'-GAT AAC TGA AAT CCT GAG CCA TAC G	1299 ^a	274-299
1936	5'-TAC CAC CCG CAC GGC	1954 ^a	205-219
1937 ^b	5'-CGG AGT CGC CGT CGA TG	1954 ^a	309-325
1942	5'-GAC TGG AAC AAA GCC TAT AAA AAA TCA	1954 ^a	148-174
1937 ^b	5'-CGG AGT CGC CGT CGA TG	1954 ^a	309-325
2040	5'-TGT GAC CCC AGA CAA ACC C	2054 ^a	33-51
2041 ^b	5'-GTT GAG CGG CAG CAC TAT CT	2054 ^a	207-226
<u>Resistance gene:</u> inhA			
2098	5'-CTG AGT CAC ACC GAC AAA CGT C	2101 ^a	910-931
2099 ^b	5'-CCA GGA CTG AAC GGG ATA CGA A	2101 ^a	1074-1095
<u>Resistance genes:</u> linA, linA'			
1536 ^b	5'-AGA TGT ATT AAC TGG AAA ACA ACA A	1540 ^a	99-123
1537 ^b	5'-CTT TGT AAT TAG TTT CTG AAA ACC A	1540 ^a	352-376
1538	5'-TTA GAA GAT ATA GGA TAC AAA ATA GAA G	1540 ^a	187-214
1539 ^b	5'-GAA TGA AAA AGA AGT TGA GCT T	1540 ^a	404-425
<u>Resistance gene:</u> linB			
1541	5'-TGA TAA TCT TAT ACG TGG GGA ATT T	1545 ^a	246-270
1542 ^b	5'-ATA ATT TTC TAA TTG CCC TGT TTC AT	1545 ^a	359-384
1543	5'-GGG CAA TTA GAA AAT TAT TTA TCA GA	1545 ^a	367-392
1544 ^b	5'-TTT TAC TCA TGT TTA GCC AAT TAT CA	1545 ^a	579-604

^a Sequence from databases.

^b These sequences are from the complementary DNA strand of the sequence of the originating fragment given in the Sequence Listing.

Annex L: Specific and ubiquitous primers for nucleic acid amplification (antimicrobial agents resistance genes sequences) (continued).

		Originating DNA fragment	
SEQ ID NO.	Nucleotide sequence	SEQ ID NO.	Nucleotide position
Resistance gene: <i>mefA</i>			
1546	5'-CAA GAA GGA ATG GCT GTA CTA C	1548 ^a	625-646
1547 ^b	5'-TAA TTC CCA AAT AAC CCT AAT AAT AGA	1548 ^a	816-842
Resistance gene: <i>mefE</i>			
1549	5'-GCT TAT TAT TAG GAA GAT TAG GGG GC	1551 ^a	815-840
1550 ^b	5'-TAG CAA GTG ACA TGA TAC TTC CGA	1551 ^a	1052-1075
Resistance genes: <i>mefA</i>, <i>mefE</i>			
1552	5'-GGC AAG CAG TAT CAT TAA TCA CTA	1548 ^a	50-73
1553 ^b	5'-CAA TGC TAC GGA TAA ACA ATA CTA TC	1548 ^a	318-343
1554	5'-AGA AAA TTA AGC CTG AAT ATT TAG GAC	1548 ^a	1010-1035
1555 ^b	5'-TAG TAA AAA CCA ATG ATT TAC ACC G	1548 ^a	1119-1143
Resistance genes: <i>mphA</i>, <i>mphK</i>			
1556	5'-ACT GTA CGC ACT TGC AGC CCG ACA T	1560 ^a	33-57
1557 ^b	5'-GAA CGG CAG GCG ATT CTT GAG CAT	1560 ^a	214-237
1558	5'-GTG GTG GTG CAT GGC GAT CTC T	1560 ^a	583-604
1559 ^b	5'-GCC GCA GCG AGG TAC TCT TCG TTA	1560 ^a	855-878
Resistance gene: <i>mupA</i>			
2142	5'-GCC TTA ATT TCG GAT AGT GC	2144 ^a	1831-1850
2143 ^b	5'-GAG AAA GAG CCC AAT TAT CTA ATG T	2144 ^a	2002-2026
Resistance gene: <i>parC</i>			
1342	5'-GAT GTT ATT GGT CAA TAT CAT CCA	1321 ^a	205-229
1343 ^b	5'-AAG AAA CTG TCT CTT TAT TAA TAT CAC GT	1321 ^a	396-425
1934	5'-GAA CGC CAG CGC GAA ATT CAA AAA G	1781	67-91
1935 ^b	5'-AGC TCG GCA TAC TTC GAC AGG	1781	277-297
2044	5'-ACC GTA AGT CGG CCA AGT CA	2055 ^a	176-195
2045 ^b	5'-GTT CTT TCT CCG TAT CGT C	2055 ^a	436-454

^a Sequence from databases.

^b These sequences are from the complementary DNA strand of the sequence of the originating fragment given in the Sequence Listing.

Annex L: Specific and ubiquitous primers for nucleic acid amplification (antimicrobial agents resistance genes sequences) (continued).

		Originating DNA fragment	
SEQ ID NO.	Nucleotide sequence	SEQ ID NO.	Nucleotide position
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<u>Resistance gene:</u> <i>ppflo-like</i>			
2163	5'-ACC TTC ATC CTA CCG ATG TGG GTT	2165 ^a	922-945
2164 ^b	5'-CAA CGA CAC CAG CAC TGC CAT TG	2165 ^a	1136-1158
<u>Resistance gene:</u> <i>rpoB</i>			
2065	5'-CCA GGA CGT GGA GGC GAT CAC A	2072 ^a	1218-1239
2066 ^b	5'-CAC CGA CAG CGA GCC GAT CAG A	2072 ^a	1485-1506
<u>Resistance gene:</u> <i>satG</i>			
1581	5'-AAT TGG GGA CTA CAC CTA TTA TGA TG	1585 ^a	93-118
1582 ^b	5'-GGC AAA TCA GTC AGT TCA GGA GT	1585 ^a	310-332
1583	5'-CGA TTG GCA ACA ATA CAC TCC TG	1585 ^a	294-316
1584 ^b	5'-TCA CCT ATT TTT ACG CCT GGT AGG AC	1585 ^a	388-413
<u>Resistance gene:</u> <i>sulII</i>			
1961	5'-GCT CAA GGC AGA TGG CAT TCC C	1965 ^a	222-243
1962 ^b	5'-GGA CAA GGC GGT TGC GTT TGA T	1965 ^a	496-517
1963	5'-CAT TCC CGT CTC GCT CGA CAG T	1965 ^a	237-258
1964 ^b	5'-ATC TGC CTG CCC GTC TTG C	1965 ^a	393-411
<u>Resistance gene:</u> <i>tetB</i>			
1966	5'-CAT GCC AGT CTT GCC AAC G	1970 ^a	66-84
1967 ^b	5'-CAG CAA TAA GTA ATC CAG CGA TG	1970 ^a	242-264
1968	5'-GGA GAG ATT TCA CCG CAT AG	1970 ^a	457-476
1969 ^b	5'-AGC CAA CCA TCA TGC TAT TCC A	1970 ^a	721-742
<u>Resistance gene:</u> <i>tetM</i>			
1586	5'-ATT CCC ACA ATC TTT TTT ATC AAT AA	1590 ^a	361-386
1587 ^b	5'-CAT TGT TCA GAT TCG GTA AAG TTC	1590 ^a	501-524
1588	5'-GTT TTT GAA GTT AAA TAG TGT TCT T	1590 ^a	957-981
1589 ^b	5'-CTT CCA TTT GTA CTT TCC CTA	1590 ^a	1172-1192

^a Sequence from databases.

^b These sequences are from the complementary DNA strand of the sequence of the originating fragment given in the Sequence Listing.

Annex L: Specific and ubiquitous primers for nucleic acid amplification (antimicrobial agents resistance genes sequences) (continued).

		Originating DNA fragment	
SEQ ID NO.	Nucleotide sequence	SEQ ID NO.	Nucleotide position
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<u>Resistance gene:</u> vatB			
1609	5'-GCC CTG ATC CAA ATA GCA TAT A	1613 ^a	11-32
1610 ^b	5'-CCT GGC ATA ACA GTA ACA TTC TG	1613 ^a	379-401
1611	5'-TGG GAA AAA GCA ACT CCA TCT C	1613 ^a	301-322
1612 ^b	5'-ACA ACT GAA TTC GCA GCA ACA AT	1613 ^a	424-446
<u>Resistance gene:</u> vatC			
1614	5'-CCA ATC CAG AAG AAA TAT ACC C	1618 ^a	26-47
1615 ^b	5'-ATT AGT TTA TCC CCA ATC AAT TCA	1618 ^a	177-200
1616	5'-ATA ATG AAT GGG GCT AAT CAT CGT AT	1618 ^a	241-266
1617 ^b	5'-GCC AAC AAC TGA ATA AGG ATC AAC	1618 ^a	463-486
<u>Resistance gene:</u> vga			
1619	5'-AAG GCA AAA TAA AAG GAG CAA AGC	1623 ^a	641-664
1620 ^b	5'-TGT ACC CGA GAC ATC TTC ACC AC	1623 ^a	821-843
1621	5'-AAT TGA AGG ACG GGT ATT GTG GAA AG	1623 ^a	843-868
1622 ^b	5'-CGA TTT TGA CAG ATG GCG ATA ATG AA	1623 ^a	975-1000
<u>Resistance gene:</u> vgaB			
1624	5'-TTC TTT AAT GCT CGT AGA TGA ACC TA	1628 ^a	354-379
1625 ^b	5'-TTT TCG TAT TCT TCT TGT TGC TTT C	1628 ^a	578-602
1626	5'-AGG AAT GAT TAA GCC CCC TTC AAA AA	1628 ^a	663-688
1627 ^b	5'-TTA CAT TGC GAC CAT GAA ATT GCT CT	1628 ^a	849-874
<u>Resistance genes:</u> vgb, vgh			
1629	5'-AAG GGG AAA GTT TGG ATT ACA CAA CA	1633 ^a	73-98
1630 ^b	5'-GAA CCA CAG GGC ATT ATC AGA ACC	1633 ^a	445-468
1631	5'-CGA CGA TGC TTT ATG GTT TGT	1633 ^a	576-596
1632 ^b	5'-GTT AAT TTG CCT ATC TTG TCA CAC TC	1633 ^a	850-875

^a Sequence from databases.

^b These sequences are from the complementary DNA strand of the sequence of the originating fragment given in the Sequence Listing.

Annex L: Specific and ubiquitous primers for nucleic acid amplification (antimicrobial agents resistance genes) (continued).

		Originating DNA fragment	
SEQ ID NO.	Nucleotide sequence	SEQ ID NO.	Nucleotide position
<hr/>			
Resistance gene: <i>vgbB</i>			
1634	5'-TTA ACT TGT CTA TTC CCG ATT CAG G	1882 ^a	23-47
1635 ^b	5'-GCT GTG GCA ATG GAT ATT CTG TA	1882 ^a	267-289
1636	5'-TTC CTA CCC CTG ATG CTA AAG TGA	1882 ^a	155-178
1637 ^b	5'-CAA AGT GCG TTA TCC GAA CCT AA	1882 ^a	442-464
 Sequencing primers			
Resistance gene: <i>gyrA</i>			
1290	5'-GAY TAY GCI ATG ISI GTI ATH GT	1299 ^a	70-83
1292 ^b	5'-ARI SCY TCI ARI ATR TGI GC	1299 ^a	1132-1152
1291	5'-GCI YTI CCI GAY GTI MGI GAY GG	1299 ^a	100-123
1292 ^b	5'-ARI SCY TCI ARI ATR TGI GC	1299 ^a	1132-1152
1293	5'-ATG GCT GAA TTA CCT CAA TC	1299 ^a	1-21
1294 ^b	5'-ATG ATT GTT GTA TAT CTT CTT CAA C	1299 ^a	2626-2651
1295 ^b	5'-CAG AAA GTT TGA AGC GTT GT	1299 ^a	1255-1275
1296	5'-AAC GAT TCG TGA GTC AGA TA	1299 ^a	1188-1208
1297	5'-CGG TCA ACA TTG AGG AAG AGC T	1300 ^a	29-51
1298 ^b	5'-ACG AAA TCG ACC GTC TCT TTT TC	1300 ^a	415-437
Resistance gene: <i>gyrB</i>			
1301	5'-GTI MGI AWI MGI CCI GSI ATG TA	1307 ^a	82-105
1302 ^b	5'-TAI ADI GGI GGI KKI GCI ATR TA	1307 ^a	1600-1623
1303	5'-GGI GAI GAI DYI MGI GAR GG	1307 ^a	955-975
1304 ^b	5'-CIA RYT TIK YIT TIG TYT G	1307 ^a	1024-1043
1305	5'-ATG GTG ACT GCA TTG TCA GAT G	1307 ^a	1-23
1306 ^b	5'-GTC TAC GGT TTT CTA CAA CGT C	1307 ^a	1858-1888

^a Sequence from databases.

^b These sequences are from the complementary DNA strand of the sequence of the originating fragment given in the Sequence Listing.

Annex L: Specific and ubiquitous primers for nucleic acid amplification (antimicrobial agents resistance genes sequences) (continued).

		Originating DNA fragment	
SEQ ID NO.	Nucleotide sequence	SEQ ID NO.	Nucleotide position
Sequencing primers (continued)			
Resistance gene: <i>parC</i>			
1308	5'-ATG TAY GTI ATI ATG GAY MGI GC	1320 ^a	67-90
1309 ^b	5'-ATI ATY TTR TTI CCY TTI CCY TT	1320 ^a	1993-2016
1310	5'-ATI ATI TSI ATI ACY TCR TC	1320 ^a	1112-1132
1311 ^b	5'-GAR ATG AAR ATI MGI GGI GAR CA	1320 ^a	1288-1311
1312	5'-AAR TAY ATI ATI CAR GAR MGI GC	1321 ^a	67-90
1313 ^b	5'-AMI AYI CKR TGI GGI TTI TTY TT	1321 ^a	2212-2235
1314	5'-TAI GAI TTY ACI GAI SMI CAR GC	1321 ^a	1228-1251
1315 ^b	5'-ACI ATI GCI TCI GCY TGI KSY TC	1321 ^a	1240-1263
1316	5'-GTG AGT GAA ATA ATT CAA GAT T	1321 ^a	1-23
1317 ^b	5'-CAC CAA AAT CAT CTG TAT CTA C	1321 ^a	2356-2378
1318	5'-ACC TAY TCS ATG TAC GTR ATC ATG GA	1320 ^a	58-84
1319 ^b	5'-AGR TCG TCI ACC ATC GGY AGY TT	1320 ^a	832-855
Resistance gene: <i>parE</i>			
1322	5'-RTI GAI AAY ISI GTI GAY GAR G	1328 ^a	133-155
1325 ^b	5'-RTT CAT YTC ICC IAR ICC YTT	1328 ^a	1732-1752
1323	5'-ACI AWR SAI GGI GGI ACI CAY G	1328 ^a	829-850
1324 ^b	5'-CCI CCI GCI SWR TCI CCY TC	1328 ^a	1280-1302
1326	5'-TGA TTC AAT ACA GGT TTT AGA G	1328 ^a	27-49
1327 ^b	5'-CTA GAT TTC CTC CTC ATC AAA T	1328 ^a	1971-1993

^a Sequence from databases.

^b These sequences are from the complementary DNA strand of the sequence of the originating fragment given in the Sequence Listing.

Ann x LI: Internal hybridization probes for specific detection of antimicrobial agents resistance genes sequences.

SEQ ID NO.	Nucleotide sequence	Originating DNA fragment	
		SEQ ID NO.	Nucleotide position
Resistance gene: <i>aph3'VIa</i>			
2252	5'-CCA CAT ACA GTG TCT CTC	1406 ^a	149-166
Resistance gene: <i>blaSHV</i>			
1886	5'-GAC GCC CGC GCC ACC ACT	1900 ^a	484-501
1887	5'-GAC GCC CGC GAC ACC ACT A	1899 ^a	514-532
1888	5'-GAC GCC CGC AAC ACC ACT A	1901 ^a	514-532
1889	5'-GTT CGC AAC TGC AGC TGC TG	1899 ^a	593-612
1890	5'-TTC GCA ACG GCA GCT GCT G	1899 ^a	594-612
1891	5'-CCG GAG CTG CCG AIC GGG	1902 ^a	692-709
1892	5'-CGG AGC TGC CAA RCG GGG	1903 ^a	693-710
1893	5'-GGA GCT GGC GAR CGG GGT	1899 ^a	694-711
1894	5'-GAC CGG AGC TAG CGA RCG	1904 ^a	690-707
1895	5'-CGG AGC TAG CAA RCG GGG T	1905 ^a	693-711
1896	5'-GAA ACG GAA CTG AAT GAG GCG	1899 ^a	484-504
1897	5'-CAT TAC CAT GGG CGA TAA CAG	1899 ^a	366-386
1898	5'-CCA TTA CCA TGA GCG ATA ACAG	1899 ^a	365-386
Resistance gene: <i>blaTEM</i>			
1909	5'-ATG ACT TGG TTA AGT ACT CAC C	1928 ^a	293-314
1910	5'-ATG ACT TGG TTG AGT ACT CAC C	1927 ^a	293-314
1911	5'-CCA TAA CCA TGG GTG ATA ACA C	1928 ^a	371-392
1912	5'-CCA TAA CCA TGA GTG ATA ACA C	1927 ^a	371-392
1913	5'-CGC CTT GAT CAT TGG GAA CC	1928 ^a	475-494
1914	5'-CGC CTT GAT CGT TGG GAA CC	1927 ^a	475-494
1915	5'-CGC CTT GAT AGT TGG GAA CC	1929 ^a	475-494
1916	5'-CGT GGG TCT TGC GGT ATC AT	1927 ^a	712-731
1917	5'-CGT GGG TCT GGC GGT ATC AT	1930 ^a	712-731
1918	5'-GTG GGT CTC ACG GTA TCA TTG	1927 ^a	713-733
1919	5'-CGT GGG TCT CTC GGT ATC ATT	1931 ^a	712-732
1920	5'-CGT GGI TCT CGC GGT ATC AT	1927 ^a	712-731
1921	5'-CGT GGG TCT AGC GGT ATC ATT	1932 ^a	713-733
1922	5'-GTT TTC CAA TGA TTA GCA CTT TTA	1927 ^a	188-211
1923	5'-GTT TTC CAA TGA TAA GCA CTT TTA	1927 ^a	188-211
1924	5'-GTT TTC CAA TGC TGA GCA CTT TT	1932 ^a	188-210
1925	5'-CGT TTT CCA ATG ATG AGC ACT TT	1927 ^a	187-209
1926	5'-GTT TTC CAA TGG TGA GCA CTT TT	1933 ^a	188-210
2006	5'-TGG AGC CGG TGA GCG TGG	1927 ^a	699-716

^a Sequence from databases.

Annex LI: Internal hybridization probes for specific detection of antimicrobial agents resistance genes sequences (continued).

		Originating DNA fragment	
SEQ ID NO.	Nucleotide sequence	SEQ ID NO.	Nucleotide position
<hr/>			
<u>Resistance gene:</u> <i>blaTEM</i> (continued)			
2007	5'-TGG AGC CAG TGA GCG TGG	2010 ^a	699-716
2008	5'-TCT GGA GCC GAT GAG CGT G	1929 ^a	697-715
2009	5'-CTG GAG CCA GTA AGC GTG G	2011 ^a	698-716
2141	5'-CAC CAG TCA CAG AAA AGC	1927 ^a	311-328
<u>Resistance gene:</u> <i>dhfrIa</i>			
2253	5'-CAT TAC CCA ACC GAA AGT A	1461 ^a	158-176
<u>Resistance gene:</u> <i>embB</i>			
2104	5'-CTG GGC ATG GCI CGA GTC	2105 ^a	910-927
<u>Resistance gene:</u> <i>gyrA</i>			
1333	5'-TCA TGG TGA CTT ATC TAT TTA TG	1299 ^a	240-263
1334	5'-CAT CTA TTT ATA AAG CAA TGG TA	1299 ^a	251-274
1335	5'-CTA TTT ATG GAG CAA TGG T	1299 ^a	254-273
1940	5'-GTA TCG TTG GTG ACG TAA T	1299 ^a	206-224
1943	5'-GCT GGT GGA CGG CCA G	1954 ^a	279-294
1945	5'-CGG CGA CTA CGC GGT AT	1954 ^a	216-232
1946	5'-CGG CGA CTT CGC GGT AT	1954 ^a	216-232
1947	5'-CGG TAT ACG GCA CCA TCG T	1954 ^a	227-245
1948	5'-GCG GTA TAC AAC ACC ATC G	1954 ^a	226-244
1949	5'-CGG TAT ACG CCA CCA TCG T	1954 ^a	227-245
2042	5'-CAC GGG GAT TTC TCT ATT TA	2054 ^a	103-122
2043	5'-CAC GGG GAT TAC TCT ATT TA	2054 ^a	103-122
<u>Resistance gene:</u> <i>inhA</i>			
2100	5'-GCG AGA CGA TAG GTT GTC	2101 ^a	1017-1034
<u>Resistance gene:</u> <i>parC</i>			
1336	5'-TGG AGA CTA CTC AGT GT	1321 ^a	232-249
1337	5'-TGG AGA CTT CTC AGT GT	1321 ^a	232-249
1338	5'-GTG TAC GGA GCA ATG	1321 ^a	245-260
1339	5'-CCA GCG GAA ATG CGT	1321 ^a	342-357
1941	5'-GCA ATG GTC CGT TTA AGT	1321 ^a	253-270
1944	5'-TTT CGC CGC CAT GCG TTA C	1781	247-265
1950	5'-GGC GAC ATC GCC TGC	1781	137-151
1951	5'-GGC GAC AGA GCC TGC TA	1781	137-153

^a Sequence from databases.

Annex LI: Internal hybridization probes for specific detection of antimicrobial agents resistance genes sequences (continued).

		Originating DNA fragment	
SEQ ID NO.	Nucleotide sequence	SEQ ID NO.	Nucleotide position
<hr/>			
<u>Resistance gene:</u> <i>parC</i> (continued)			
1952	5'-CCT GCT ATG GAG CGA TGG T	1781	147-165
1953	5'-CGC CTG CTA TAA AGC GAT GGT	1781	145-165
2046	5'-ACG GGG ATT TTT CTA TCT AT	2055 ^a	227-246
<hr/>			
<u>Resistance gene:</u> <i>rpoB</i>			
2067	5'-AGC TGA GCC AAT TCA TGG	2072 ^a	1304-1321
2068	5'-ATT CAT GGA CCA GAA CAA C	2072 ^a	1314-1332
2069	5'-CGC TGT CGG GGT TGA CCC	2072 ^a	1334-1351
2070	5'-GTT GAC CCA CAA GCG CCG	2072 ^a	1344-1361
2071	5'-CGA CTG TCG GCG CTG GGG	2072 ^a	1360-1377
<hr/>			
<u>Resistance gene:</u> <i>tetM</i>			
2254	5'-ACC TGA ACA GAG AGA AAT G	1590 ^a	1062-1080

^a Sequence from databases.

Annex LII: Molecular beacon internal hybridization probes for specific detection of atpD sequences.

		Originating DNA fragment	
SEQ ID NO.	Nucleotide sequence ^a	SEQ ID NO.	Nucleotide position
<hr/>			
<u>Bacterial species:</u> <i>Bacteroides fragilis</i>			
2136	5'- <u>CCA</u> <u>ACG</u> <u>CGT</u> CCT CAA TCA TTT CTA ACT TCT ATG GCC GGC <u>GTT</u> GG	929	353-382
<u>Bacterial species:</u> <i>Bordetella pertussis</i>			
2182	5'- <u>GCG</u> <u>CGC</u> CAA CGA CTT CTA CCA CGA AAT GGA AGA GTC <u>GCG</u> <u>CGC</u>	1672	576-605
<u>Bacterial group:</u> <i>Campylobacter jejuni</i> and <i>C. coli</i>			
2133	5'- <u>CCA</u> <u>CGC</u> ACA WAA ACT TGT TTT AGA AGT AGC AGC WCA <u>GCG</u> <u>TGG</u>	1576, 1600,1849, 1863,2139 ^{b,c}	44-73 ^d
<u>Fungal species:</u> <i>Candida glabrata</i>			
2078	5'- <u>CCG</u> <u>AGC</u> CTT GGT CTT CGG CCA AAT GAA <u>CGC</u> <u>TCG</u> G	463	442-463
<u>Fungal species:</u> <i>Candida krusei</i>			
2075	5'- <u>CCG</u> <u>AGC</u> CAG GTT CTG AAG TCT CTG CAT TAT TAG GTG <u>CTC</u> <u>GG</u>	468	720-748
<u>Fungal species:</u> <i>Candida lusitanae</i>			
2080	5'- <u>CCG</u> <u>AGC</u> CGA AGA GGG CCA AGA TGT <u>CGC</u> <u>TCG</u> G	470	520-538
<u>Fungal species:</u> <i>Candida parapsilosis</i>			
2079	5'- <u>CCG</u> <u>AGC</u> GTT CAG TTA CTT CAG TCC AAG CCG <u>GCT</u> <u>CGG</u>	472	837-860
<u>Fungal species:</u> <i>Candida tropicalis</i>			
2077	5'- <u>CCG</u> <u>AGC</u> AAC CGA TCC AGC TCC AGC TAC <u>GCT</u> <u>CGG</u>	475	877-897
<u>Bacterial species:</u> <i>Klebsiella pneumoniae</i>			
2281	5'- <u>CCC</u> <u>CCA</u> GCT GGG CGG CGG TAT CGA <u>TGG</u> <u>GGG</u>	317	40-59

^a Underlined nucleotides indicate the molecular beacon's stem.

^b Sequence from databases.

^c These sequences were aligned to derive the corresponding primer.

^d The nucleotide positions refer to the *C. jejuni* atpD sequence fragment (SEQ ID NO. 1576).

Annex LII: Molecular beacon internal hybridization probes for specific detection of *atpD* sequences (continued).

		Originating DNA fragment	
SEQ ID NO.	Nucleotide sequence ^a	SEQ ID NO.	Nucleotide position
<hr/>			
<u>Fungal genus:</u>		<i>Candida sp.</i>	
2076	5'- <u>CCG</u> <u>AGC</u> YGA YAA CAT TTT CAG ATT CAC CCA 460-478, RGC <u>GCT</u> <u>CGG</u>		697-723 ^c 663 ^b

^a Underlined nucleotides indicate the molecular beacon's stem.

^b These sequences were aligned to derive the corresponding primer.

^c The nucleotide positions refer to the *C. albicans atpD* sequence fragment (SEQ ID NO. 460).

1/27

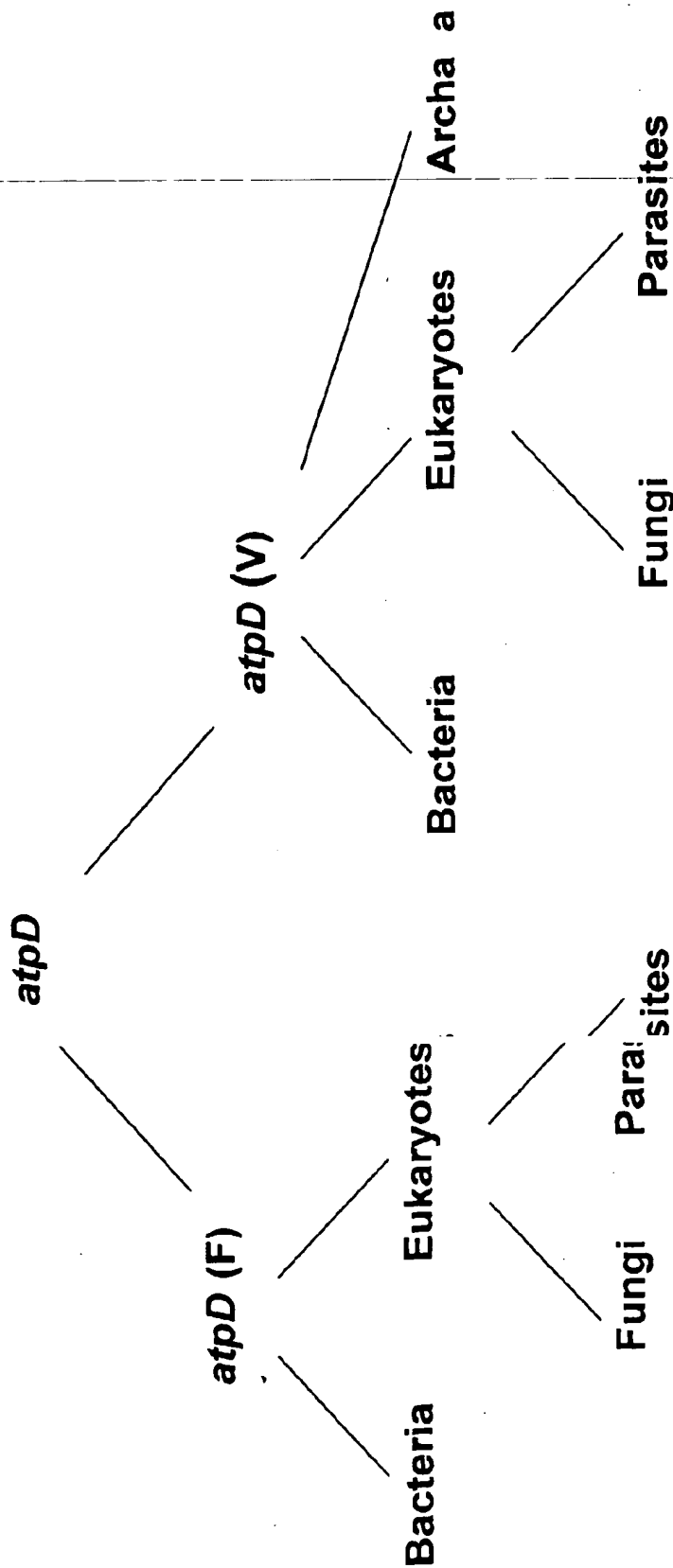
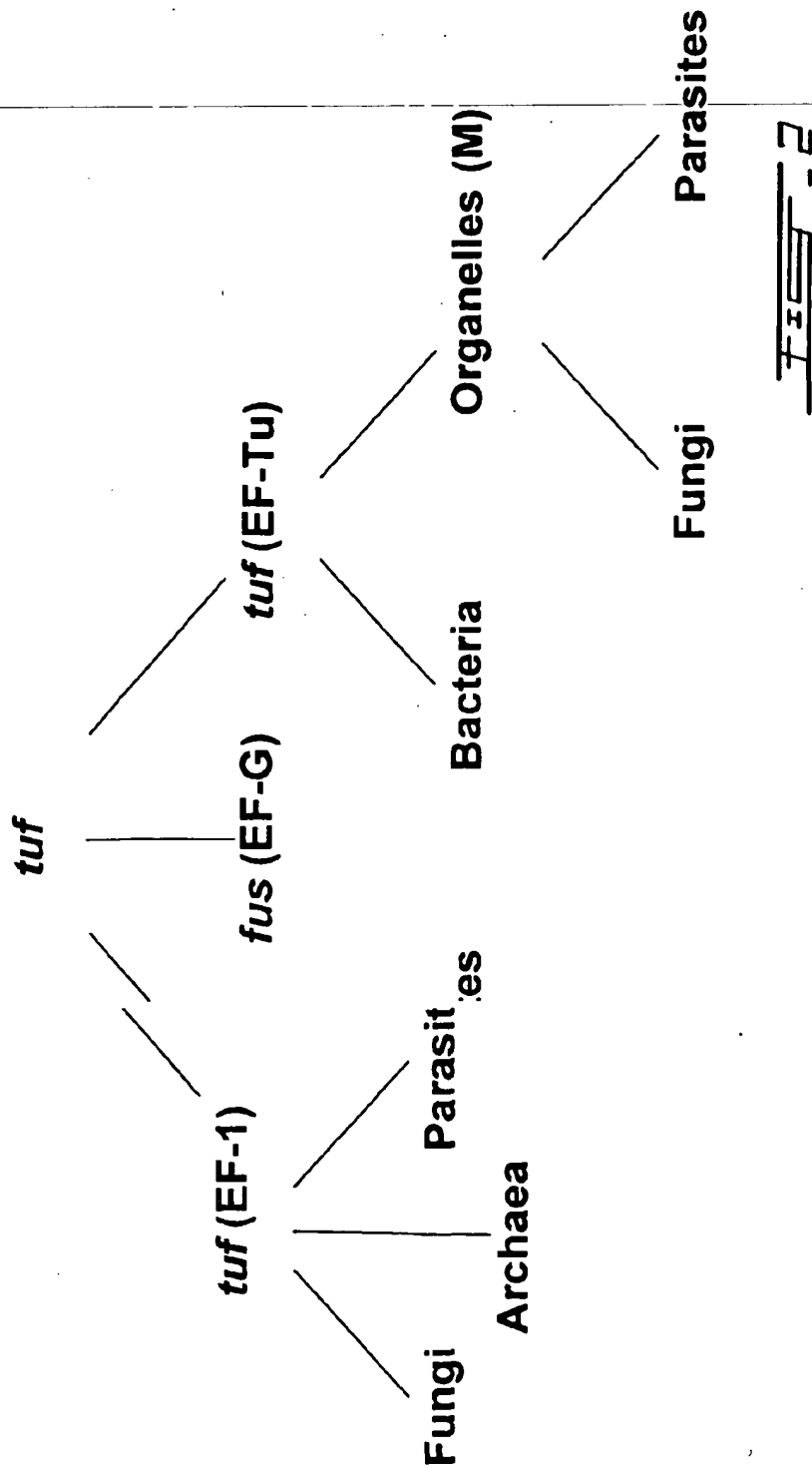


FIG. 1

2 / 27



Annex LIII: Internal hybridization probes for specific detection of *atpD* sequences.

		Originating DNA fragment	
SEQ ID NO.	Nucleotide sequence	SEQ ID NO.	Nucleotide position
<hr/>			
<hr/>			
<u>Bacterial species:</u> <i>Acinetobacter baumannii</i>			
2169	5'-CCC GTT TGC GAA AGG TGG	243	304-321
<u>Bacterial species:</u> <i>Klebsiella pneumoniae</i>			
2167	5'-CAG CAG CTG GGC GGC GGT	317	36-53

Annex LIV: Internal hybridization probes for specific detection of *ddl* and *mtl* sequences.

SEQ ID NO.	Nucleotide sequence	Originating DNA fragment	
		SEQ ID NO.	Nucleotide position

Bacterial species: *Enterococcus faecium (ddl)*

2286	5'-AGT TGC TGT ATT AGG AAA TG	2288 ^a	784-803
2287	5'-TCG AAG TTG CTG TAT TAG GA	2288 ^a	780-799

Bacterial species: *Enterococcus faecalis mtl*

2289	5'-CAC CGA AGA AGA TGA AAA AA	1243 ^a	264-283
2290	5'-TGG CAC CGA AGA AGA TGA	1243 ^a	261-278
2291	5'-ATT TTG GCA CCG AAG AAG A	1243 ^a	257-275

^a Sequence from databases.

What is claimed is:

1. A method for generating a repertory of nucleic acids of *tuf*, *fus*, *atpD* and/or *recA* genes from which are derived probes or primers, or both, useful for the detection of one, more than one related microorganisms, or substantially all microorganisms of a group selected from algae, archaea, bacteria, fungi and parasites, which comprises the step of:

- amplifying the nucleic acids of a plurality of determined algal, archaeal, bacterial, fungal and parasitical species with any combination of the primer pairs defined in SEQ ID NOs.: 543, 556-574, 636-655, 664, 681-683, 694, 696-697, 699-700, 708, 812-815, 911-917, 919-922, 935-938, 1203-1207, 1212-1213, 1221-1229, 1605-1606, 1974-1984, 1999-2003, 2282-2285.

2. A method for generating a repertory of nucleic acid sequences, which comprises the steps of:

- reproducing the method of claim 1, and
- adding the step of:
 - sequencing said nucleic acids.

3. A method for generating sequences of probes, or primers, or both, useful for the detection of one, more than one related microorganisms, or substantially all microorganisms of a group selected from algae, archaea, bacteria, fungi and parasites, which comprises the steps of:

- reproducing the method of claim 2, and
- adding the steps of:
 - aligning a subset of nucleic acid sequences of said repertory,
 - locating nucleic acid stretches that are present in the nucleic acids of strains or representatives of said one, more than one related microorganisms, or substantially all microorganisms of said group, and not present in the nucleic acid sequences of other microorganisms, and

- deriving consensus nucleic acid sequences useful as probes or primers from said stretches.

4. A bank of nucleic acids comprising the repertory of nucleic acids obtained from the method of claim 1.

5. A bank of nucleic acid sequences comprising the repertory of nucleic acid sequences obtained from the method of claim 2.

6. A method for generating sequences of probes, or primers, or both, useful for the detection of one, more than one related microorganisms, or substantially all microorganisms of a group selected from algae, archaea, bacteria, fungi and parasites, which comprises the steps of:

- aligning a subset of nucleic acid sequences of the bank as defined in claim 5,
- locating nucleic acid sequence stretches that are present in the nucleic acid sequences of strains or representatives of said one, more than one related microorganisms, or substantially all microorganisms of said group, and not present in the nucleic acid sequences of other microorganisms, and
- deriving consensus nucleic acid sequences useful as probes or primers from said stretches.

7. A method for generating probes, or primers or both, useful for the detection of one, more than one related microorganisms, or substantially all microorganisms of a group selected from algae, archaea, bacteria, fungi and parasites, which comprises the steps of:

- reproducing the method of claim 3 or 6, and
- adding the step of:
 - synthesising said probes or primers upon the nucleic acid sequences thereof.

8. A nucleic acid used for universal detection of any one of alga, archaeon, bacterium, fungus and parasite which is obtained from the method of claim 7.

9. A nucleic acid used for universal detection as set forth in claim 8, which has a nucleic acid sequence of at least 12 nucleotides capable of hybridizing with said any one of alga, archaeon, bacterium, fungus and parasite and with any one of SEQ ID NOs.: 543, 556-574, 636-655, 658-661, 664, 681-683, 694, 696, 697, 699, 700, 708, 812-815, 911-917, 919-922, 935-938, 1203-1207, 1212-1213, 1221-1229, 1605-1606, 1974-1984, 1999-2003, 2282-2285.

10. A nucleic acid used for the specific and ubiquitous detection and for identification of any one of a algal, archaeal, bacterial, fungal and parasitital species, genus, family and group, which is obtained from the method of claim 7.

11. A nucleic acid as set forth in claim 10 having any one of the nucleotide sequences which are defined in SEQ ID NOs.:

- | | |
|--|--|
| 539, 540 | for the detection and/or identification of <i>Mycobacteriaceae</i> family |
| 541, 542, 544, 2121 | for the detection and/or identification of Pseudomonads group |
| 545, 546 | for the detection and/or identification of <i>Corynebacterium</i> sp. |
| 547, 548, 1202 | for the detection and/or identification of <i>Streptococcus</i> sp. |
| 549, 550, 582, 583, 625, 626, 627, 628, | for the detection and/or identification of <i>Streptococcus agalactiae</i> |
| 1199 ¹¹⁹⁹ | |
| 551, 552, 2166, 2173, 2174, 2175, 2176, 2177, 2178, 2179 | for the detection and/or identification of <i>Neisseria gonorrhoeae</i> |
| 553, 575, 605, 606, 707, 1175, 1176 | for the detection and/or identification of <i>Staphylococcus</i> sp. |
| 554, 555, 2213 | for the detection and/or identification of <i>Chlamydia trachomatis</i> |

- 576, 631, 632, 633, for the detection and/or identification of *Candida* sp.
 634, 635, 1163,
 1164, 1167, 2076,
 2108, 2109
 577, 1156, 1160 for the detection and/or identification of *Candida albicans*
 2073
-
- 578, 1166, 1168, for the detection and/or identification of *Candida dubliniensis*
 2074
 579, 2168 for the detection and/or identification of *Escherichia coli*
 580, 603, 1174, for the detection and/or identification of *Enterococcus*
 1236, 1238, 2289, *faecalis*
 2290, 2291
 581 for the detection and/or identification of *Haemophilus*
influenzae
 584, 585, 586, 587, for the detection and/or identification of *Staphylococcus*
 588, 1232, 1234, *aureus*
 2186
 589, 590, 591, 592, for the detection and/or identification of *Staphylococcus*
 593 *epidermidis*
 594, 595 for the detection and/or identification of *Staphylococcus*
haemolyticus
 596, 597, 598 for the detection and/or identification of *Staphylococcus*
hominis
 599, 600, 601, 695, for the detection and/or identification of *Staphylococcus*
 1208, 1209 *saprophyticus*
 602, 1235, 1237, for the detection and/or identification of *Enterococcus*
 1696, 1697, 1698, *faecium*
 1699, 1700, 1701,
 2286, 2287
 604 for the detection and/or identification of *Enterococcus*
gallinarum
 620, 1122 for the detection and/or identification of *Enterococcus*
casseliflavus, *E. flavescens* and *E. gallinarum*
 629, 630, 2085, for the detection and/or identification of *Chlamydia*
 2086, 2087, 2088, *pneumoniae*
 2089, 2090, 2091,
 2092

636, 637, 638, 639, for the detection and/or identification of at least the following:
640, 641, 642

Abiotrophia adiacens, *Abiotrophia defectiva*, *Acinetobacter baumannii*, *Acinetobacter lwoffii*, *Aerococcus viridans*, *Bacillus anthracis*, *Bacillus cereus*, *Bacillus subtilis*, *Brucella abortus*, *Burkholderia cepacia*, *Citrobacter diversus*, *Citrobacter freundii*, *Enterobacter aerogenes*, *Enterobacter agglomerans*, *Enterobacter cloacae*, *Enterococcus avium*, *Enterococcus casseliflavus*, *Enterococcus dispar*, *Enterococcus durans*, *Enterococcus faecalis*, *Enterococcus faecium*, *Enterococcus flavescens*, *Enterococcus gallinarum*, *Enterococcus mundtii*, *Enterococcus raffinosus*, *Enterococcus solitarius*, *Escherichia coli*, *Gemella morbillorum*, *Haemophilus ducreyi*, *Haemophilus haemolyticus*, *Haemophilus influenzae*, *Haemophilus parahaemolyticus*, *Haemophilus parainfluenzae*, *Hafnia alvei*, *Kingella kingae*, *Klebsiella oxytoca*, *Klebsiella pneumoniae*, *Legionella pneumophila*, *Megamonas hypermegale*, *Moraxella atlantae*, *Moraxella catarrhalis*, *Morganella morganii*, *Neisseria gonorrhoeae*, *Neisseria meningitidis*, *Pasteurella aerogenes*, *Pasteurella multocida*, *Peptostreptococcus magnus*, *Proteus mirabilis*, *Providencia alcalifaciens*, *Providencia rettgeri*, *Providencia rustigianii*, *Providencia stuartii*, *Pseudomonas aeruginosa*, *Pseudomonas fluorescens*, *Pseudomonas stutzeri*, *Salmonella bongori*, *Salmonella choleraesuis*, *Salmonella enteritidis*, *Salmonella gallinarum*, *Salmonella typhimurium*, *Serratia liquefaciens*, *Serratia marcescens*, *Shigella flexneri*, *Shigella sonnei*, *Staphylococcus aureus*, *Staphylococcus capitis*, *Staphylococcus epidermidis*, *Staphylococcus haemolyticus*, *Staphylococcus hominis*, *Staphylococcus lugdunensis*, *Staphylococcus saprophyticus*, *Staphylococcus simulans*, *Staphylococcus warneri*, *Stenotrophomonas maltophilia*, *Streptococcus acidominimus*, *Streptococcus agalactiae*, *Streptococcus anginosus*, *Streptococcus bovis*, *Streptococcus constellatus*, *Streptococcus cricetus*, *Streptococcus cristatus*, *Streptococcus dysgalactiae*, *Streptococcus equi*, *Streptococcus ferus*, *Streptococcus gordonii*, *Streptococcus intermedius*, *Streptococcus macacae*, *Streptococcus mitis*, *Streptococcus mutans*, *Streptococcus oralis*, *Streptococcus parasanguinis*, *Streptococcus parauberis*, *Streptococcus pneumoniae*, *Streptococcus pyogenes*, *Streptococcus rattus*, *Streptococcus salivarius*, *Streptococcus sanguinis*, *Streptococcus sobrinus*, *Streptococcus uberis*, *Streptococcus vestibularis*, *Vibrio cholerae*, *Yersinia enterocolitica*, *Yersinia pestis*, *Yersinia pseudotuberculosis*.

656, 657, 271, for the detection and/or identification of *Enterococcus* sp.

1136, 1137

701, 702 for the detection and/or identification of *Leishmania* sp.

- 703, 704, 705, 706, for the detection and/or identification of *Entamoeba* sp.
793
- 794, 795 for the detection and/or identification of *Trypanosoma cruzi*
- 796, 797, 808, 809, for the detection and/or identification of *Clostridium* sp.
810, 811
-
- 798, 799, 800, 801, for the detection and/or identification of *Cryptosporidium*
802, 803, 804, 805, *parvum*
806, 807
- 816, 817, 818, 819 for the detection and/or identification of *Giardia* sp.
- 820, 821, 822 for the detection and/or identification of *Trypanosoma*
brucei
- 823, 824 for the detection and/or identification of *Trypanosoma* sp.
- 825, 826 for the detection and/or identification of *Bordetella* sp.
- 923, 924, 925, 926, for the detection and/or identification of *Trypanosomatidae*
927, 928 family
- 933, 934 for the detection and/or identification of *Enterobacteriaceae*
group
- 994, 995, 996, 997, for the detection and/or identification of *Streptococcus*
998, 999, 1000, *pyogenes*
1001, 1200, 1210,
1211
- 1157, 2079, 2118 for the detection and/or identification of *Candida*
parapsilosis
- 1158, 1159, 2078, for the detection and/or identification of *Candida glabrata*
2110, 2111
- 1160, 2077, 2119, for the detection and/or identification of *Candida tropicalis*
2120
- 1161, 2075, 2112, for the detection and/or identification of *Candida krusei*
2113, 2114
- 1162 for the detection and/or identification of *Candida*
guilliermondii
- 1162, 2080, 2115 for the detection and/or identification of *Candida lusitaniae*
2116, 2117
- 1165 for the detection and/or identification of *Candida*
zeylanoides
- 1201 for the detection and/or identification of *Streptococcus*
pneumoniae

1233	for the detection and/or identification of <i>Staphylococcus</i> sp. other than <i>S. aureus</i>
1329, 1330, 1331, 1332, 2167, 2281	for the detection and/or identification of <i>Klebsiella pneumoniae</i>
1661, 1665	for the detection and/or identification of <i>Escherichia coli</i> and <i>Shigella</i> sp.
1690, 1691, 1692, 1693, 2169	for the detection and/or identification of <i>Acinetobacter baumannii</i>
1694, 1695, 2122	for the detection and/or identification of <i>Pseudomonas aeruginosa</i>
1971, 1972, 1973	for the detection and/or identification of <i>Cryptococcus</i> sp.
2081, 2082, 2083	for the detection and/or identification of <i>Legionella</i> sp.
2084	for the detection and/or identification of <i>Legionella pneumophila</i>
2093, 2094, 2095, 2096	for the detection and/or identification of <i>Mycoplasma pneumoniae</i>
2106, 2107	for the detection and/or identification of <i>Cryptococcus neoformans</i>
2131, 2132, 2133	for the detection and/or identification of <i>Campylobacter jejuni</i> and <i>C. coli</i>
2134, 2135, 2136	for the detection and/or identification of <i>Bacteroides fragilis</i>
2170	for the detection and/or identification of <i>Abiotrophia adiacens</i>
2171	for the detection and/or identification of <i>Gemella</i> sp.
2172	for the detection and/or identification of <i>Enterococcus</i> sp., <i>Gemella</i> sp., <i>A. adiacens</i>
2180, 2181, 2182	for the detection and/or identification of <i>Bordetella pertussis</i> .

12. A method for detecting the presence in a test sample of a microorganism that is an alga, archaeum, bacterium, fungus or parasite, which comprises:

- a) putting in contact any test sample *tuf* or *atpD* or *recA* nucleic acids and nucleic acid primers and/or probes, said primers and/or probes having

been selected to be sufficiently complementary to hybridize to one or more *tuf* or *atpD* or *recA* nucleic acids that are specific to said group of microorganisms;

b) allowing the primers and/or probes and any test sample *tuf* or *atpD* or *recA* nucleic acids to hybridize under specified conditions such as said primers and/or probes hybridize to the *tuf* or *atpD* or *recA* nucleic acids of said microorganism and does not detectably hybridize to *tuf* or *atpD* or *recA* sequences from other microorganisms; and,

c) testing for hybridization of said primers and/or probes to any test sample *tuf* or *atpD* or *recA* nucleic acids.

13. The method of claim 12 wherein c) is based on a nucleic acid target amplification method.

14. The method of claim 12 wherein c) is based on a signal amplification method.

15. The method of any one of claims 12 to 14 wherein said primers and/or probes that are sufficiently complementary are perfectly complementary.

16. The method of any one of claims 12 to 14 wherein said primers and/or probes that are sufficiently complementary are not perfectly complementary.

17. A method for the specific detection and/or identification of a microorganism that is an algal, archaeal, bacterial, fungal or parasitical species, genus, family or group in any sample, using a panel of probes or amplification primers or both, each individual probe or primer being derived from a nucleic acid which has a nucleotide sequence of at least 12 nucleotides in length capable of hybridizing with the nucleic acids of said microorganism and with a nucleic acid having any one of the nucleotide sequences defined in SEQ ID NOs.:

539, 540 for the detection and/or identification of *Mycobacteriaceae* family

541, 542, 544, 2121 for the detection and/or identification of *Pseudomonads* group

545, 546	for the detection and/or identification of <i>Corynebacterium</i> sp.
547, 548, 1202	for the detection and/or identification of <i>Streptococcus</i> sp.
549, 550, 582, 583, 625, 626, 627, 628,	for the detection and/or identification of <i>Streptococcus agalactiae</i>
1199	
551, 552, 2166, 2173, 2174, 2175, 2176, 2177, 2178, 2179	for the detection and/or identification of <i>Neisseria gonorrhoeae</i>
553, 575, 605, 606, 707, 1175, 1176	for the detection and/or identification of <i>Staphylococcus</i> sp.
554, 555, 2213	for the detection and/or identification of <i>Chlamydia trachomatis</i>
576, 631, 632, 633, 634, 635, 1163, 1164, 1167, 2076, 2108, 2109	for the detection and/or identification of <i>Candida</i> sp.
577, 1156, 1160 2073	for the detection and/or identification of <i>Candida albicans</i>
578, 1166, 1168, 2074	for the detection and/or identification of <i>Candida dubliniensis</i>
579, 2168	for the detection and/or identification of <i>Escherichia coli</i>
580, 603, 1174, 1236, 1238, 2289, 2290, 2291	for the detection and/or identification of <i>Enterococcus faecalis</i>
581	for the detection and/or identification of <i>Haemophilus influenzae</i>
584, 585, 586, 587, 588, 1232, 1234, 2186	for the detection and/or identification of <i>Staphylococcus aureus</i>
589, 590, 591, 592, 593	for the detection and/or identification of <i>Staphylococcus epidermidis</i>
594, 595	for the detection and/or identification of <i>Staphylococcus haemolyticus</i>
596, 597, 598	for the detection and/or identification of <i>Staphylococcus hominis</i>

- 599, 600, 601, 695, for the detection and/or identification of *Staphylococcus saprophyticus*
1208, 1209
- 602, 1235, 1237, for the detection and/or identification of *Enterococcus faecium*
1696, 1697, 1698,
1699, 1700, 1701,
2286, 2287
- 604 for the detection and/or identification of *Enterococcus gallinarum*
- 620, 1122 for the detection and/or identification of *Enterococcus casseliflavus*, *E. flavescens* and *E. gallinarum*
- 629, 630, 2085, for the detection and/or identification of *Chlamydia pneumoniae*
2086, 2087, 2088,
2089, 2090, 2091,
2092
- 636, 637, 638, 639, for the detection and/or identification of at least the following:
640, 641, 642
Abiotrophia adiacens, *Abiotrophia defectiva*, *Acinetobacter baumannii*, *Acinetobacter lwoffii*, *Aerococcus viridans*, *Bacillus anthracis*, *Bacillus cereus*, *Bacillus subtilis*, *Brucella abortus*, *Burkholderia cepacia*, *Citrobacter diversus*, *Citrobacter freundii*, *Enterobacter aerogenes*, *Enterobacter agglomerans*, *Enterobacter cloacae*, *Enterococcus avium*, *Enterococcus casseliflavus*, *Enterococcus dispar*, *Enterococcus durans*, *Enterococcus faecalis*, *Enterococcus faecium*, *Enterococcus flavescens*, *Enterococcus gallinarum*, *Enterococcus mundtii*, *Enterococcus raffinosus*, *Enterococcus solitarius*, *Escherichia coli*, *Gemella morbillorum*, *Haemophilus ducreyi*, *Haemophilus haemolyticus*, *Haemophilus influenzae*, *Haemophilus parahaemolyticus*, *Haemophilus parainfluenzae*, *Hafnia alvei*, *Kingella kingae*, *Klebsiella oxytoca*, *Klebsiella pneumoniae*, *Legionella pneumophila*, *Megamonas hypermegale*, *Moraxella atlantae*, *Moraxella catarrhalis*, *Morganella morganii*, *Neisseria gonorrhoeae*, *Neisseria meningitidis*, *Pasteurella aerogenes*, *Pasteurella multocida*, *Peptostreptococcus magnus*, *Proteus mirabilis*, *Providencia alcalifaciens*, *Providencia rettgeri*, *Providencia rustigianii*, *Providencia stuartii*, *Pseudomonas aeruginosa*, *Pseudomonas fluorescens*, *Pseudomonas stutzeri*, *Salmonella bongori*, *Salmonella choleraesuis*, *Salmonella enteritidis*, *Salmonella gallinarum*, *Salmonella typhimurium*, *Serratia liquefaciens*, *Serratia marcescens*, *Shigella flexneri*, *Shigella sonnei*, *Staphylococcus aureus*, *Staphylococcus capitis*, *Staphylococcus epidermidis*, *Staphylococcus haemolyticus*, *Staphylococcus hominis*, *Staphylococcus lugdunensis*, *Staphylococcus saprophyticus*, *Staphylococcus simulans*, *Staphylococcus warneri*, *Stenotrophomonas*

maltophilia, Streptococcus acidominimus, Streptococcus agalactiae, Streptococcus anginosus, Streptococcus bovis, Streptococcus constellatus, Streptococcus cricetus, Streptococcus cristatus, Streptococcus dysgalactiae, Streptococcus equi, Streptococcus ferus, Streptococcus gordonii, Streptococcus intermedius, Streptococcus macacae, Streptococcus mitis, Streptococcus mutans, Streptococcus oralis, Streptococcus parasanguinis, Streptococcus parauberis, Streptococcus pneumoniae, Streptococcus pyogenes, Streptococcus rattus, Streptococcus salivarius, Streptococcus sanguinis, Streptococcus sobrinus, Streptococcus uberis, Streptococcus vestibularis, Vibrio cholerae, Yersinia enterocolitica, Yersinia pestis, Yersinia pseudotuberculosis.

- 656, 657, 271, 1136, 1137 for the detection and/or identification of *Enterococcus* sp.
- 701, 702 for the detection and/or identification of *Leishmania* sp.
- 703, 704, 705, 706, 793 for the detection and/or identification of *Entamoeba* sp.
- 794, 795 for the detection and/or identification of *Trypanosoma cruzi*
- 796, 797, 808, 809, 810, 811 for the detection and/or identification of *Clostridium* sp.
- 798, 799, 800, 801, 802, 803, 804, 805, 806, 807 for the detection and/or identification of *Cryptosporidium parvum*
- 816, 817, 818, 819 for the detection and/or identification of *Giardia* sp.
- 820, 821, 822 for the detection and/or identification of *Trypanosoma brucei*
- 823, 824 for the detection and/or identification of *Trypanosoma* sp.
- 825, 826 for the detection and/or identification of *Raxdetella* sp.
- 923, 924, 925, 926, 927, 928 for the detection and/or identification of *Trypanosomatidae* family
- 933, 934 for the detection and/or identification of *Enterobacteriaceae* group
- 994, 995, 996, 997, 998, 999, 1000, 1001, 1200, 1210, 1211 for the detection and/or identification of *Streptococcus pyogenes*
- 1157, 2079, 2118 for the detection and/or identification of *Candida parapsilosis*

1158, 1159, 2078, 2110, 2111	for the detection and/or identification of <i>Candida glabrata</i>
1160, 2077, 2119, 2120	for the detection and/or identification of <i>Candida tropicalis</i>
1161, 2075, 2112, 2113, 2114	for the detection and/or identification of <i>Candida krusei</i>
1162	for the detection and/or identification of <i>Candida guilliermondii</i>
1162, 2080, 2115 2116, 2117	for the detection and/or identification of <i>Candida lusitaniae</i>
1165	for the detection and/or identification of <i>Candida zeylanoides</i>
1201	for the detection and/or identification of <i>Streptococcus pneumoniae</i>
1233	for the detection and/or identification of <i>Staphylococcus</i> sp. other than <i>S. aureus</i>
1329, 1330, 1331, 1332, 2167, 2281	for the detection and/or identification of <i>Klebsiella pneumoniae</i>
1661, 1665	for the detection and/or identification of <i>Escherichia coli</i> and <i>Shigella</i> sp.
1690, 1691, 1692, 1693, 2169	for the detection and/or identification of <i>Acinetobacter baumannii</i>
1694, 1695, 2122	for the detection and/or identification of <i>Pseudomonas aeruginosa</i>
1971, 1972, 1973	for the detection and/or identification of <i>Cryptococcus</i> sp.
2081, 2082, 2083	for the detection and/or identification of <i>Legionella</i> sp.
2084	for the detection and/or identification of <i>Legionella pneumophila</i>
2093, 2094, 2095, 2096	for the detection and/or identification of <i>Mycoplasma pneumoniae</i>
2106, 2107	for the detection and/or identification of <i>Cryptococcus neoformans</i>
2131, 2132, 2133	for the detection and/or identification of <i>Campylobacter jejuni</i> and <i>C. coli</i>
2134, 2135, 2136	for the detection and/or identification of <i>Bacteroides fragilis</i>

- 2170 for the detection and/or identification of *Abiotrophia adiacens*
 2171 for the detection and/or identification of *Gemella* sp.
 2172 for the detection and/or identification of *Enterococcus* sp.,
Gemella sp., *A. adiacens*
 2180, 2181, 2182 for the detection and/or identification of *Bordetella pertussis*,

said method comprising the step of contacting the nucleic acids of the sample with said primers or probes under suitable conditions of hybridization or of amplification and detecting the presence of hybridized probes or amplified products as an indication of the presence of said specific algal, archaeal, bacterial, fungal or parasitical species, genus, family or group.

18. A method for the universal detection of any bacterium, fungus or parasite in a sample, using a panel of probes or amplification primers or both, each individual probe or primer being derived from a nucleic acid as defined in claims 8 or 9, the method comprising the step of contacting the nucleic acids of the sample with said primers or probes under suitable conditions of hybridization or of amplification and detecting the presence of any alga, archaeon, bacterium, fungus or parasite.

19. A method as set forth in claim 17 or 18, which further comprises probes or primers, or both, for the detection of at least one antimicrobial agent resistance gene.

20. A method as set forth in claim 17, 18 or 19, which further comprises probes or primers, or both, for the detection of at least one toxin gene.

21. A method as set forth in claim 19 or 20, wherein the probes or primers for the detection of said antimicrobial agent resistance gene or toxin gene have at least 12 nucleotides in length capable of hybridizing with an antimicrobial agent resistance gene and/or toxin gene selected from SEQ ID NOs.:

- 1078, 1079, 1085 for the detection and/or identification of the *E. coli* Shiga-like toxin 2 (*stx*₂) gene

1080, 1081, 1084, 2012	for the detection and/or identification of the <i>E. coli</i> Shiga-like toxin 1 (<i>stx</i> ₁) gene
1082, 1083	for the detection and/or identification of <i>E. coli</i> Shiga-like toxins 1 and 2 (<i>stx</i>) genes
1086, 1087, 1088, 1089, 1090, 1091, 1092, 1170, 1239, 1240, 2292	for the detection and/or identification of the <i>vanA</i> resistance gene
1095, 1096, 1171, 1241, 2294, 2295	for the detection and/or identification of the <i>vanB</i> resistance gene
1111, 1112, 1113, 1114, 1115, 1116, 1118, 1119, 1120, 1121, 1123, 1124	for the detection and/or identification of the <i>vanAB</i> resistance genes
1103, 1104, 1109, 1110	for the detection and/or identification of the <i>vanC1</i> resistance gene
1105, 1106, 1107, 1108	for the detection and/or identification of the <i>vanC2</i> and <i>vanC3</i> resistance genes
1097, 1098, 1099, 1100, 1101, 1102	for the detection and/or identification of the <i>vanC1</i> , <i>vanC2</i> and <i>vanC3</i> resistance genes
1150, 1153, 1154, 1155	for the detection and/or identification of the <i>vanAXY</i> resistance genes
1094, 1125, 1126, 1127, 1128, 1129, 1130, 1131, 1132, 1133, 1134, 1135, 1192, 1193, 1194, 1195, 1196, 1197, 1214, 1216, 1217, 1218, 1219, 1220, 2015, 2016, 2017, 2018, 2019, 2020, 2021, 2022, 2023, 2024, 2025, 2026, 2027, 2028, 2029, 2030, 2031, 2032, 2033, 2034, 2035, 2036, 2037, 2038, 2039	for the detection and/or identification of the <i>S. pneumoniae</i> <i>pbpla</i> gene

1142, 1143, 1144, 1145	for the detection and/or identification of the <i>S. pneumoniae</i> <i>pbp2b</i> gene
1146, 1147, 1148, 1149	for the detection and/or identification of the <i>S. pneumoniae</i> <i>pbp2x</i> gene
1177, 1231	for the detection and/or identification of the <i>mecA</i> resistance gene
1290, 1291, 1292, 1293, 1294, 1295, 1296, 1297, 1298, 1333, 1334, 1335, 1340, 1341, 1936, 1937, 1940, 1942, 1943, 1945, 1946, 1947, 1948, 1949, 2040, 2041, 2042, 2043, 2250, 2251	for the detection and/or identification of the <i>gyrA</i> resistance gene
1301, 1302, 1303, 1304, 1305, 1306	for the detection and/or identification of the <i>gyrB</i> resistance gene
1308, 1309, 1310, 1311, 1312, 1313, 1314, 1315, 1316, 1317, 1318, 1319, 1336, 1337, 1338, 1339, 1342, 1343, 1934, 1935, 1938, 1939, 1941, 1944, 1950, 1951, 1952, 1953, 1955, 2044, 2045, 2046	for the detection and/or identification of the <i>parC</i> resistance gene
1322, 1323, 1324, 1325, 1326, 1327	for the detection and/or identification of the <i>parE</i> resistance gene
1344, 1345, 1346, 1347	for the detection and/or identification of the <i>aac(2')-Ia</i> resistance gene
1349, 1350	for the detection and/or identification of the <i>aac(3')-Ib</i> resistance gene
1352, 1353, 1354, 1355	for the detection and/or identification of the <i>aac(3')-IIIb</i> resistance gene
1357, 1358, 1359, 1360	for the detection and/or identification of the <i>aac(3')-IVa</i> resistance gene
1362, 1363, 1364, 1365	for the detection and/or identification of the <i>aac(3')-VIa</i> resistance gene

1367, 1368, 1369, 1370	for the detection and/or identification of the <i>aac(6')-Ia</i> resistance gene
1372, 1373, 1374, 1375	for the detection and/or identification of the <i>aac(6')-Ic</i> resistance gene
1377, 1378, 1379, 1380	for the detection and/or identification of the <i>ant(3')-Ia</i> resistance gene
1382, 1383, 1384, 1385	for the detection and/or identification of the <i>ant(4')-Ia</i> resistance gene
1387, 1388, 1389, 1390	for the detection and/or identification of the <i>aph(3')-Ia</i> resistance gene
1392, 1393, 1394, 1395	for the detection and/or identification of the <i>aph(3')-IIa</i> resistance gene
1397, 1398, 1399, 1400	for the detection and/or identification of the <i>aph(3')-IIIa</i> resistance gene
1402, 1403, 1404, 1405, 2252	for the detection and/or identification of the <i>aph(3')-VIa</i> resistance gene
1407, 1408, 1409 1410	for the detection and/or identification of the <i>blaCARB</i> resistance gene
1412, 1413, 1414, 1415	for the detection and/or identification of the <i>blaCMY-2</i> resistance gene
1417, 1418	for the detection and/or identification of the <i>blaCTX-M- I</i> and <i>blaCTX-M-2</i> resistance genes
1419, 1420, 1421, 1422	for the detection and/or identification of the <i>blaCTX-M-1</i> resistance gene
1424, 1425, 1426, 1427	for the detection and/or identification of the <i>blaCTX-M-2</i> resistance gene
1429, 1430, 1431, 1432	for the detection and/or identification of the <i>blaIMP</i> resistance gene
1434, 1435	for the detection and/or identification of the <i>blaOXA2</i> resistance gene
1436, 1437	for the detection and/or identification of the <i>blaOXA10</i> resistance gene
1440, 1441	for the detection and/or identification of the <i>blaPER-1</i> resistance gene

1443, 1444	for the detection and/or identification of the <i>blaPER-2</i> resistance gene
1446, 1447, 1448, 1449	for the detection and/or identification of the <i>blaPER-1</i> and <i>blaPER-2</i> resistance genes
1450, 1451	for the detection and/or identification of the <i>dhfrA</i> resistance gene
1453, 1454, 1455, 1456	for the detection and/or identification of the <i>dhfrIa</i> and <i>dhfrXV</i> resistance genes
1457, 1458, 1459, 1460, 2253	for the detection and/or identification of the <i>dhfrIa</i> resistance gene
1462, 1463, 1464, 1465	for the detection and/or identification of the <i>dhfrIb</i> and <i>dhfrV</i> resistance genes
1466, 1467, 1468, 1469	for the detection and/or identification of the <i>dhfrIb</i> resistance gene
1471, 1472, 1473, 1474	for the detection and/or identification of the <i>dhfrV</i> resistance gene
1476, 1477, 1478, 1479	for the detection and/or identification of the <i>dhfrVI</i> resistance gene
1481, 1482, 1483, 1484	for the detection and/or identification of the <i>dhfrVII</i> and <i>dhfrXVII</i> resistance genes
1485, 1486, 1487, 1488	for the detection and/or identification of the <i>dhfrVII</i> resistance gene
1490, 1491, 1492, 1493	for the detection and/or identification of the <i>dhfrVIII</i> resistance gene
1495, 1496, 1497, 1498	for the detection and/or identification of the <i>dhfrIX</i> resistance gene
1500, 1501, 1502, 1503	for the detection and/or identification of the <i>dhfrXII</i> resistance gene
1505, 1506	for the detection and/or identification of the <i>dhfrXIII</i> resistance gene
1508, 1509, 1510, 1511	for the detection and/or identification of the <i>dhfrXV</i> resistance gene
1513, 1514, 1515, 1516	for the detection and/or identification of the <i>dhfrXVII</i> resistance gene

1528, 1529	for the detection and/or identification of the <i>ereA</i> and <i>ereA2</i> resistance genes
1531, 1532, 1533, 1534	for the detection and/or identification of the <i>ereB</i> resistance gene
1536, 1537, 1538, 1539	for the detection and/or identification of the <i>linA</i> and <i>linA'</i> resistance genes
1541, 1542, 1543, 1544	for the detection and/or identification of the <i>linB</i> resistance gene
1546, 1547	for the detection and/or identification of the <i>mefA</i> resistance gene
1549, 1550	for the detection and/or identification of the <i>mefE</i> resistance gene
1552, 1553, 1554, 1555	for the detection and/or identification of the <i>mefA</i> and <i>mefE</i> resistance genes
1556, 1557, 1558, 1559	for the detection and/or identification of the <i>mphA</i> and <i>mphK</i> resistance genes
1581, 1582, 1583, 1584	for the detection and/or identification of the <i>satG</i> resistance gene
1586, 1587, 1588, 1589, 2254	for the detection and/or identification of the <i>tetM</i> resistance gene
1591, 1592, 1593, 2297	for the detection and/or identification of the <i>vanD</i> resistance gene
1595, 1596, 1597, 1598	for the detection and/or identification of the <i>vanE</i> resistance gene
1609, 1610, 1611, 1612	for the detection and/or identification of the <i>vatB</i> resistance gene
1614, 1615, 1616, 1617	for the detection and/or identification of the <i>vatC</i> resistance gene
1619, 1620, 1621, 1622	for the detection and/or identification of the <i>vga</i> resistance gene
1624, 1625, 1626, 1627	for the detection and/or identification of the <i>vgaB</i> resistance gene
1629, 1630, 1631, 1632	for the detection and/or identification of the <i>vgb</i> and <i>vgh</i> resistance genes

1634, 1635, 1636, 1637	for the detection and/or identification of the <i>vgbB</i> resistance gene
1883, 1884, 1885, 1886, 1887, 1888, 1889, 1890, 1891, 1892, 1893, 1894, 1895, 1896, 1897, 1898	for the detection and/or identification of the <i>blaSHV</i> resistance gene
1906, 1907, 1908, 1909, 1910, 1911, 1912, 1913, 1914, 1915, 1916, 1917, 1918, 1919, 1920, 1921, 1922, 1923, 1924, 1925, 1926, 2006, 2007, 2008, 2009, 2141	for the detection and/or identification of the <i>blaTEM</i> resistance gene
1961, 1962, 1963, 1964	for the detection and/or identification of the <i>sulII</i> resistance gene
1966, 1967, 1968, 1969	for the detection and/or identification of the <i>tetB</i> resistance gene
2065, 2066, 2067, 2068, 2069, 2070, 2071	for the detection and/or identification of the <i>rpoB</i> resistance gene
2098, 2099, 2100	for the detection and/or identification of the <i>inhA</i> resistance gene
2102, 2103, 2104	for the detection and/or identification of the <i>embB</i> resistance gene
2123, 2124, 2125	for the detection and/or identification of the <i>C. difficile cdtA</i> toxin gene
2126, 2127, 2128	for the detection and/or identification of the <i>C. difficile cdtB</i> toxin gene
2142, 2143	for the detection and/or identification of the <i>mupA</i> resistance gene
2145, 2146	for the detection and/or identification of the <i>catI</i> resistance gene
2148, 2149	for the detection and/or identification of the <i>catII</i> resistance gene

2151, 2152	for the detection and/or identification of the <i>catIII</i> resistance gene
2154, 2155	for the detection and/or identification of the <i>catP</i> resistance gene
2157, 2158, 2160, 2161	for the detection and/or identification of the <i>cat</i> resistance gene
2163, 2164	for the detection and/or identification of the <i>ppflo</i> -like resistance gene.

22. A composition of matter comprising a specific nucleic acid as set forth in claim 10 or 11, which is specific for a bacterial, fungal or parasitical species, genus, family, or group, or a nucleic acid as set forth in claim 8 or 9 which is universal for a bacterium, fungus or parasite, or both specific and universal nucleic acids, in conjunction with a nucleic acid sequence of at least 12 nucleotides capable of hybridizing with an antimicrobial agent resistance gene and/or toxin gene.

23. A composition as set forth in claim 22, wherein the nucleic acid capable of hybridizing with an antimicrobial agent resistance gene and/or toxin gene is any one of:

1078, 1079, 1085	for the detection and/or identification of the <i>E. coli</i> Shiga-like toxin 2 (<i>stx₂</i>) gene
1080, 1081, 1084, 2012	for the detection and/or identification of the <i>E. coli</i> Shiga-like toxin 1 (<i>stx₁</i>) gene
1082, 1083	for the detection and/or identification of <i>E. coli</i> Shiga-like toxins 1 and 2 (<i>stx</i>) genes
1086, 1087, 1088, 1089, 1090, 1091, 1092, 1170, 1239, 1240, 2292	for the detection and/or identification of the <i>vanA</i> resistance gene
1095, 1096, 1171, 1241, 2294, 2295	for the detection and/or identification of the <i>vanB</i> resistance gene
1111, 1112, 1113, 1114, 1115, 1116, 1118, 1119, 1120, 1121, 1123, 1124	for the detection and/or identification of the <i>vanAB</i> resistance genes

1103, 1104, 1109, 1110	for the detection and/or identification of the <i>vanC1</i> resistance gene
1105, 1106, 1107, 1108	for the detection and/or identification of the <i>vanC2</i> and <i>vanC3</i> resistance genes
1097, 1098, 1099, 1100, 1101, 1102	for the detection and/or identification of the <i>vanC1</i> , <i>vanC2</i> and <i>vanC3</i> resistance genes
1150, 1153, 1154, 1155	for the detection and/or identification of the <i>vanAXY</i> resistance genes
1094, 1125, 1126, 1127, 1128, 1129, 1130, 1131, 1132, 1133, 1134, 1135, 1192, 1193, 1194, 1195, 1196, 1197, 1214, 1216, 1217, 1218, 1219, 1220, 2015, 2016, 2017, 2018, 2019, 2020, 2021, 2022, 2023, 2024, 2025, 2026, 2027, 2028, 2029, 2030, 2031, 2032, 2033, 2034, 2035, 2036, 2037, 2038, 2039	for the detection and/or identification of the <i>S. pneumoniae pbp1a</i> gene
1142, 1143, 1144, 1145	for the detection and/or identification of the <i>S. pneumoniae pbp2b</i> gene
1146, 1147, 1148, 1149	for the detection and/or identification of the <i>S. pneumoniae pbp2x</i> gene
1177, 1231	for the detection and/or identification of the <i>mechA</i> resistance gene
1290, 1291, 1292, 1293, 1294, 1295, 1296, 1297, 1298, 1333, 1334, 1335, 1340, 1341, 1936, 1937, 1940, 1942, 1943, 1945, 1946, 1947, 1948, 1949, 2040, 2041, 2042, 2043, 2250, 2251	for the detection and/or identification of the <i>gyrA</i> resistance gene

1301, 1302, 1303, 1304, 1305, 1306	for the detection and/or identification of the <i>gyrB</i> resistance gene
1308, 1309, 1310, 1311, 1312, 1313, 1314, 1315, 1316, 1317, 1318, 1319, 1336, 1337, 1338, 1339, 1342, 1343, 1934, 1935, 1938, 1939, 1941, 1944, 1950, 1951, 1952, 1953, 1955, 2044, 2045, 2046	for the detection and/or identification of the <i>parC</i> resistance gene
1322, 1323, 1324, 1325, 1326, 1327	for the detection and/or identification of the <i>parE</i> resistance gene
1344, 1345, 1346, 1347	for the detection and/or identification of the <i>aac(2')-Ia</i> resistance gene
1349, 1350	for the detection and/or identification of the <i>aac(3')-Ib</i> resistance gene
1352, 1353, 1354, 1355	for the detection and/or identification of the <i>aac(3')-IIb</i> resistance gene
1357, 1358, 1359, 1360	for the detection and/or identification of the <i>aac(3')-IVa</i> resistance gene
1362, 1363, 1364, 1365	for the detection and/or identification of the <i>aac(3')-VIa</i> resistance gene
1367, 1368, 1369, 1370	for the detection and/or identification of the <i>aac(6')-Ia</i> resistance gene
1372, 1373, 1374, 1375	for the detection and/or identification of the <i>aac(6')-Ic</i> resistance gene
1377, 1378, 1379, 1380	for the detection and/or identification of the <i>ant(3')-Ia</i> resistance gene
1382, 1383, 1384, 1385	for the detection and/or identification of the <i>ant(4')-Ia</i> resistance gene
1387, 1388, 1389, 1390	for the detection and/or identification of the <i>aph(3')-Ia</i> resistance gene
1392, 1393, 1394, 1395	for the detection and/or identification of the <i>aph(3')-IIa</i> resistance gene
1397, 1398, 1399, 1400	for the detection and/or identification of the <i>aph(3')-IIIa</i> resistance gene

1402, 1403, 1404, 1405, 2252	for the detection and/or identification of the <i>aph(3')-VIIa</i> resistance gene
1407, 1408, 1409 1410	for the detection and/or identification of the <i>blaCARB</i> resistance gene
1412, 1413, 1414, 1415	for the detection and/or identification of the <i>blaCMY-2</i> resistance gene
1417, 1418	for the detection and/or identification of the <i>blaCTX-M-1</i> and <i>blaCTX-M-2</i> resistance genes
1419, 1420, 1421, 1422	for the detection and/or identification of the <i>blaCTX-M-1</i> resistance gene
1424, 1425, 1426, 1427	for the detection and/or identification of the <i>blaCTX-M-2</i> resistance gene
1429, 1430, 1431, 1432	for the detection and/or identification of the <i>blaIMP</i> resistance gene
1434, 1435	for the detection and/or identification of the <i>blaOXA2</i> resistance gene
1436, 1437	for the detection and/or identification of the <i>blaOXA10</i> resistance gene
1440, 1441	for the detection and/or identification of the <i>blaPER-1</i> resistance gene
1443, 1444	for the detection and/or identification of the <i>blaPER-2</i> resistance gene
1446, 1447, 1448, 1449	for the detection and/or identification of the <i>blaPER-1</i> and <i>blaPER-2</i> resistance genes
1450, 1451	for the detection and/or identification of the <i>dhfrA</i> resistance gene
1453, 1454, 1455, 1456	for the detection and/or identification of the <i>dhfrIa</i> and <i>dhfrXV</i> resistance genes
1457, 1458, 1459, 1460, 2253	for the detection and/or identification of the <i>dhfrIa</i> resistance gene
1462, 1463, 1464, 1465	for the detection and/or identification of the <i>dhfrIb</i> and <i>dhfrV</i> resistance genes
1466, 1467, 1468, 1469	for the detection and/or identification of the <i>dhfrIb</i> resistance gene

1471, 1472, 1473, 1474	for the detection and/or identification of the <i>dhfrV</i> resistance gene
1476, 1477, 1478, 1479	for the detection and/or identification of the <i>dhfrVI</i> resistance gene
1481, 1482, 1483, 1484	for the detection and/or identification of the <i>dhfrVII</i> and <i>dhfrXVII</i> resistance genes
1485, 1486, 1487, 1488	for the detection and/or identification of the <i>dhfrVII</i> resistance gene
1490, 1491, 1492, 1493	for the detection and/or identification of the <i>dhfrVIII</i> resistance gene
1495, 1496, 1497, 1498	for the detection and/or identification of the <i>dhfrIX</i> resistance gene
1500, 1501, 1502, 1503	for the detection and/or identification of the <i>dhfrXII</i> resistance gene
1505, 1506	for the detection and/or identification of the <i>dhfrXIII</i> resistance gene
1508, 1509, 1510, 1511	for the detection and/or identification of the <i>dhfrXV</i> resistance gene
1513, 1514, 1515, 1516	for the detection and/or identification of the <i>dhfrXVII</i> resistance gene
1528, 1529	for the detection and/or identification of the <i>ereA</i> and <i>ereA2</i> resistance genes
1531, 1532, 1533, 1534	for the detection and/or identification of the <i>ereB</i> resistance gene
1536, 1537, 1538, 1539	for the detection and/or identification of the <i>linA</i> and <i>linA'</i> resistance genes
1541, 1542, 1543, 1544	for the detection and/or identification of the <i>linB</i> resistance gene
1546, 1547	for the detection and/or identification of the <i>mefA</i> resistance gene
1549, 1550	for the detection and/or identification of the <i>mefE</i> resistance gene
1552, 1553, 1554, 1555	for the detection and/or identification of the <i>mefA</i> and <i>mefE</i> resistance genes

1556, 1557, 1558, 1559	for the detection and/or identification of the <i>mphA</i> and <i>mphK</i> resistance genes
1581, 1582, 1583, 1584	for the detection and/or identification of the <i>satG</i> resistance gene
1586, 1587, 1588, 1589, 2254	for the detection and/or identification of the <i>tetM</i> resistance gene
1591, 1592, 1593, 2297	for the detection and/or identification of the <i>vanD</i> resistance gene
1595, 1596, 1597, 1598	for the detection and/or identification of the <i>vanE</i> resistance gene
1609, 1610, 1611, 1612	for the detection and/or identification of the <i>vatB</i> resistance gene
1614, 1615, 1616, 1617	for the detection and/or identification of the <i>vatC</i> resistance gene
1619, 1620, 1621, 1622	for the detection and/or identification of the <i>vga</i> resistance gene
1624, 1625, 1626, 1627	for the detection and/or identification of the <i>vgaB</i> resistance gene
1629, 1630, 1631, 1632	for the detection and/or identification of the <i>vgb</i> and <i>vgh</i> resistance genes
1634, 1635, 1636, 1637	for the detection and/or identification of the <i>vgbB</i> resistance gene
1883, 1884, 1885, 1886, 1887, 1888, 1889, 1890, 1891, 1892, 1893, 1894, 1895, 1896, 1897, 1898	for the detection and/or identification of the <i>blaSHV</i> resistance gene
1906, 1907, 1908, 1909, 1910, 1911, 1912, 1913, 1914, 1915, 1916, 1917, 1918, 1919, 1920, 1921, 1922, 1923, 1924, 1925, 1926, 2006, 2007, 2008, 2009, 2141	for the detection and/or identification of the <i>blaTEM</i> resistance gene
1961, 1962, 1963, 1964	for the detection and/or identification of the <i>sulII</i> resistance gene

1966, 1967, 1968, 1969	for the detection and/or identification of the <i>tetB</i> resistance gene
2065, 2066, 2067, 2068, 2069, 2070, 2071	for the detection and/or identification of the <i>therpoB</i> resistance gene
2098, 2099, 2100	for the detection and/or identification of the <i>inhA</i> resistance gene
2102, 2103, 2104	for the detection and/or identification of the <i>embB</i> resistance gene
2123, 2124, 2125	for the detection and/or identification of the <i>C. difficile cdtA</i> toxin gene
2126, 2127, 2128	for the detection and/or identification of the <i>C. difficile cdtB</i> toxin gene
2142, 2143	for the detection and/or identification of the <i>mupA</i> resistance gene
2145, 2146	for the detection and/or identification of the <i>catI</i> resistance gene
2148, 2149	for the detection and/or identification of the <i>catII</i> resistance gene
2151, 2152	for the detection and/or identification of the <i>catIII</i> resistance gene
2154, 2155	for the detection and/or identification of the <i>catP</i> resistance gene
2157, 2158, 2160, 2161	for the detection and/or identification of the <i>cat</i> resistance gene
2163, 2164	for the detection and/or identification of the <i>ppflo</i> -like resistance gene.

24. A nucleic acid having at least 12 nucleotides in length, capable of hybridizing with the nucleotide sequence of any one of the *tuf* sequences defined in SEQ ID NOs.: 1-73, 75-241, 399-457, 498-529, 612-618, 621-624, 675, 677, 717-736, 779-792, 840-855, 865, 868-888, 897-910, 932, 967-989, 992, 1266-1287, 1518-1526, 1561-1575, 1578-1580, 1662-1664, 1666-1667, 1669-1670, 1673-1683, 1685-1689, 1786-1843, 1874-1881, 1956-1960, 2183-2185, 2187-2188, 2193-2201, 2214-2249, 2255-2272.

25. A nucleic acid having at least 12 nucleotides in length, capable of hybridizing with the nucleotide sequence of any one of the *atpD* sequences defined in SEQ ID NOs.: 242-270, 272-398, 458-497, 530-538, 663, 667, 673, 674, 676, 678-680, 737-778, 827-832, 834-839, 856-862, 866-867, 889-896, 929-931, 941-966, 1245-1254, 1256-1265, 1527, 1576-1577, 1600-1604, 1638-1647, 1649-1660, 1671, 1684, 1844-1848, 1849-1865, 2189-2192.

26. A nucleic acid having at least 12 nucleotides in length, capable of hybridizing with the nucleotide sequence of any one of the *recA* sequences defined in SEQ ID NOs.: 990-991, 1003, 1288-1289, 1714, 1756-1763, 1866-1873 and 2202-2212.

27. A nucleic acid having at least 12 nucleotides in length, capable of selectively hybridizing with the nucleotide sequence of any one of the antimicrobial agent resistance gene sequences defined in SEQ ID NOs.: 1004-1075, 1255, 1607-1608, 1648, 1764-1785, 2013-2014, 2056-2064, 2273-2280.

28. The nucleic acid sequences of the nucleic acids of any one of claims 24 to 27.

29. The use of a nucleic acid having at least 12 nucleotides in length capable of hybridizing with the nucleic acids of any one of the antimicrobial agent resistance genes sequences defined in SEQ ID NOs.: 1004-1075, 1255, 1607-1608, 1648, 1764-1785, 2013-2014, 2056-2064, 2273-2280 for the detection and identification of microbial species.

30. The use of a nucleic acid having at least 12 nucleotides in length capable of hybridizing with the nucleic acids of any one of the toxin genes defined in SEQ ID NOs.: 1078-1085, 2012 and 2123 to 2128 for the detection and identification of microbial species.

31. A repertory of *hexA* nucleic acids used for the detection and/or identification of *Streptococcus pneumoniae*, which repertory is created by amplifying

the nucleic acids of any streptococcal species with any combination of primers SEQ ID NOs.: 1179, 1181 and 1182.

32. A repertory as defined in claim 31, which comprises the nucleic acids having a nucleotide sequence defined in SEQ ID NOs.: 1184 to 1191.

33. A repertory of nucleic acid sequences derived from the repertory of claim 31 or 32.

34. A nucleic acid used for the specific and ubiquitous detection and for identification of *Streptococcus pneumoniae*, which is derived from the repertory of claim 31.

35. A nucleic acid as set forth in claim 34 which has a nucleic acid sequence of at least 12 nucleotides capable of hybridizing with said any *Streptococcus pneumoniae* and with any one of SEQ ID NOs.: 1184 to 1187.

36. A nucleic acid as set forth in claim 34, which has a nucleic acid sequence of at least 12 nucleotides capable of hybridizing with the nucleic acids of *Streptococcus pneumoniae* and with any one of the nucleic acids having SEQ ID NOs.: 1179, 1180, 1181, 1182.

37. A peptide derived from the translation of the nucleic acids from the repertory obtained from the method of claim 1, 31 or 32, or of the nucleic acids defined in any one of claims 24 to 27, 33 and 36.

38. A peptide sequence derived from the peptide of claim 37.

39. A recombinant vector comprising a nucleic acid obtained from the method of claim 1, 31 or 32, or from the nucleic acids defined in any one of claims 24 to 27, 35 and 36.

40. A recombinant vector as defined in claim 39 which is an expression vector.

41. A recombinant host cell comprising the recombinant vector defined in claim 39 or 40.

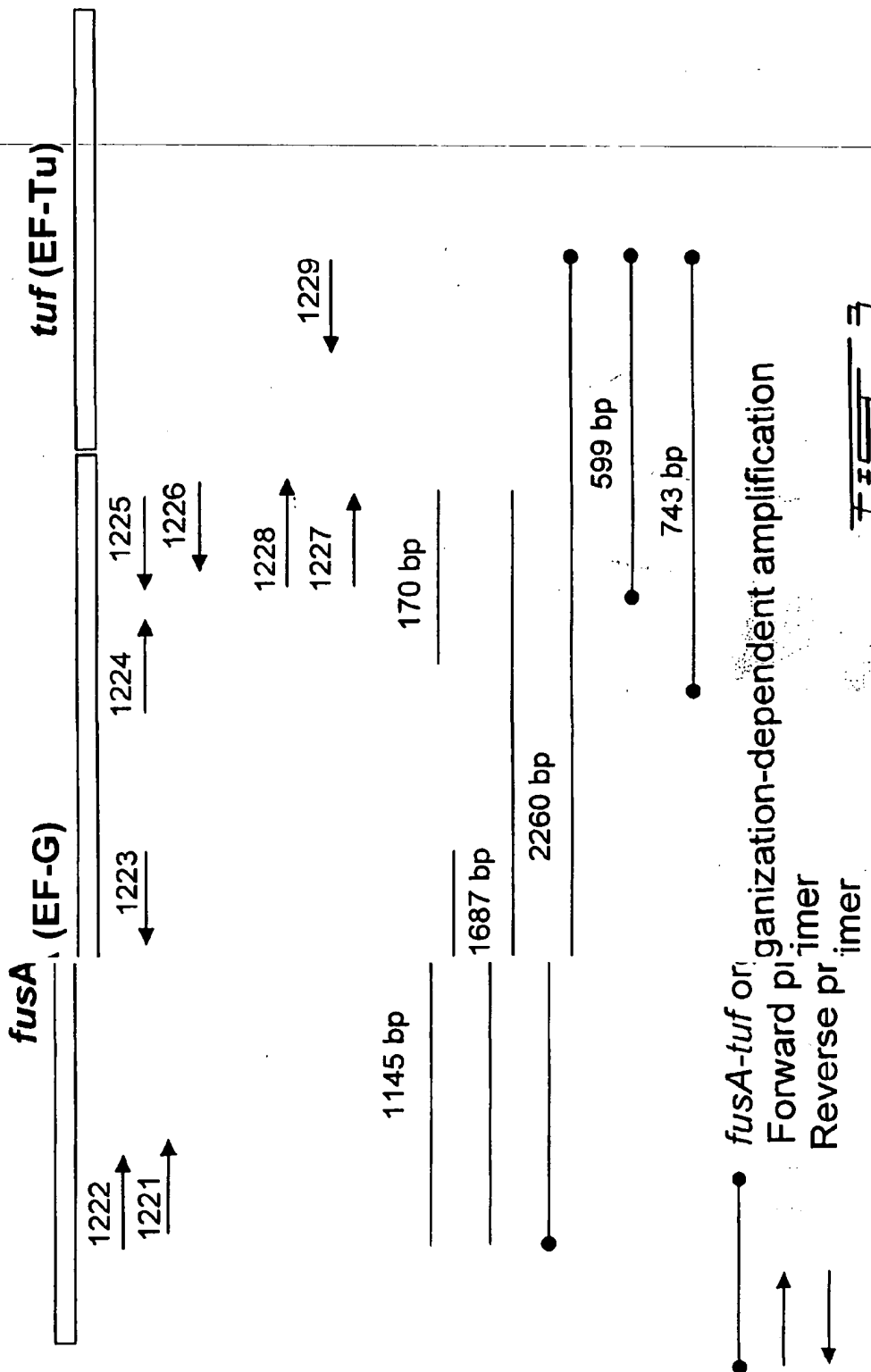
42. The use of the nucleic acid sequences defined in claim 28 or 33, or obtained from the method of claim 2 and of the protein sequences deduced from said nucleic acid sequences, for the design of a therapeutic agent effective against said microorganisms.

43. The use as defined in claim 42, wherein said therapeutic agent is an antimicrobial agent, a vaccine or a genic therapeutic agent.

44. A method for identification of a microorganism in a test sample, comprising the steps of:

- a) obtaining a nucleic acid sequence for a *tuf*, *atpD*, and/or *recA* genes of said microorganisms, and
- b) comparing said nucleic acid sequence with the nucleic acid sequences of a bank as defined in claim 5, said repertory comprising a nucleic acid sequence obtained from the nucleic acids of said microorganism, whereby said microorganism is identified when said comparison results in a match between said sequences.

3/27



4/27

<i>S. aureus</i>	REHLLSRNVGVPYIWF	120	130	140	150	160	170	180	190	200
<i>S. epidermidis</i>	REHLLSRNVGVPYIWF	INKMDVDDDEELLELMEMEVRLD	SEYDFPGDDVPVIAGS	KALE	GD	AEYEQKILDLMAAV	DEYIP		
<i>E. durans (A)</i>	REHLLSRQVGPYIWF	INKMDVDDDEELLELMEMEVRLD	SEYDFPGDDVPVIAGS	KALE	GD	AEYEQKILDLMAAV	DEYIP		
<i>E. hirae (A)</i>	REHLLSRQVGPYIWF	INKMDVDDDEELLELMEMEVRLD	TEYDFPGDDVPVIAGS	KALE	GD	AEYEQKILDLMAAV	DEYIP		
<i>E. mundtii (A)</i>	REHLLSRQVGPYIWF	INKMDVDDDEELLELMEMEVRLD	TEYDFPGDDVPVAGS	KALE	GD	AEYEQKILDLMAAV	DEYIP		
<i>E. faecium (A)</i>	REHLLSRQVGPYIWF	INKMDVDDDEELLELMEMEVRLD	TEYDFPGDDVPVIAGS	AL	RALE	GD	AEYEQKILDLMAAV	DEYIP	
<i>E. cecorum</i>	REHLLSRNVGVPYIWF	INKMDVDDDEELLELMEMEVRLD	TEYDFPGDDVPVAGS	KALE	GD	AEYEQKILDLMAAV	DEYIP		
<i>E. columbae</i>	REHLLSRNVGVPYIWF	INKMDVDDDEELLELMEMEVRLD	TEYDFPGDDVPVIAGS	KALE	GD	AEYEQKILDLMAAV	DEYIP		
<i>E. cassel. flavus (A)</i>	REHLLSRNVGVPYIWF	INKMDVDDDEELLELMEMEVRLD	TEYDFPGDDVPVIAGS	KALE	GD	AEYEQKILDLMAAV	DEYIP		
<i>E. gallinarum (A)</i>	REHLLSRNVGVPYIWF	INKMDVDDDEELLELMEMEVRLD	TEYDFPGDDVPVIAGS	KALE	GD	AEYEQKILDLMAAV	DEYIP		
<i>E. faecalis</i>	REHLLSRNVGVPYIWF	INKMDVDDDEELLELMEMEVRLD	SEYDFPGDDVPVIAGS	KALE	GD	AEYEQKILDLMAAV	DEYIP		
<i>E. avium (A)</i>	REHLLSRNVGVPYIWF	INKMDVDDDEELLELMEMEVRLD	SEYDFPGDDVPVIAGS	KALE	GD	AEYEQKILDLMAAV	DEYIP		
<i>E. raffinosus (A)</i>	REHLLSRNVGVPYIWF	INKMDVDDDEELLELMEMEVRLD	SEYDFPGDDVPVIAGS	KALE	GD	AEYEQKILDLMAAV	DEYIP		
<i>E. dispar (A)</i>	REHLLSRNVGVPYIWF	INKMDVDDDEELLELMEMEVRLD	TEYDFPGDDVPVIAGS	KALE	GD	AEYEQKILDLMAAV	DEYIP		
<i>E. malodoratus (A)</i>	REHLLSRNVGVPYIWF	INKMDVDDDEELLELMEMEVRLD	SEYDFPGDDVPVIAGS	KALE	GD	AEYEQKILDLMAAV	DEYIP		
<i>E. pseudoavium (A)</i>	REHLLSRNVGVPYIWF	INKMDVDDDEELLELMEMEVRLD	SEYDFPGDDVPVIAGS	KALE	GD	AEYEQKILDLMAAV	DEYIP		
<i>E. sulfureus</i>	REHLLSRNVGVPYIWF	INKMDVDDDEELLELMEMEVRLD	SEYDFPGDDVPVIAGS	KALE	GD	AEYEQKILDLMAAV	DEYIP		
<i>E. saccharolyticus</i>	REHLLSRNVGVPYIWF	INKMDVDDDEELLELMEMEVRLD	SEYDFPGDDVPVIAGS	KALE	GD	AEYEQKILDLMAAV	DEYIP		
<i>E. solitarius</i>	REHLLSRNVGVPYIWF	INKMDVDDDEELLELMEMEVRLD	SEYDFPGDDVPVIGS	KALE	GD	AEYEQKILDLMD	AV	DEYIP	

FE-4a

5/27

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TIPERDSDKPFMMPVEDVI 220
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TIPERDSDKPFMMPVEDVI 680
TIPERDSDKPFMMPVEDVI 690
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TIPERDSDKPFMMPVEDVI 850
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TIPERDSDKPFMMPVEDVI 970
TIPERDSDKPFMMPVEDVI 980
TIPERDSDKPFMMPVEDVI 990
TIPERDSDKPFMMPVEDVI 1000

46

- S. aureus*
- S. epidermidis*
- E. durans* (A)
- E. hirae* (A)
- E. mundtii* (A)
- E. faecium* (A)
- E. cecorum*
- E. columbae*
- E. cassel. flavus* (A)
- E. gallinarum* (A)
- E. faecalis*
- E. avium* (A)
- E. raffinosus* (A)
- E. dispar* (A)
- E. malodoratus* (A)
- E. pseudoavium* (A)
- E. sulfureus*
- E. saccharolyticus*
- E. solitarius*

6/27

<i>L. monocytogenes</i>	REHLLSRQGVGYIWI	FNKKDINVDDEELLEVEMEIROLLTEYFPGDDIPVIGSALKALQ	GEADWEAKIDELMEAVDSYIP
<i>E. cassel.flavus (B)</i>	REHLLSRQGVGYHLLIV	FINKTIDVDDDELIDLVEVEVRELLTEYDFPGDDIPVIGSALKALE	GDPAEAAIILTMDTVDEYIP
<i>E. gallinarum (B)</i>	REHLLSRQGVGYHLLIV	FINKTIDVDDDELIDLVEVEVRELLSEYNFPGDDIPVIGSALKALE	GDPAEAAIMELMDTVDSYIP
<i>E. durans (B)</i>	REHLLSRQGVGYHLLIV	FINKTIDVDDDELIDLVEVEVRELLSEYFPGDDTPVIGSALKALQ	GDPAEAAIMELTDTVDEYIP
<i>E. faecium (B)</i>	REHLLSRQGVGYHLLIV	FINKTIDVDDDELIDLVEVEVRELLSEYFPGDDTPVIGSALKALQ	GDPAEAAIMELMDTVDEYIP
<i>E. hirae (B)</i>	REHLLSRQGVGYHLLIV	FINKTIDVDDDELIDLVEVEVRELLSEYFPGDDTPVIGSALKALQ	GDPAEAAIMELMDTVDEYIP
<i>E. mundtii (B)</i>	REHLLSRQGVGYHLLIV	FINKTIDVDDDELIDLVEVEVRELLSEYFPGDDTPVIGSALKALQ	GDPAEAAIMELMDTVDEYIP
<i>E. avium (B)</i>	REHLLSRQGVGYHLLIV	FINKTIDVDDDELIDLVEVEVRELLSEYFPGDDTPVIGSALKALQ	GDPAEAAIMELMDTVDEYIP
<i>E. pseudoavium (B)</i>	REHLLSRQGVGYHLLIV	FINKTIDVDDDELIDLVEVEVRELLSEYFPGDDTPVIGSALKALQ	GDPAEAAIMELMDTVDEYIP
<i>E. malodoratus (B)</i>	REHLLSRQGVGYHLLIV	FINKTIDVDDDELIDLVEVEVRELLSEYFPGDDTPVIGSALKALQ	GDPAEAAIMELMDTVDEYIP
<i>E. raffinosus (B)</i>	REHLLSRQGVGYHLLIV	FINKTIDVDDDELIDLVEVEVRELLSEYFPGDDTPVIGSALKALQ	GDPAEAAIMELMDTVDEYIP
<i>E. dispar (B)</i>	REHLLSRQGVGYHLLIV	FINKTIDVDDDELIDLVEVEVRELLSEYFPGDDTPVIGSALKALQ	GDPAEAAIMELMDTVDEYIP
<i>S. pneumoniae</i>	REHLLSRQGVGYHLLIV	FINKTIDVDDDELIDLVEVEVRELLSEYFPGDDTPVIGSALKALQ	GDPAEAAIMELMDTVDEYIP
<i>S. suis</i>	REHLLSRQGVGYHLLIV	FINKTIDVDDDELIDLVEVEVRELLSEYFPGDDTPVIGSALKALQ	GDPAEAAIMELMDTVDEYIP
<i>S. pyogenes</i>	REHLLSRQGVGYHLLIV	FINKTIDVDDDELIDLVEVEVRELLSEYFPGDDTPVIGSALKALQ	GDPAEAAIMELMDTVDEYIP
<i>S. mutans</i>	REHLLSRQGVGYHLLIV	FINKTIDVDDDELIDLVEVEVRELLSEYFPGDDTPVIGSALKALQ	GDPAEAAIMELMDTVDEYIP
<i>L. lactis</i>	REHLLSRQGVGYHLLIV	FINKTIDVDDDELIDLVEVEVRELLSEYFPGDDTPVIGSALKALQ	GDPAEAAIMELMDTVDEYIP
<i>T. aquaticus</i>	REHLLSRQGVGYHLLIV	FINKTIDVDDDELIDLVEVEVRELLSEYFPGDDTPVIGSALKALQ	GDPAEAAIMELMDTVDEYIP
<i>E. coli</i>	REHLLSRQGVGYHLLIV	FINKTIDVDDDELIDLVEVEVRELLSEYFPGDDTPVIGSALKALQ	GDPAEAAIMELMDTVDEYIP

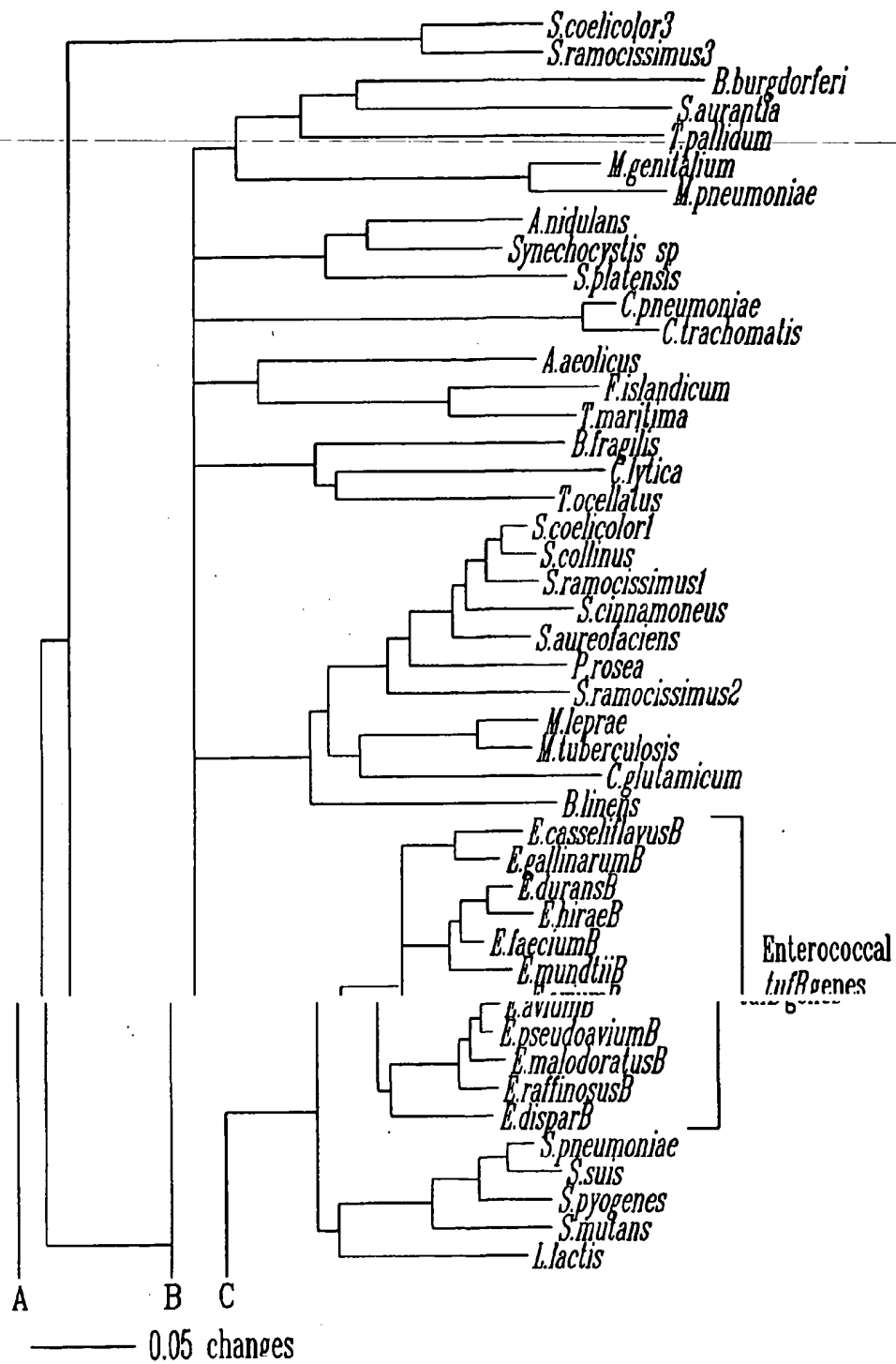
C f → D g E F
 7-4c

7/27

L. monocytogenes THEROTDKPFWMPVEG
E. casselii THEROTDKPILLPIED
E. gallinarum THEROTDKPILLPVEG
E. durans THEROTDKPILLPVED
E. faecium THEROTDKPILLPVED
E. hirae THEROTDKPILLPAED
E. mundtii THEROTDKPILLPVED
E. avium THEROTDKPILLPVED
E. pseudovarium THEROTDKPELLPVED
E. malodoratus THERONDKPELLPVEG
E. raffinosus THEROTDKPELLPVEG
E. dispar THERONDKPELLPVEG
S. pneumoniae EPEROTDKPELLPVEL
S. suis EPEROTDKPELLPVEL
S. pyogenes EPEROTDKPELLPVEL
S. mutans DPEROTDKPELLPVEL
L. lactis TPEROTDKPELLPVEL
T. aquaticus TPVROVDKPELLPVEL
E. coli EBERAIDKPELLPIEL

700-44

8/27



9/27

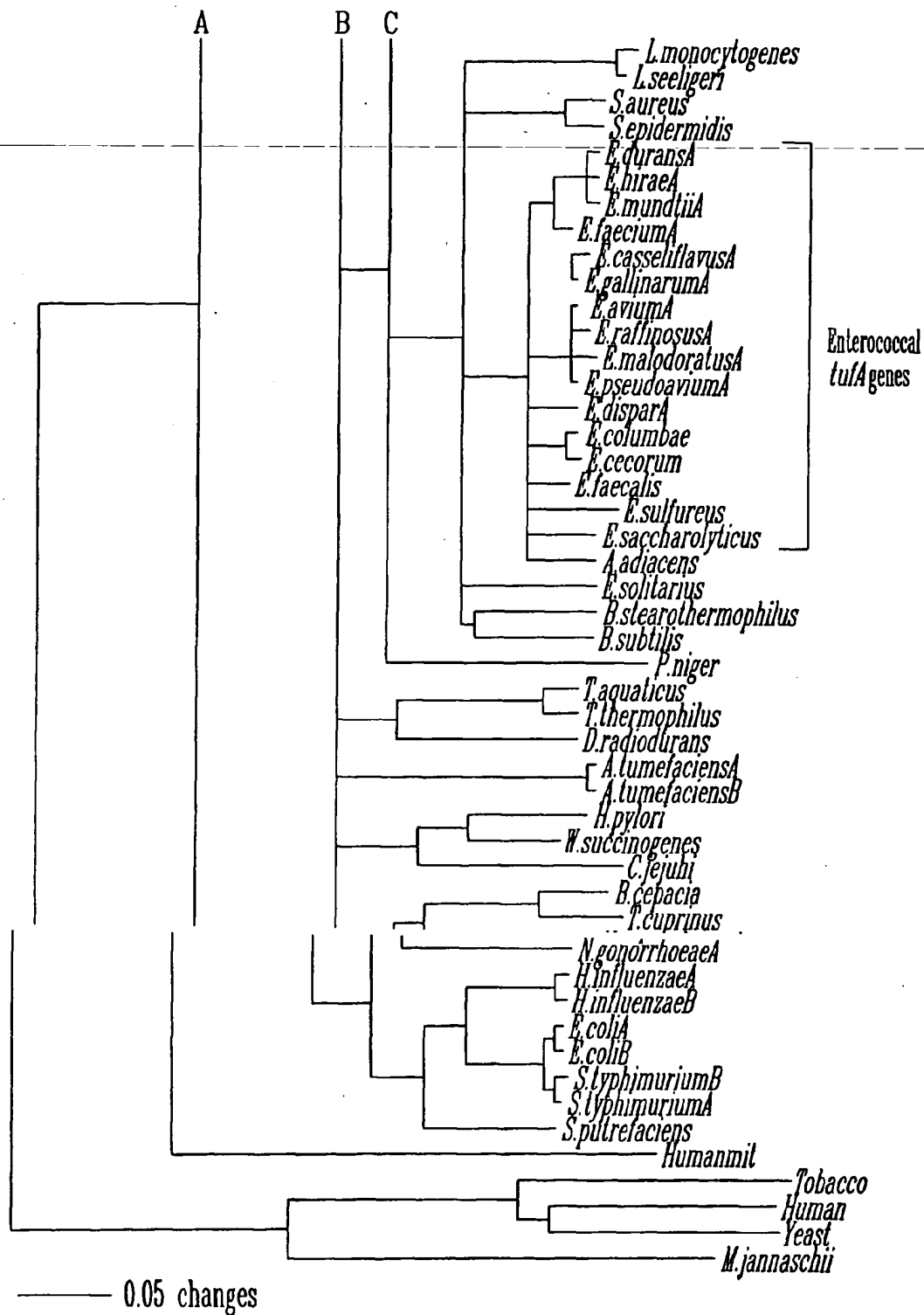
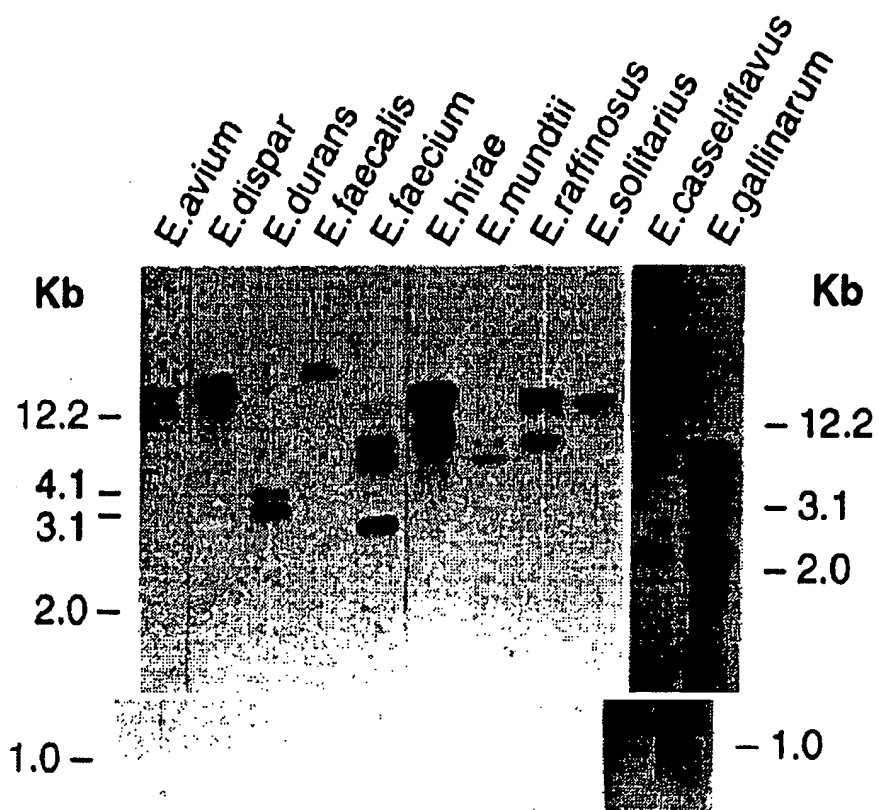


FIG. 5b

10/27

FIG. 6

11/27

	301	311	321	331
E. coli	GAGATCGGT ¹	AAGAAGAGCG	TTGGG	CGATTCACCG
E. agglomerans	GACATCGGT ¹	AAGAAGAGCG	TTGGG	CGATCCACCG
P. agglomerans	GAGCTGAAA ¹	AAGAAGATGG	CAGCGCAGTA	CTATTCACCG
P. dispersa	GACCTGAAA ¹	AAGAAGACGG	CAGCGCTGTA	CTATTCATCG
T. ptyseos	GACCTGAAG ¹	ACGAAGATGG	TAGCAATGTT	CTATTCACCG
E. coli	~I~G~E~	E~E~R~W	~A~	I~H~R~
E. agglomerans	~I~G~E~	E~E~R~W	~A~	I~H~R~
P. agglomerans	~L~K~E~	E~D~G~S	~A~V~E~	I~H~R~
P. dispersa	~L~K~E~	E~D~G~S	~A~V~E~	I~H~R~
T. ptyseos	~L~K~N~	E~D~G~S	~N~V~E~	I~H~R~

FIG. 7

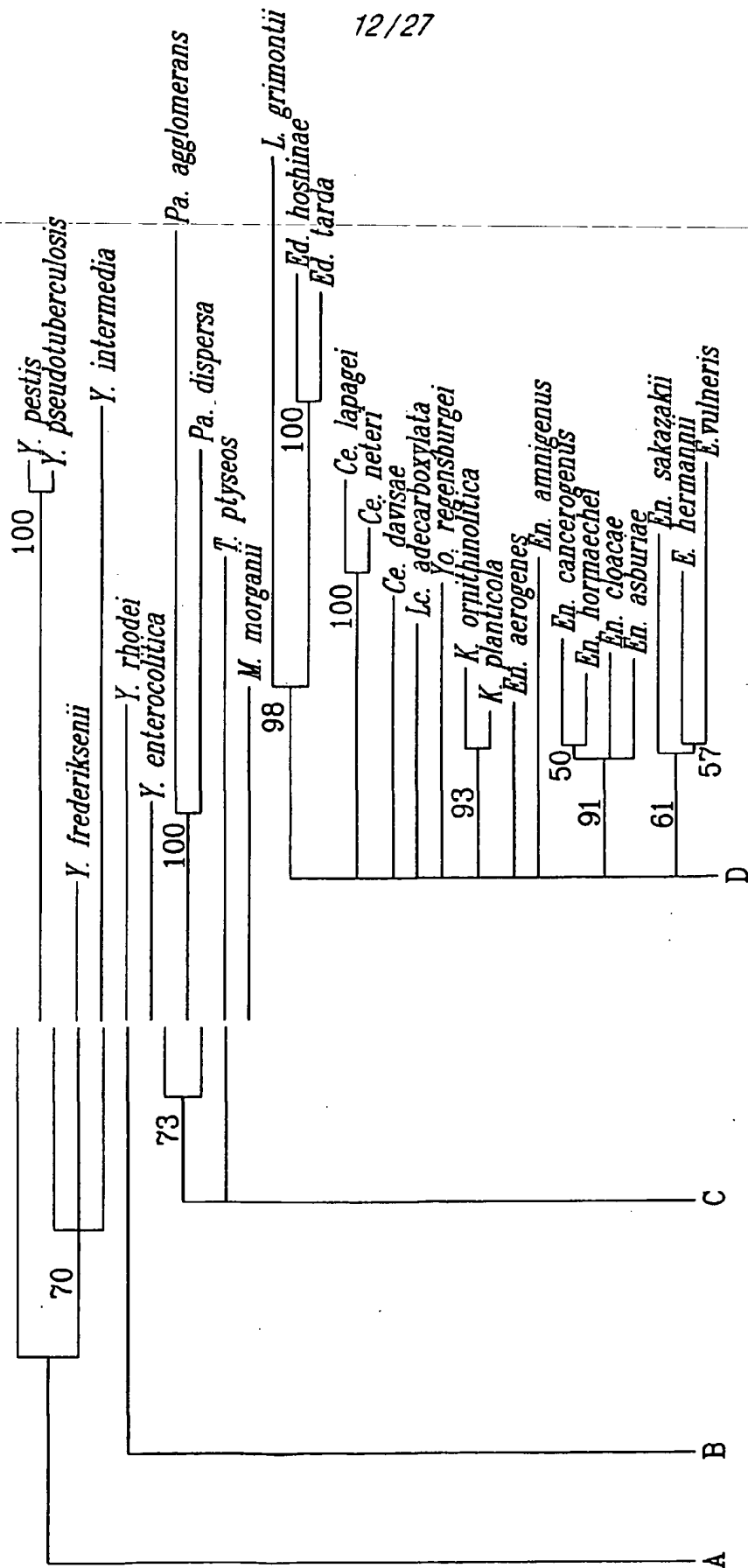


FIG. 8a

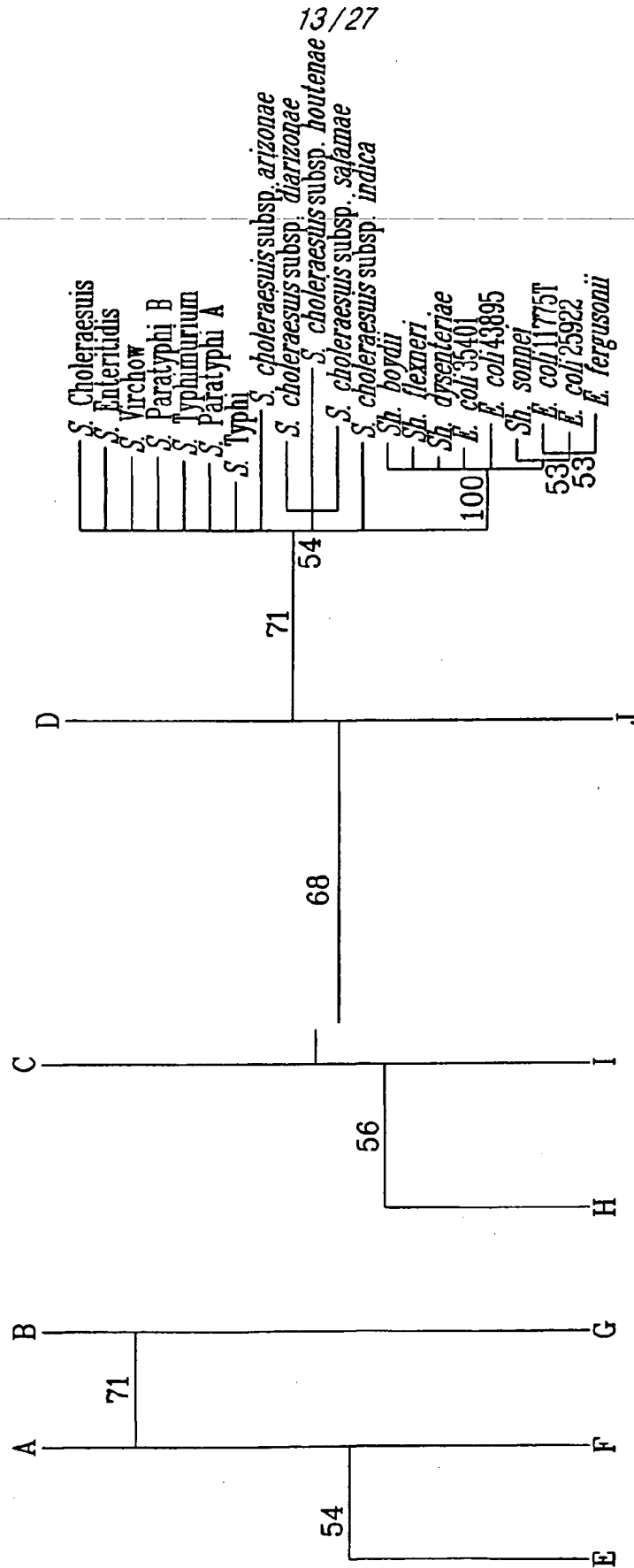


FIG. 1

14/27

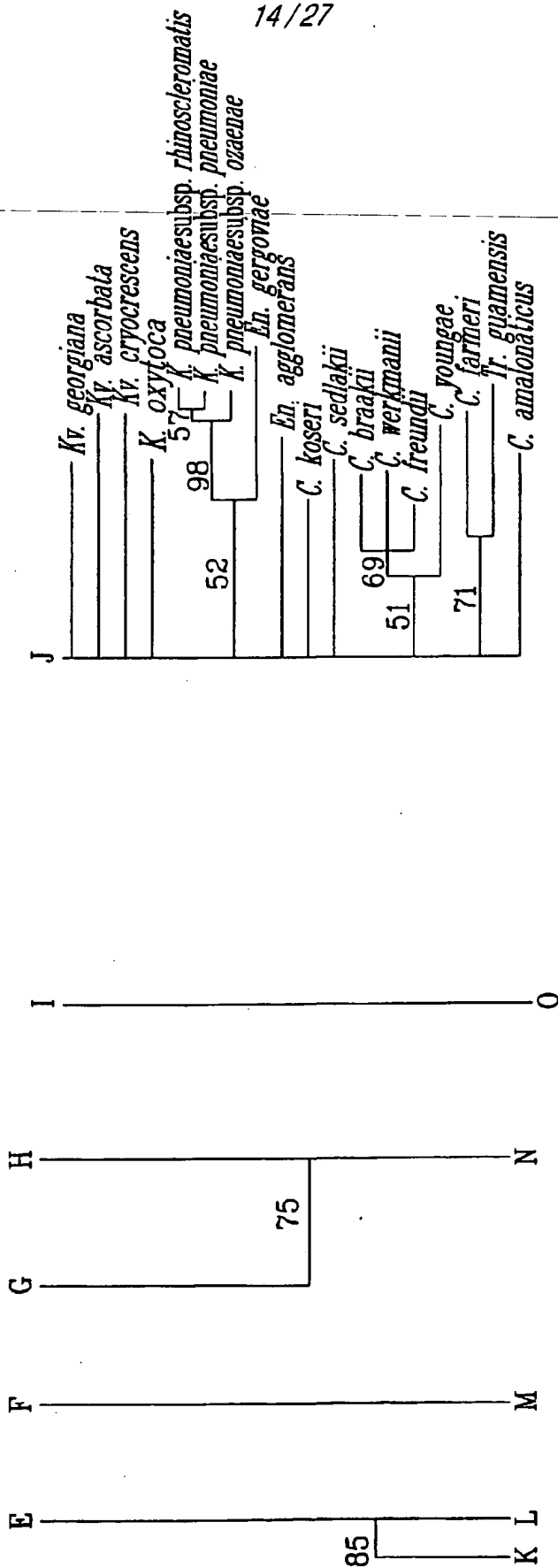
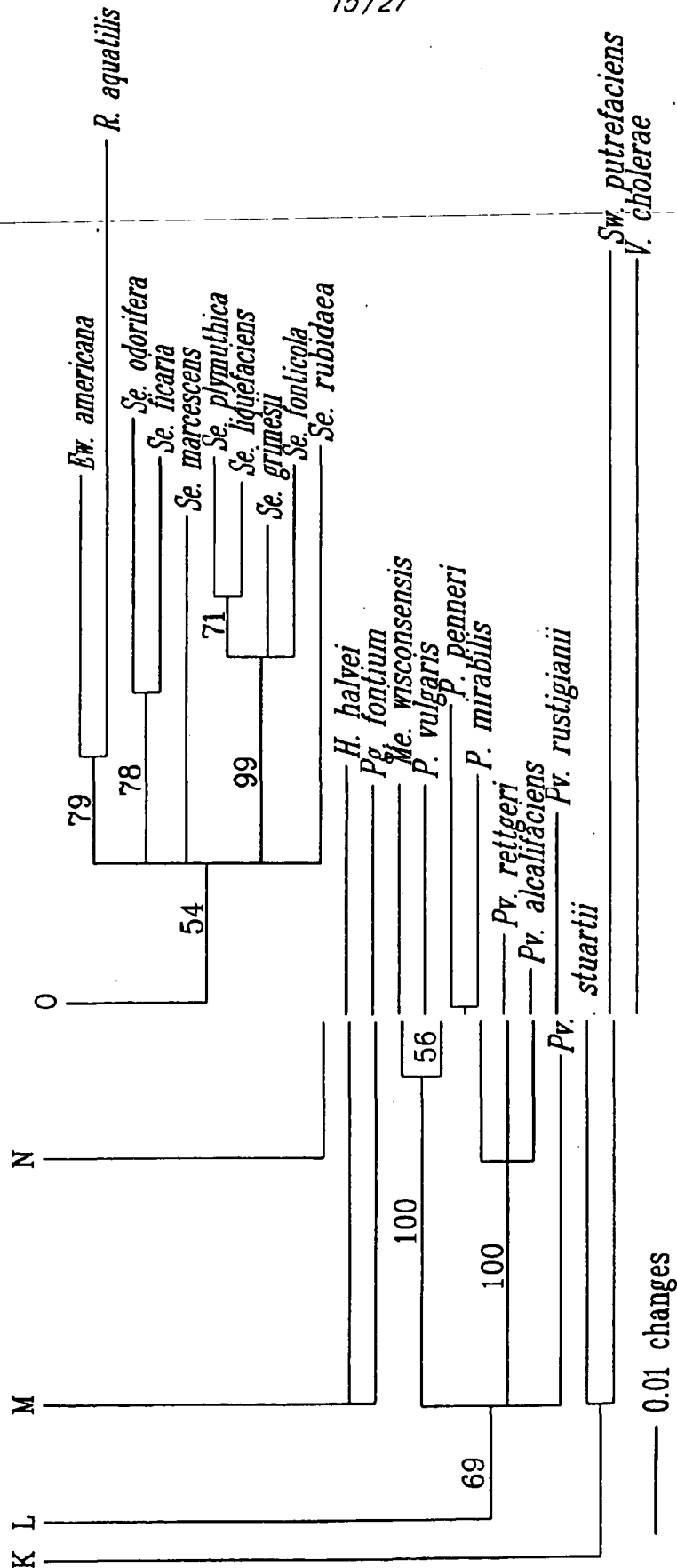
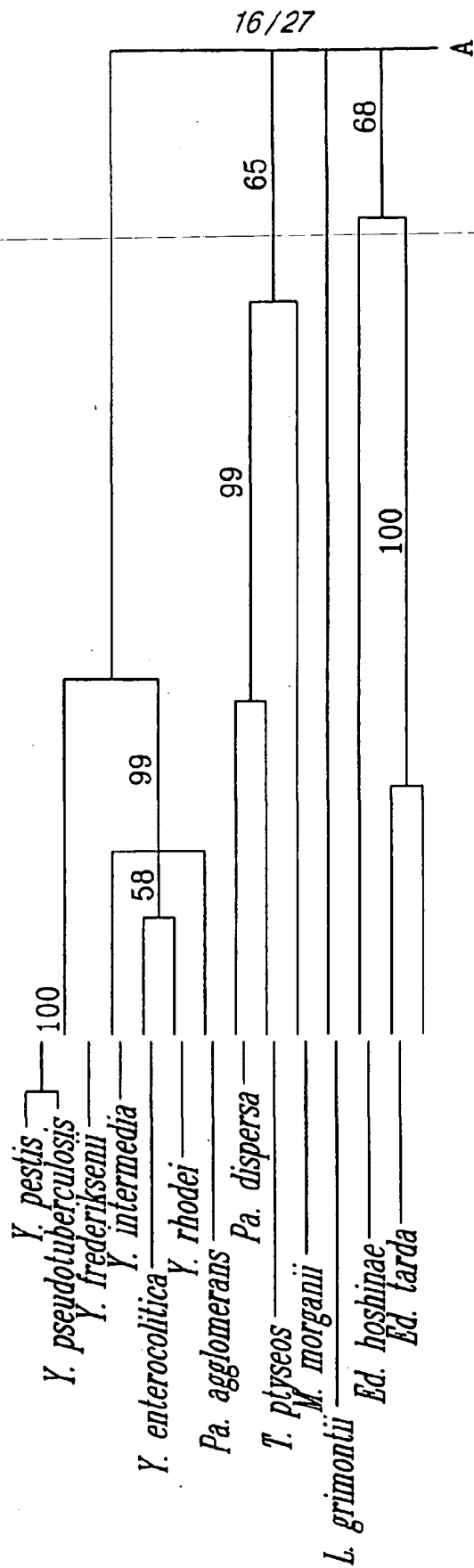


FIG. 1 - Bc

15/27



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17/27

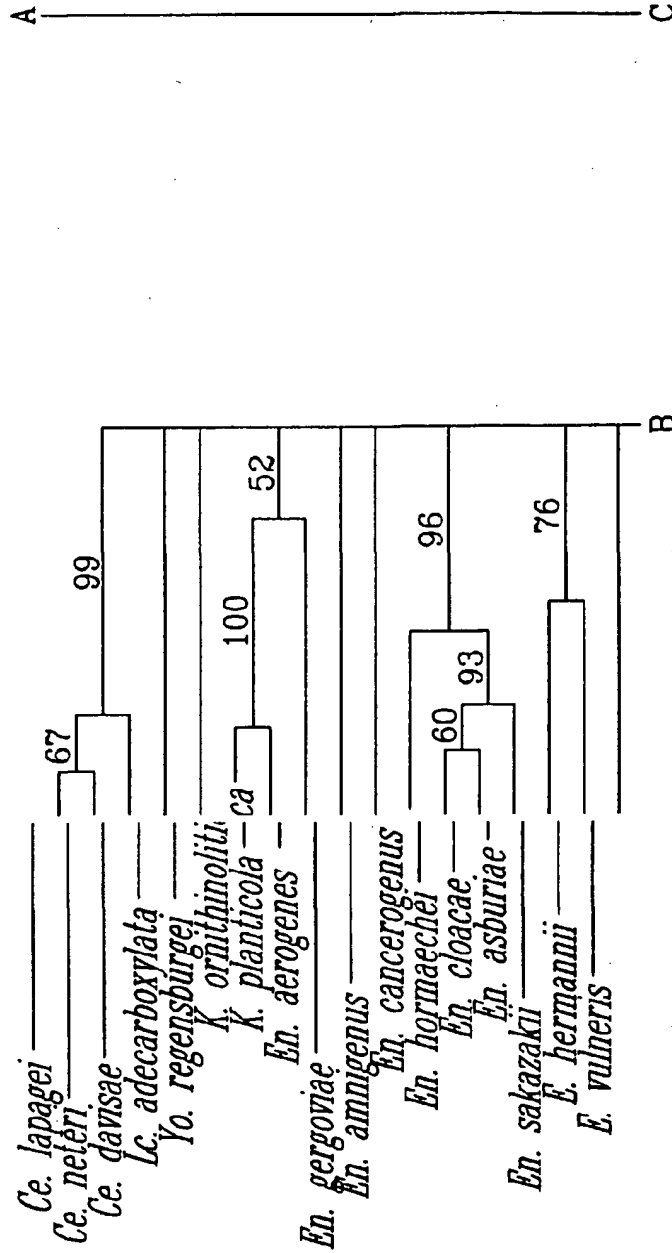
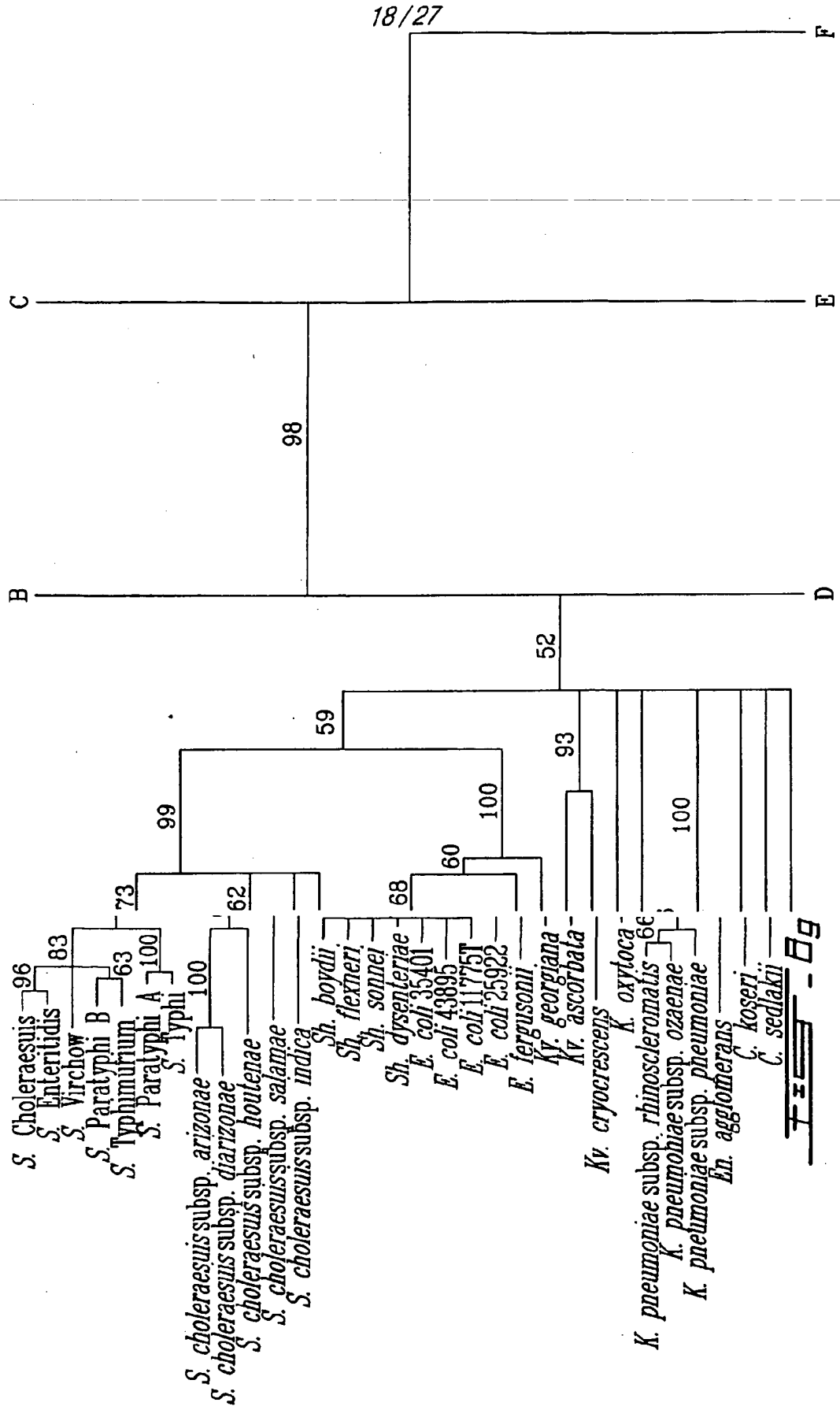
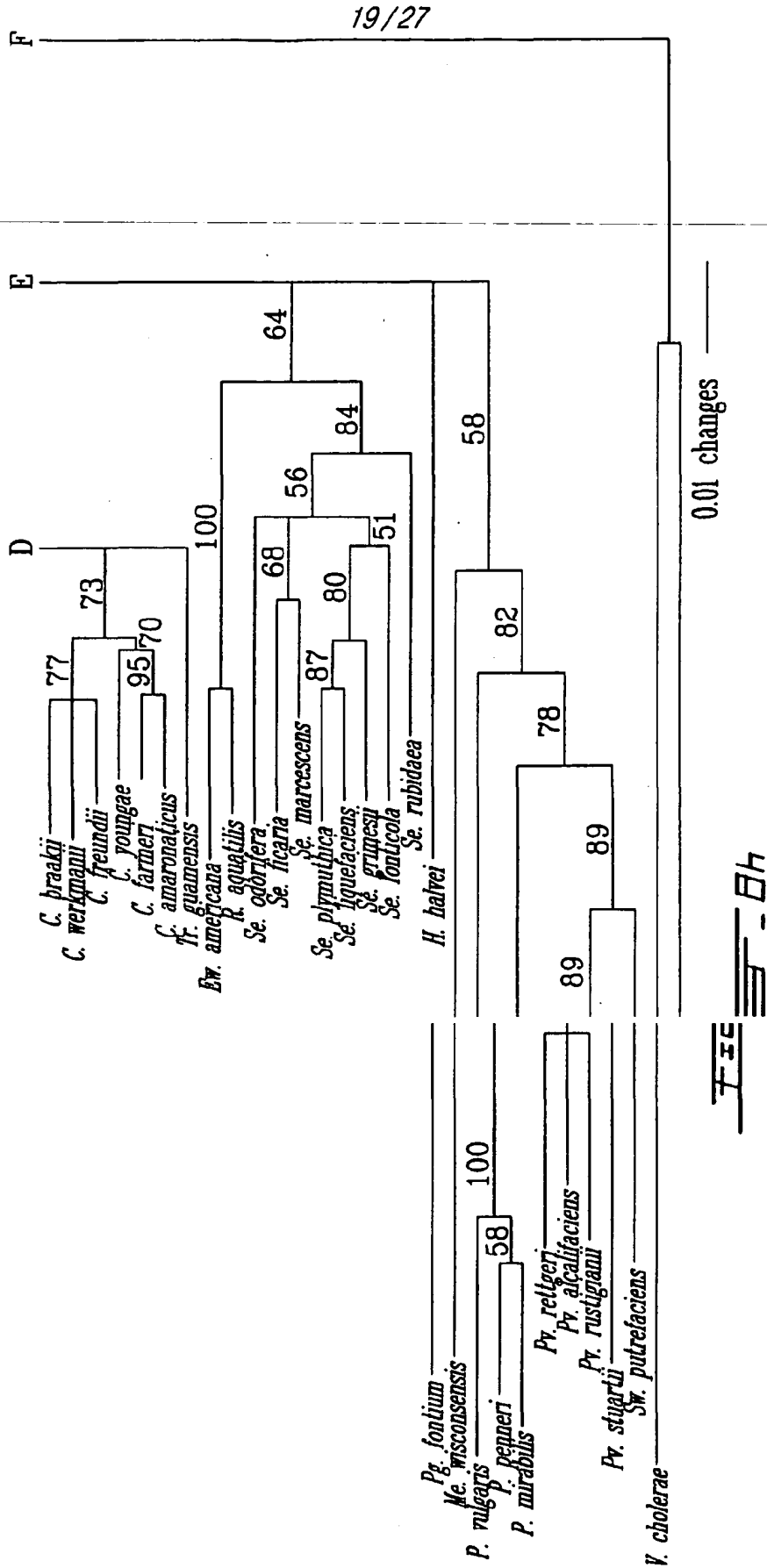
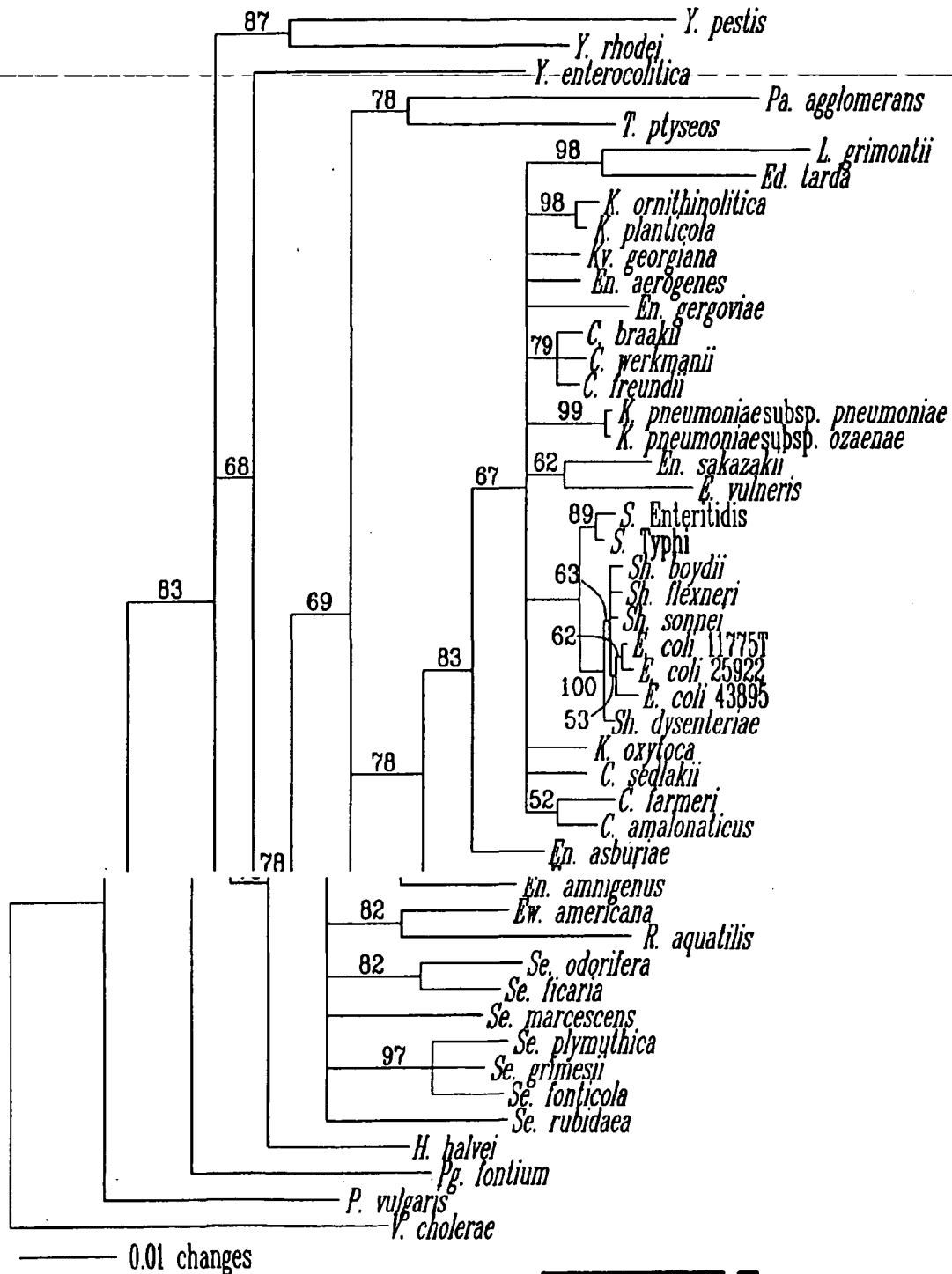


FIG. 1

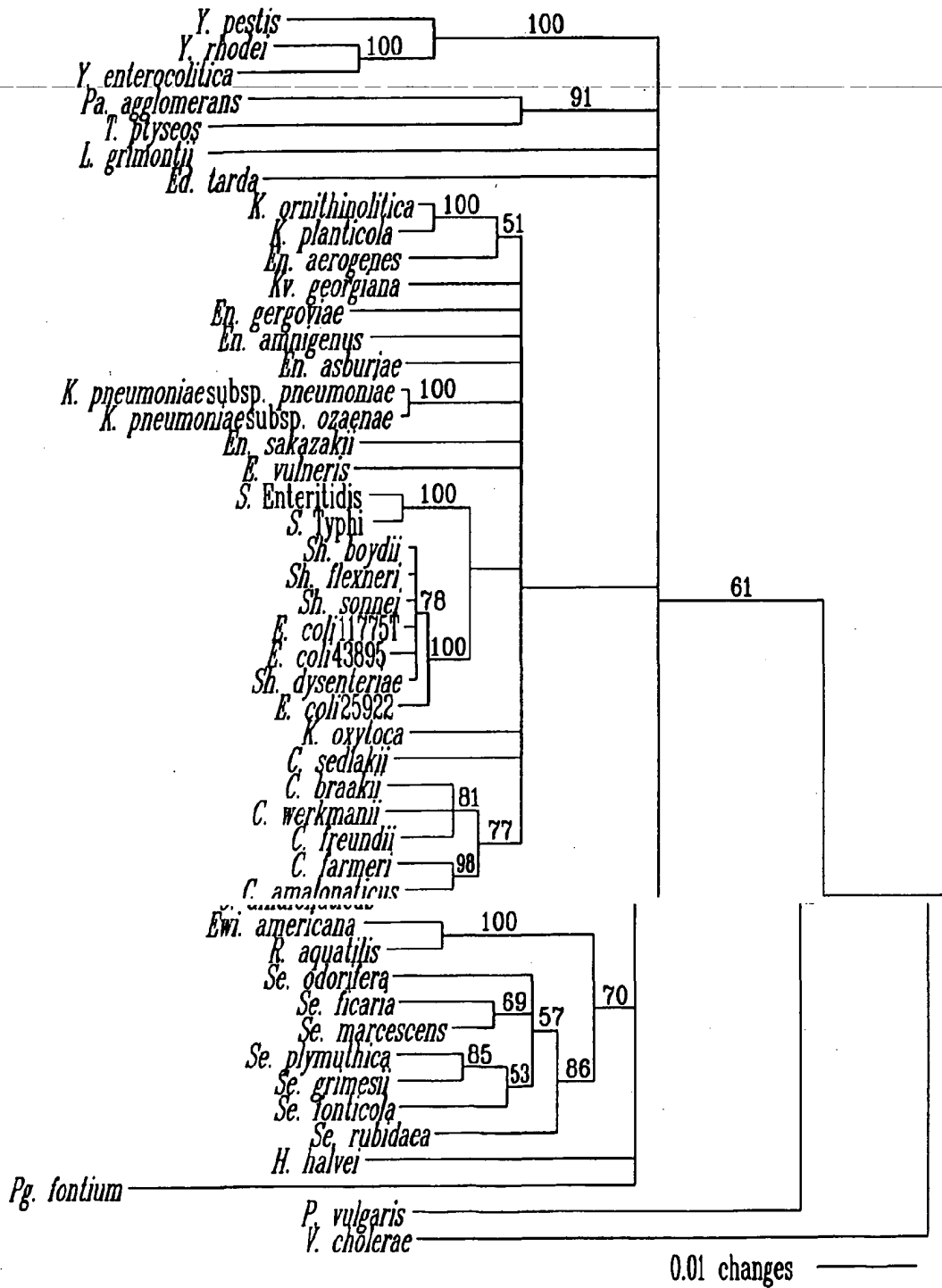




20/27

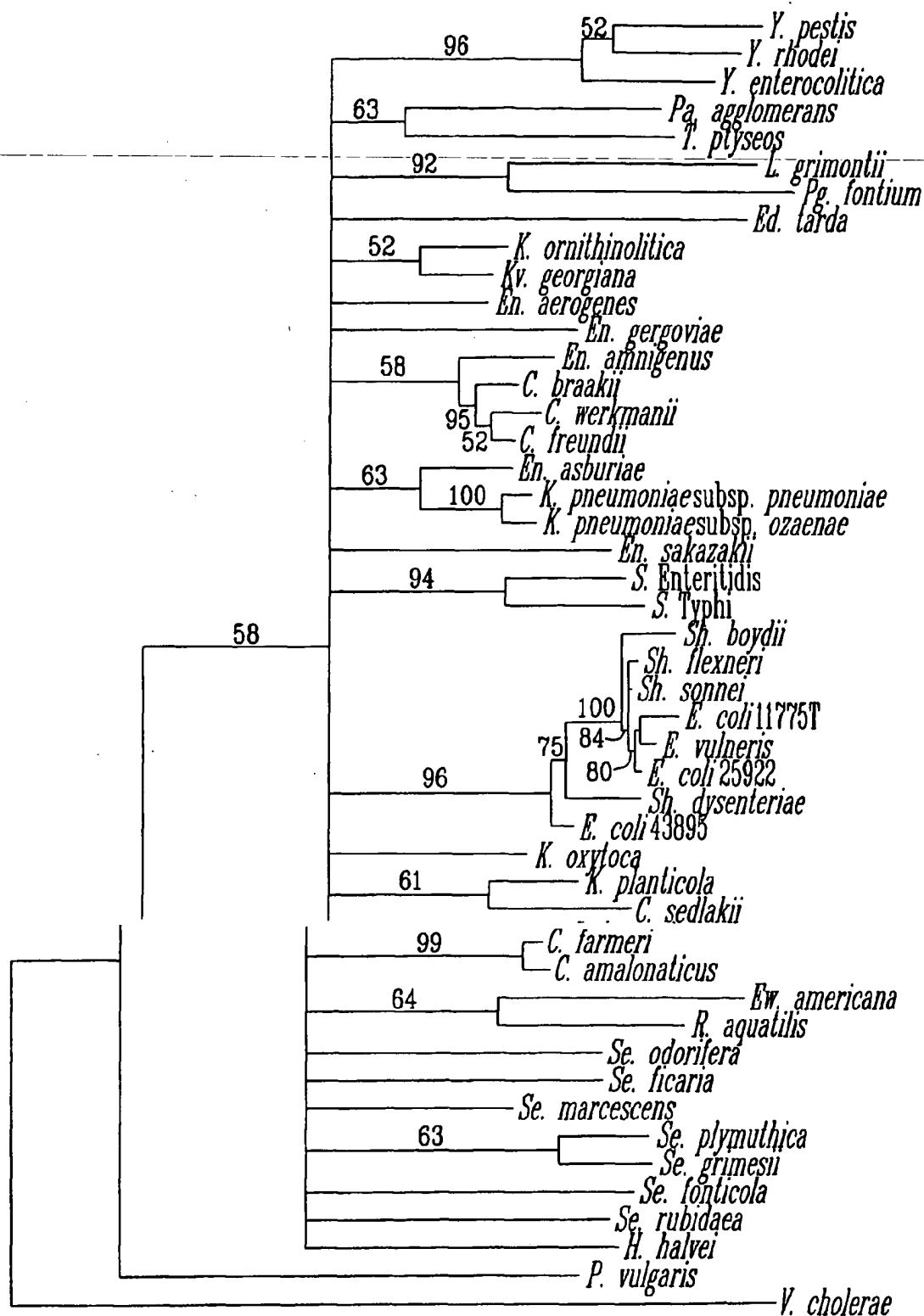


21 / 27

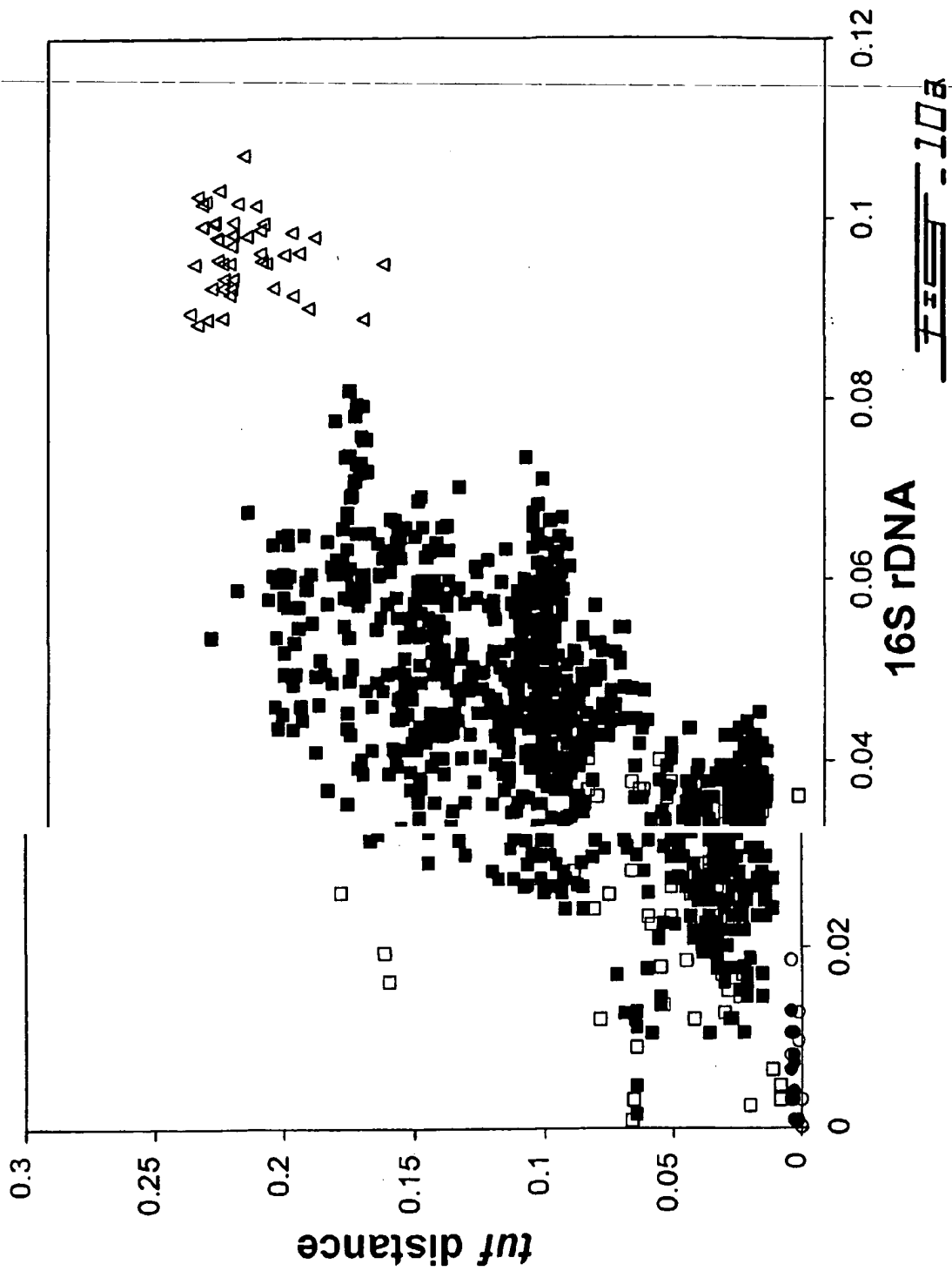


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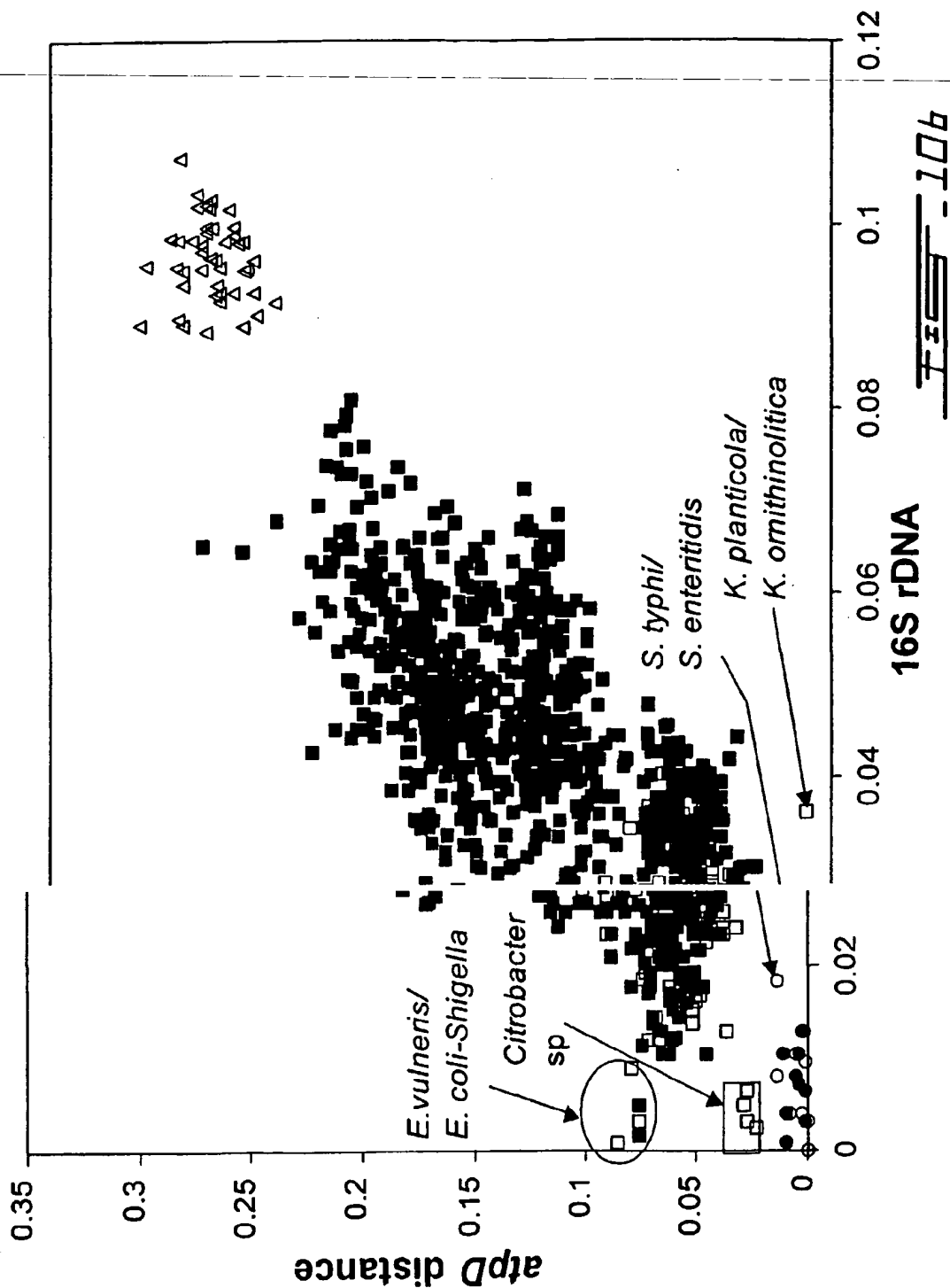
22/27



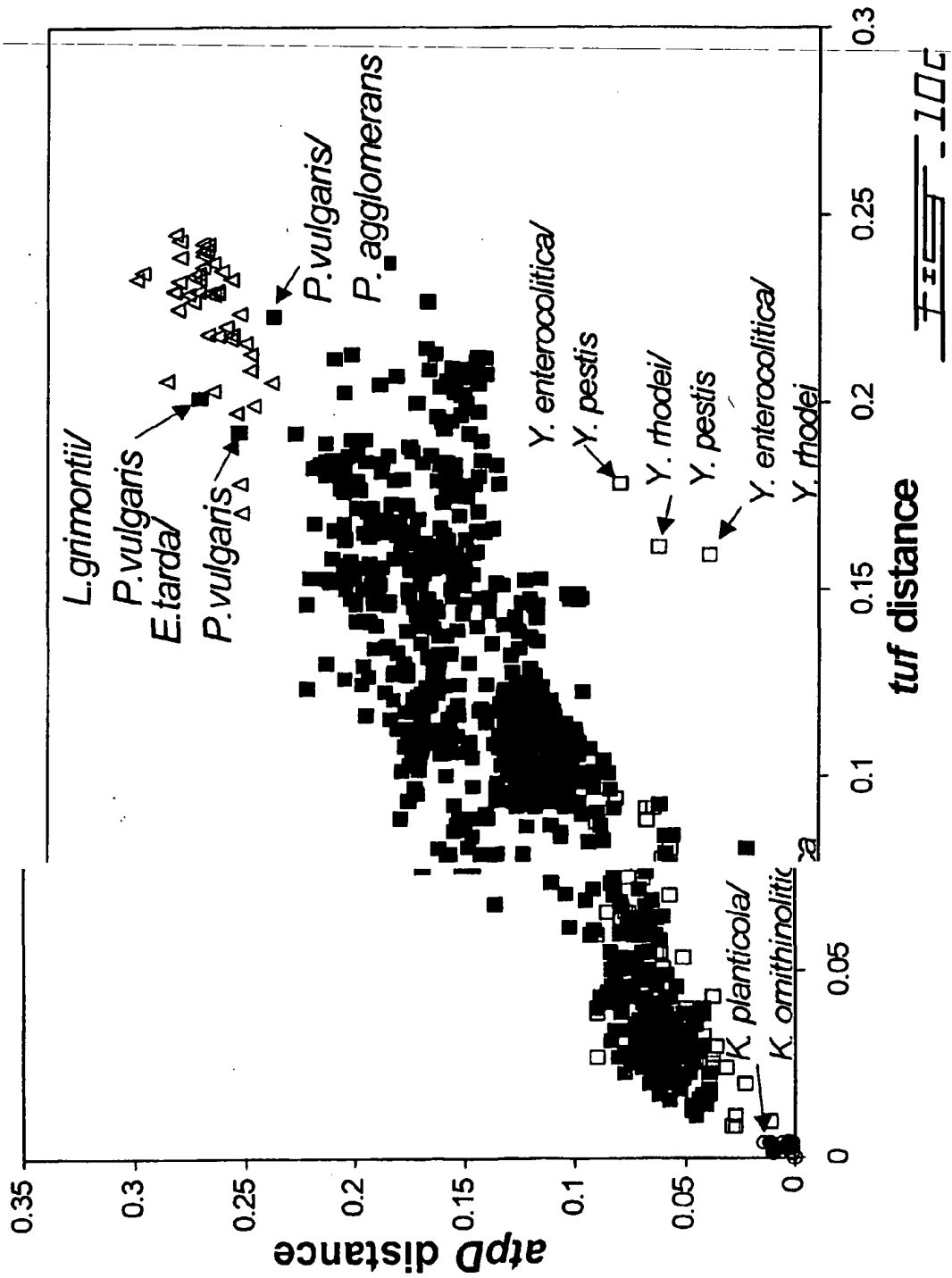
23/27



24/27



25/27



SEQ ID NO: 118+SEQ ID NO: 119 (118 bp)

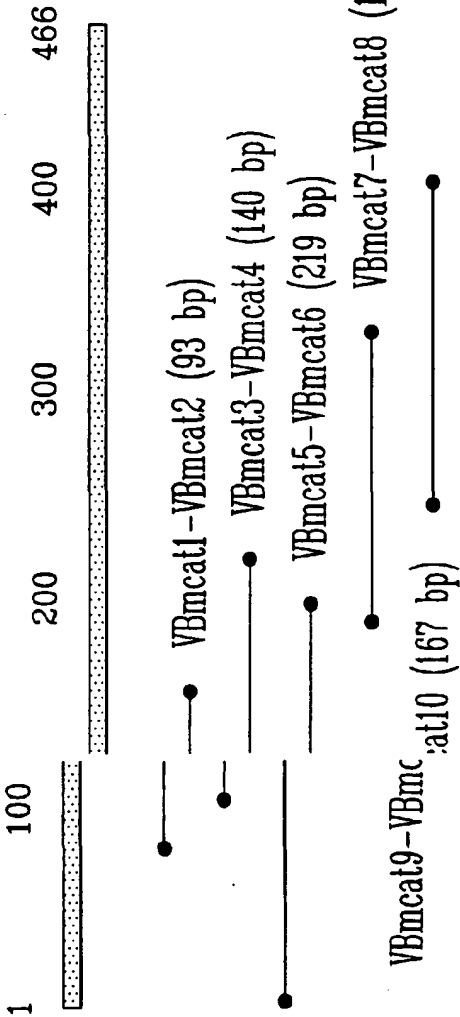


FIG. 11

27 / 27

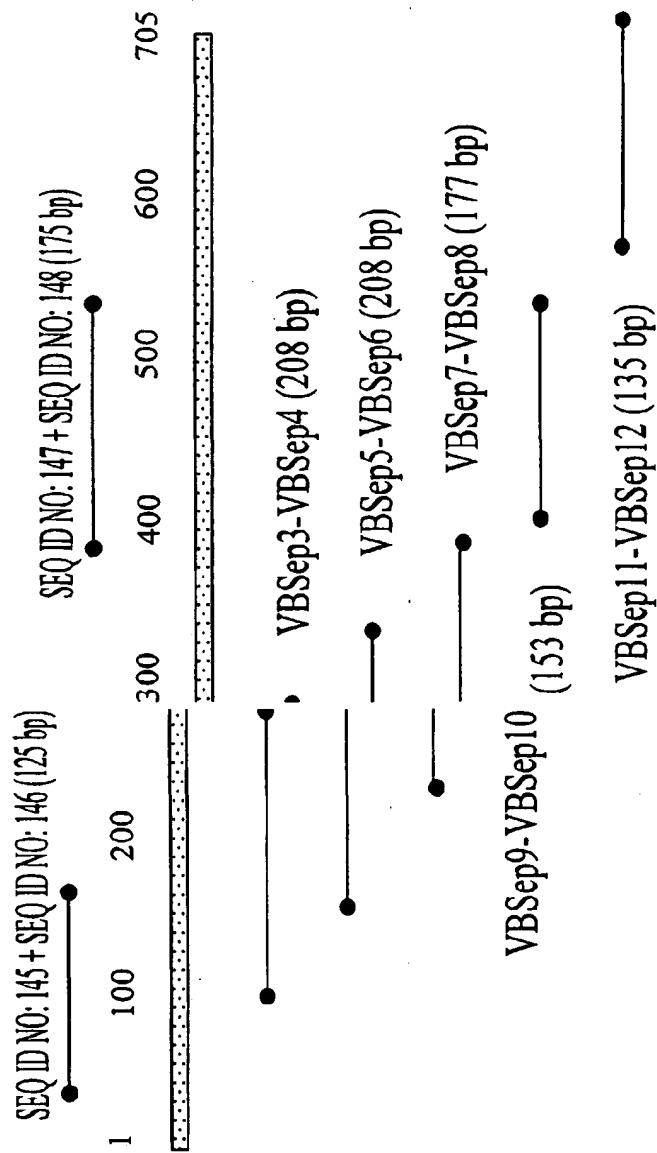


FIG. 12

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANTS:

5 BERGERON, Michel G. ¹, 1145 des Érables, Québec City,
 Québec, Canada, G2K 1T8
 BOISSINOT, Maurice ¹, 109 Jean-Bruchési, St-Augustin-
 de-Desmaures, Québec, Canada, G3A 2N2
 10 HULETSKY, Ann ¹, 1231 Av des Pins, Sillery, Québec,
 Canada, G1S 4J3
 MÉNARD, Christian ¹, 1174 Rue du Pont, St-Lambert-de-
 Lévis, Québec, Canada, G0S 2W0
 OUELLETTE, Marc ¹, 1035 de Ploërmel, Sillery, Québec,
 Canada, G1S 3S1
 15 PICARD, François J. ¹, 1245 de la Sapinière, Cap-
 Rouge, Québec, Canada, G1Y 1A1
 ROY, Paul H. ², 28 Charles Garnier, Loretteville,
 Québec, Canada, G2A 2X8

20 ¹:Canadian citizenship
²:American citizenship

(ii) TITLE OF THE INVENTION: HIGHLY CONSERVED GENES AN THEIR
 25 USE TO GENERATE SPECIES-SPECIFIC, GENUS-SPECIFIC AND
 UNIVERSAL NUCLEIC ACID PROBES AND AMPLIFICATION PRIMERS TO
 RAPIDLY DETECT AND IDENTIFY ALGAL, ARCHAEAL, BACTERIAL,
 FUNGAL AND PARASITICAL MICROORGANISMS FROM CLINICAL
 SPECIMENS FOR DIAGNOSIS

30 (iii) NUMBER OF SEQUENCES: 2297

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE:
 35 (B) STREET:
 (C) CITY:
 (D) STATE:
 (E) COUNTRY:
 (F) ZIP:

40 (v) COMPUTER READABLE:

(A) MEDIUM TYPE:
 (B) COMPUTER:
 45 (C) OPERATING:
 (D) SOFTWARE:

(vi) CURRENT APPLICATION DATA:

50 (A) APPLICATION:
 (B) FILING DATE:
 (C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

55 (A) APPLICATION:
 (B) FILING DATE:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME:

(B) REGISTRATION NUMBER:

5

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE:

(B) TELEFAX:

2) INFORMATION FOR SEQ ID NO: 1

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 750 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

10 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Acinetobacter baumannii*
 (B) STRAIN: ATCC 19606

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1

CAAACCTCGTG AGCACATCCT TCTTCTCGT CAGGTAGGTG TACCTTACAT 50
 CATCGTATTC TTAAACAAAT GCGACCTTGT TGATGACGAA GAATTACTTG 100
 20 AATTAGTAGA AATGGAAGTA CGTGAACCTC TTTCTACTTA TGACTTCCCA 150
 GGTGATGACA CTCCAGTAAT CCGTGGTTCA GCTCTGCGAG CGCTTAACGG 200
 TGAAGCTGGT CCTTACGGTG AAGAATCAGT TCTTGCTCTT GTAGCAGCAC 250
 TTGACTCTTA CATCCCAGAG CCAGAGCGTG CAATCGACAA AGCATTCTTG 300
 ATGCCAATCG AAGACGTATT CTCATTTTCT GGTGCGTGGTA CAGTAGTAAC 350
 25 AGGCCGTGTT GAAGCTGGTA TCATCAAAGT TGGTGAAGAA GTAGAGATCG 400
 TTGGTATTAA AGATACAGTT AAAACAACCTG TAACTGGCGT AGAAATGTTC 450
 CGTAAACTTC TTGACGAAGG CCGTGCAGGT GAGAACTGTG GTATCTTACT 500
 TCGTGGTACT AAGCGTGAAG AAGTACAACG TGGTCAAGTA CTTGCTAAAC 550
 CAGGTACAAT CAAGCCGCAC ACTAAATTCG ACGCAGAAAGT ATACGTACTT 600
 30 TCTAAAGAAG AAGGTGGTCG TCACACTCCA TTCTTAAATG GTTACCGTCC 650
 ACAGTTCTAC TTCCGTACAA CTGACGTAAC TGGTGCRAAT CAGTTGAAAG 700
 AAGGCGTTGA AATGGTAATG CCAGGTGACA ACGTTGAAAT GTCAGTAGAA 750

35

2) INFORMATION FOR SEQ ID NO: 2

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 826 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

45

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Actinomyces meyeri*
 (B) STRAIN: ATCC 35568

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2

CGGTGCGATC CTCGTGGTCG CCGCGACCGA CGGCCCATG GCCCAGACCC 50
 GCGAGCACGT CCTGCTCGCC CGTCAGGTCG GCGTCCAC CATCCTCATC 100
 GCCCTCAACA AGTCCGACAT GGTGACGAC GAGGAAATGA TGGAAGTGGT 150
 55 CGAGGAGGAG TGCCGCGACC TGCTGGAGTC CCAGGACTTC GATCGCGATG 200
 CCCCAGTCGT CCAGGTTTCC GCTCTGAAGG CCCTCGAGGG CGACGCGGAG 250
 TGGGTGGCCA AGATCGAGGA GCTCATGGAG GCTGTGGATT CCTACATCCC 300
 CACCCCGGAG CGCGATATGG ACAAGCCCTT CCTCATGCCG ATCGAGGACG 350
 TCTTCACGAT CACAGGTCGT GGCACGGTCG TCACGGGGCG TGTTGAGCGT 400
 60 GGCAAGCTGC CGATCAACTC CGAGGTCGAG ATCCTCGGTA TCCGTGATCC 450

CCAGAAGACC ACGGTCACCG GCATCGAGAT GTTCCACAAG TCGATGGACG 500
 AGGCATGGGC CGGCGAGAAC TGTGGCCTGC TGCTGCGCGG TACCAAGCGC 550
 GATGAGGTTG AGCGCGGCCA GGTTGTGGCC ATTCCCGGCT CCATCACGCC 600
 TCACACCGAG TTCGAGGGCC AGGTTTACAT CCTCAAGAAG GAAGAGGGCG 650
 5 GCCGTCACAA CCCGTTCTTC TCGAACTACC GTCCGCAGTT CTACTTCCGT 700
 ACCACGGACG TGACCGGCGT CATCACCTC CCCGAGGGCA CCGACATGGT 750
 CATGCCTGGC GACACCACCG AGATCTCCGT TCAGCTGATC CAGCCCATCG 800
 CCATGGAGCC CGGCTGGGCT TCGCCA 826

10

2) INFORMATION FOR SEQ ID NO: 3

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 835 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

20 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Aerococcus viridans*
 (B) STRAIN: ATCC 11563

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3

TGGTGCATC TTAGTAGTAT CTGCTGCTGA TGGTCCAATG CCACAACTC 50
 GTGAGCACAT CCTTTTAGCT GGCCAAATCG GTGTCCTGC ATTCGTAGTA 100
 30 TTCTTAAACA AAGTTGACCA AGTTGACGAT GAAGAATTAC TAGAATTAGT 150
 TGAAATGGAA GTTCGTGACT TATTATCTGA GTACAACTAC CCAGGTGACG 200
 ATCTACCTGT AATCGCTGGT TCTGCTTTAT TAGCATTACA AGGCGATGAA 250
 GCTCAAGAAG CTAAATCAT GGAATTAATG GAAGCTGTAG ACTCTTACAT 300
 TCCAGAACCA GAACGTGACA ACGACAAACC ATTCATGATG CCAATTGAGG 350
 35 ATGTATTCTC AATCACTGGT CGTGGTACTG TTGCTACAGG TCGTGTGAA 400
 CGTGGTGAAG TTCGTACAGG TGACGAAGTT GACATCGTTG GTATTGCTGA 450
 ACAATCGGT AAATCAGTTG TAACTGGTGT TGAAATGTTT CGTAAAACT 500
 TAGACTACGC TCAAGCTGGT GACAACATCG GTGCATTATT ACGTGGTGT 550
 CAACGTGAAG ACATCCAACG TGGTCAAGTA TTGGCTGCTC CTGGTTCAAT 600
 40 CACTCCACAT ACTAAATTTA AAGCGCAAGT TTACGTTTTA TCTAAAGAAG 650
 AAGGTGGACG TCATACACCA TTCTTAACTA ACTACCGTCC ACAATTCTAC 700
 TTCCGTACIA CTGACATTAC TGGTGTATC ACTTTACCAG AAGACGTAGC 750
 TATGGTTATG CCTGGTGACA ACGTTGATAT GGACGTTGAA TTGATTACCC 800
 CAGTTGCGAT CGAAGATGGT ACTAAATTCT CTATC 835

45

2) INFORMATION FOR SEQ ID NO: 4

(i) SEQUENCE CHARACTERISTICS:

- 50 (A) LENGTH: 827 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

55

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Achromobacter xylosoxidans* subsp.
 60 *denitrificans*

(B) STRAIN: ATCC 15173

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4

5	CCTGGTGGTG	TCGGCCGCTG	ACGGCCCCGAT	GCCGCAAACG	CGCGAACACA	50
	TCCTGCTGAG	CCGCCAGGTT	GGCGTGCCGT	ACATCATCGT	CTTCCTGAAC	100
	AAGGCCGACA	TGGTTGACGA	CGCCGAGCTG	CTTGAGCTGG	TGGAAATGGA	150
	AGTTTCGCGAR	CTGCTGAGCA	AGTACGACTT	CCCGGGCGAC	GACACCCCGA	200
	TCGTGAAGGG	TTCGGCCAAG	CTGGCGCTGG	AAGGCGACAA	GGGCGAACTG	250
10	GGCGAACAGG	CCATCATGGC	GCTGGCCGCT	GCGCTGGACT	CGTACATCCC	300
	GACGCCTGAG	CGTGCCGTTG	ACGGCGCGTT	CCTGATGCCG	GTTGAAGACG	350
	TGTTCTCGAT	CTCGGGTCGC	GGCACCGTGG	TGACCGGCCG	TATCGAACGC	400
	GGCATCATCA	AGGTCGGCGA	GGAAATCGAA	ATCGTCGGTC	TGGTGCCGAC	450
	GGTGAAGACG	ACCTGCACGG	GCGTGGAAT	GTTCCGCAAG	CTGCTGGACC	500
15	AAGGTCAAGC	CGGCGACAAC	GTGGGCATCC	TRCTGCGCGG	CACCAAGCGT	550
	GAAGACGTCC	AGCGCGGCCA	GGTTCTGGCC	AAGCCGGGCT	CGATCACCCC	600
	GCACACGGAC	TTCACGTCCG	AGGTGTACAT	CCTGTCCAAG	GAAGAAGGCG	650
	GCCGTACAC	TCCGTTCTTC	CAAGGCTATC	GTCCCCAGTT	CTACTTCCGC	700
	ACGACGGACG	TGACGGGCAC	GATCGAGCTG	CCGGCCGACA	AGGAAATGGT	750
20	CCTGCCGGGC	GACAACGTGG	CCATGACGGT	CAAGCTGCTG	GCTCCGATCG	800
	CCATGGAAGA	AGGCCTGCGT	TCGCCAC			827

25 2) INFORMATION FOR SEQ ID NO: 5

(i) SEQUENCE CHARACTERISTICS:

	(A)	LENGTH: 823 bases
	(B)	TYPE: Nucleic acid
30	(C)	STRANDEDNESS: Double
	(D)	TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

35 (vi) ORIGINAL SOURCE:

(A)	ORGANISM: <i>Anaerorhabdus furcosus</i>
(B)	STRAIN: ATCC 25662

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5

40	TGGATCAATC	CTAGTAGTTG	CTGCAACTGA	TGGACCAATG	CCTCAAATC	50
	GTGAACATAT	CTTACTTGCT	CGTCAAGTAG	GTGTTCCAAG	AATGGTTGTA	100
	TTCTTGAACA	AATGCGACAT	GGTTGAAGAT	GAAGAATTAA	TCGACCTTGT	150
	TGAAATGGAA	GTTCGTGAAC	TTCTAAGTGC	TTACGGTTTC	GAAGGTGATG	200
45	ATACACCACT	TATCCGTGGT	TCTGCATTAA	AATCTCTTGA	AGGAAATGCT	250
	GATTGGGAAG	CAAAAGTTGC	TGAATTAATG	GATGCAGTTG	ACTCTTGGAT	300
	TCCAATCCA	ACTCATGAAA	CAGACAAACC	ATTCTTAATG	GCTGTTGAAG	350
	ATGTATTAC	AATTACAGGT	CGTGGTACAG	TTGCTACTGG	ACGTGTTGAA	400
	CGTGGACACT	TAAACCTTAA	CGAAGAAGTT	GAAATCGTTG	GTATTCATGA	450
50	TACTAAGAAA	TCAGTTGTTA	CTGGTATCGA	AATGTTCCGT	AAATTATTAG	500
	ACTATGCTGA	AGCAGGAGAC	AACATTGGTG	CATTATTACG	TGGTGTTTCT	550
	CGTGATGAAA	TCGAACGTGG	ACAATGTCTA	GCTAAACCTG	GATCAGTTAC	600
	TCCACATACA	GCTTTCAAAG	CTCAAGTATA	CGTATTAAT	AAAGAAGAAG	650
	GTGGACGTCA	TACACCATT	GTAACATACT	ACCGTCCTCA	ATTCTATTT	700
55	CGTACAACTG	ACGTAACAGG	AGTTGTAA	CTTCCTGAAG	GTAAGTAAAT	750
	GGTTATGCCT	GGAGACAACA	TCGAAATGAT	CGTTGAATTA	ATCGCTCCAA	800
	TCGCTGTTGA	ACAAGGAAT	AAG			823

60

2) INFORMATION FOR SEQ ID NO: 6

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 825 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacillus anthracis*
 (B) STRAIN: 4229

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6

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CGGCGGTATC TTAGTAGTAT CTGCTGCTGA TGGCCCAATG CCTCAAACCTC      50
GTGAGCACAT CCTTCTTTCT CGTCAAGTAG GTGTACCTTA CATCGTTGTA      100
TTCTTAAACA AATGCGACAT GGTAGACGAC GAAGAATTAT TAGAATTAGT      150
20 AGAAATGGAA GTTCGCGACC TATTATCTGA ATACGGATTG CCAGGCGACG      200
ACATTCCTGT AATCAAAGGT TCTGCTCTTA AAGCTCTTCA AGGAGAAGCT      250
GATTGGGAAG CAAAAATCAT TGAATTAATG GCTGAAGTTG ATGCTTACAT      300
CCCAACTCCA GAACGTGAAA CTGACAAACC ATTCTTAATG CCTGTAGAGG      350
ACGTATTCTC TATCACAGGT CGTGGTACAG TTGCTACTGG TCGTGTTGAG      400
25 CGCGGTATCG TTAAAGTTGG TGACGTAGTA GAAATCATCG GTCTTGCTGA      450
AGAAAATGCT TCTACAACTG TAACTGGTGT AGAGATGTTC CGTAAACTTC      500
TTGACCAAGC TCAAGCTGGA GACAACATCG GTGCTTTACT TCGTGGGGTT      550
GCTCGTGAAG ACATCCAACG TGGACAAGTA CTTGCAAAAA GCGGTTCTGT      600
AAAAGCTCAC GCTAAATTC AAGCTGAAGT TTTTCGTATTA TCTAAAGAAG      650
30 AAGGTGGACG TCACACTCCA TTCTTCGCTA ACTACCGTCC TCAGTTCTAC      700
TTCCGTACAA CTGACGTAAC TGGTATCATC CAATTACCAG AAGGTACTGA      750
AATGGTAATG CCTGGTGACA ACATCGAAAT GACTATCGAA CTTATCGCTC      800
CAATCGCTAT CGAAGAGGGA ACTAA      825

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2) INFORMATION FOR SEQ ID NO: 7

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 829 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacillus cereus*
 (B) STRAIN: ATCC 14579

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7

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CGGCGGTATC TTAGTAGTAT CTGCTGCTGA TGGCCCAATG CCTCAAACAC      50
GTGAGCACAT CCTTCTTTCT CGTCAAGTAG GTGTTCCTTA CATCGTTGTA      100
55 TTCTTAAACA AATGCGACAT GGTAGATGAC GAAGAATTAT TAGAATTAGT      150
AGAAATGGAA GTTCGCGACC TATTATCTGA ATACGGATTG CCAGGCGACG      200
ACATTCCTGT AATCAAAGGT TCTGCTCTTA AAGCTCTTCA AGGAGAAGCT      250
GATTGGGAAG CAAAAATCAT TGAATTAATG GCTGAAGTTG ATGCTTACAT      300
CCCAACTCCA GAACGTGAAA CTGACAAACC ATTCTTAATG CCTGTAGAGG      350
60 ACGTATTCTC TATCACAGGT CGTGGTACAG TTGCTACTGG TCGTGTTGAG      400

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	CGCGGTATCG	TTAAAGTTGG	TGACGTAGTA	GAAATCATCG	GTCTTGCTGA	450
	AGAAAATGCT	TCTACAACTG	TAACTGGTGT	AGAGATGTTT	CGTAAACTTC	500
	TTGACCAAGC	TCAAGCTGGA	GACAACATCG	GTGCTTTACT	TCGTGGGGTT	550
	GCTCGTGAAG	ACATCCAACG	TGGACAAGTA	CTTGCAAAAA	GCGGTTCTGT	600
5	AAAAGCTCAC	GCTAAATTCA	AAGCTGAAGT	TTTCGTATTA	TCTAAAGAAG	650
	AAGGTGGACG	TCACACTCCA	TTCTTCGCTA	ACTACCGTCC	TCAGTTCTAC	700
	TTCCGTACAA	CTGACGTAAC	TGGTATCATC	CAATTACCAG	AAGGTACTGA	750
	AATGGTAATG	CCTGGTGACA	ACATTGAAAT	GACTATCGAA	CTTATCGCTC	800
	CAATCGCTAT	CGAAGAGGGA	ACTAAATTC			829

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2) INFORMATION FOR SEQ ID NO: 8

15 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 818 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacteroides distasonis*
 (B) STRAIN: ATCC 8503

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8

	CGGTGCTATC	ATCGTAGTTG	CTGCTACTGA	TGGTCCTATG	CCTCAAACCTC	50
30	GCGAGCACAT	CCTTTTGGCT	CGTCAGGTAA	ACGTTCCGAG	ATTGGTTGTA	100
	TTTCATGAACA	AGTGTGACAT	GGTTGACGAC	GAGGAAATGT	TGGAATTGGT	150
	TGAGATGGAG	ATGAGAGAGT	TGCTTTTCATT	CTATCAATTC	GACGGTGACA	200
	ACACTCCGAT	CATCCGTGGT	TCTGCTCTTG	GTGCATTGAA	CGGTGATGCT	250
	CAATGGGAAG	ATAAAGTAAT	GGAGTTGATG	GAAGCTTGTTG	ATACTTGGAT	300
35	TCCTCTGCCT	CCGCGCGAAA	TCGACAAGCC	GTTCTTGATG	CCGGTTGAGG	350
	ACGTATTCTC	AATCACGGGT	CGTGGTACTG	TTGCTACAGG	TCGTATCGAG	400
	ACAGGTATTG	TTAAGGTTGG	TGAGGAAGTT	CAGATCATCG	GTCTTGCGCG	450
	TGCTGGTAAG	AAATCTGTTG	TTACAGGTGT	TGAGATGTTT	CGTAAGTTAT	500
	TGGATCAAGG	TGAGGCTGGT	GATAACGTTG	GTTTGTTGCT	TCGCGGTATC	550
40	GATAAGAATG	AGATCAAGCG	TGGTATGGTA	ATCTGCCACC	CGGGTCAGGT	600
	TAAAGAGCAT	TCTAAGTTCA	AGGCTGAGGT	TTATATCTTG	AAGAAAGAGG	650
	AAGGTGGTCG	TCACACTCCG	TTCCACAACA	AATATCGTCC	TCAGTTCTAT	700
	ATCCGTACAT	TGGATGTAAC	TGGTGAGATC	ACTTTGCCGG	AAGGAACCTGA	750
	AATGGTAATG	CCGGGTGATA	ACGTAACGAT	CGAGGTTGAG	TTGATCTATC	800
45	CGGTAGCATG	TAGCGTAG				818

2) INFORMATION FOR SEQ ID NO: 9

50

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 639 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

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(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus casseliflavus*

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(B) STRAIN: R763

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9

5	GGTCCTATGC	CTCAAACACG	TGAACACATC	TTGTTATCAC	GTAACGTTGG	50
	TGTACCATAC	ATCGTTGTTT	TCTTAAACAA	AATGGATATG	GTTGATGACG	100
	AAGAATTACT	AGAATTAGTT	GAAATGGAAG	TTCGTGACTT	ATTGTCAGAA	150
	TATGACTTCC	CAGGCGACGA	TGTTCTGTGA	ATCGCTGGTT	CTGCTTTGAA	200
	AGCTCTTGAA	GGCGATGCTT	CATACGAAGA	AAAAATCATG	GAATTAATGG	250
10	CTGCAGTTGA	CGAATACGTT	CCAACTCCAG	AACGTGACAC	TGACAAACCA	300
	TTCATGATGC	CAGTCGAAGA	CGTATTCTCA	ATCACTGGAC	GTGGTACTGT	350
	TGCTACAGGC	CGTGTGGAAC	GTGGACAAGT	TCGCGTTGGT	GACGAAGTTG	400
	AAATCGTTGG	TATTGCTGAA	GAAACTGCTA	AAACAACGTG	AACTGGTGTG	450
	GAAATGTTCC	GTAAATTGTT	AGACTATGCT	GAAGCAGGGG	ATAACATTGG	500
15	TGCATTGCTA	CGTGGTGTTG	CTCGTGAAGA	CATCCAACGT	GGACAAGTAT	550
	TGGCTAAAGC	TGGTACAATC	ACACCTCATA	CAAAATTTAA	AGCTGAAGTT	600
	TACGTTTTTA	CAAAAGAAGA	AGGTGGACGT	CACACACCA		639

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2) INFORMATION FOR SEQ ID NO: 10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 692 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

30

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus saprophyticus*
 (B) STRAIN: CSG 197

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10

	GAACACATTC	TTTTATCACG	TAACGTTGGT	GTTCCAGCAT	TAGTTGTATT	50
	CTTAAACAAA	GTTGACATGG	TTGACGATGA	AGAATTATTA	GAATTAGTAG	100
	AAATGGAAGT	TCGTGACTTA	TTAAGCGAAT	ATGACTTCCC	AGGTGACGAT	150
40	GTACCTGTAA	TCTCTGGTTC	TGCATTAAAA	GCTTTAGAAG	GCGACGCTGA	200
	CTATGAGCAA	AAAATCTTAG	ACTTAATGCA	AGCTGTTGAT	GACTTCATTC	250
	CAACACCAGA	ACGTGATTCT	GACAAACCAT	TCATGATGCC	AGTTGAGGAC	300
	GTATTCTCAA	TCACTGGTGC	TGGTACTGTT	GCTACAGGCC	GTGTTGAACG	350
	TGGTCAAATC	AAAGTCGGTG	AAGAAATCGA	AATCATCGGT	ATGCAAGAAG	400
45	AATCAAGCAA	AACAACGTG	ACTGGTGTAG	AAATGTTCCG	TAAATTATTA	450
	GACTACGCTG	AAGCTGGTGA	CAACATTGGT	GCATTATTAC	GTGGTGTTC	500
	ACGTGATGAC	GTACAACGTG	GTCAAGTTTT	AGCTGCTCCT	GGTACTATTA	550
	CACCACATAC	AAAATTCAAA	GCGGATGTTT	ACGTTTTATC	TAAAGATGAA	600
	GGTGGTCGTC	ATACACCATT	CTTCACTAAC	TACCGCCAC	AATTCTATTT	650
50	CCGTACTACT	GACGTAACGT	GTGTTGTAA	CTTACCAGAA	GG	692

2) INFORMATION FOR SEQ ID NO: 11

55

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 821 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

60

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 5 (A) ORGANISM: *Bacteroides ovatus*
(B) STRAIN: ATCC 8483

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11

10	CGGTGCTATC ATCGTTTGTG CTGCAACTGA TGGTCCGATG CCTCAAAC	50
	GCGAACACAT TCTGTTAGCT CGTCAGGTAA ACGTACCTCG TCTGGTTGTA	100
	TTCTTGAACA AATGCGATAT GGTAGACGAC GAAGAAATGT TGGAAC	150
	TGAAATGGAA ATGAGAGAAC TCCTTTCATT CTATGATTTC GATGGTGACA	200
	ATACTCCTAT CATCCGTGGT TCTGCTCTTG GCGCATTGAA CGGTGTTGAA	250
15	AAATGGGAAG ACAAAGTTAT GGAAGTATG GATGCAGTTG ATAAGTGGAT	300
	TCCACTGCCT CCGCGCGATG TTGATAAACC ATTCTTGATG CCGGTTGAAG	350
	ACGTGTTCTC TATCACAGGT CGTGGTACTG TAGCAACAGG TCGTATCGAA	400
	ACAGGTGTCA TCCACGTTGG TGATGAAGTC GAAATTCTTG GTTTAGGTGA	450
	AGATAAGAAA TCAGTTGTAA CTGGTGTGTA AATGTTCCGT AAAGTGTGG	500
20	ATCAAGGTGA AGCTGGTGAC AACGTAGGTC TTTTGCTTCG TGGTATTGAC	550
	AAGAACGAAA TCAAACGTGG TATGGTTCTT TGTAACACAG GTCAGATTAA	600
	ACCGCACTCT AAATTCAAAG CTGAGGTTTA TATCTTGAAG AAAGAAGAAG	650
	GTGGTCGTCA CACTCCGTTT CACAACAAAT ACCGTCCTCA GTTCTACTTG	700
	CGTACTATGG ACTGTACAGG TGAATCACT TTGCCGGAAG GAACAGAAAT	750
25	GGTAATGCCG GGTGATAACG TAACTATTAC AGTTGAGTTG ATTTACCCAG	800
	TAGCATTGAA CCCGGGCTTC G	821

30 2) INFORMATION FOR SEQ ID NO: 12

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 838 bases
(B) TYPE: Nucleic acid
35 (C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

40 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bartonella henselae*
(B) STRAIN: ATCC 49882

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12

45	TGGTGCGATT TTGGTTGTTT CAGCTGCTGA TGGTCCGATG CCTCAAACAC	50
	GTGAGCATAT TCTTCTTGCC CGTCAGGTTG GTGTTCCAGC GATTGTTGTT	100
	TTTCTTAATA AGGTTGATCA GGTGATGAT GCTGAGCTTT TGGAGCTTGT	150
	TGAGCTTGAA GTTCGGGAGT TATTGTCGAA ATATGATTTT CCAGGAGACG	200
50	ATATTCCGAT CGTTAAAGGT TCTGCTTTGG CAGCGCTTGA AGATAAAGAT	250
	AAAAGCATTG GTGAAGATGC GGTTCGTCTT TTGATGAGTG AAGTTGATAA	300
	TTATATACCG ACGCCTGAAC GTCCTGTTGA TCAGCCGTTT TTGATGCCAA	350
	TTGAAGATGT TTTTTCGATT TCGGGTCGTG GAACTGTTGT GACGGGTCGT	400
	GTTGAGCGTG GTGTTATTAA GGTGGTGAA GAAGTTGAGA TTATCGGCAT	450
55	TCGTCCAAC TCTAAGACAA CAGTTACAGG GGTGAAATG TTCCGCAAGC	500
	TTTTAGATCA GGGGCAAGCG GGTGATAATA TTGGAGCGCT GCTTCGTGGT	550
	ATTGATCGTG AAGGGATTGA GCGTGGACAA GTTTTGCGA AGCCTGCTTC	600
	GGTTACACCT CATACGAGAT TTAAAGCAGA GGCTTACATT TTGACGAAAG	650
	ATGAAGGTGG TCGTCATACT CCATTTTCA CGAATTATCG TCCTCAGTTT	700
60	TATTTCCGTA CTACGGATGT AACGGGAATT GTTACGCTTC CAGAAGGTAC	750

AGAGATGGTT ATGCCTGGTG ATAATGTTGC TATGGATGTC TCTCTGATTG 800
 TTCCAATTGC CATGGAAGAA AACTTCGTT TTGCTATC 838

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2) INFORMATION FOR SEQ ID NO: 13

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 839 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bifidobacterium adolescentis*
 (B) STRAIN: ATCC 15703

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13

TGGCGCCATC CTTGTTGTGG CCGCCACCGA CGGCCCGATG GCTCAGACCC 50
 GCGAGCACGT GCTGCTCGCT CGTCAGGTGG GCGTCCCGAA GATCCTCGTC 100
 GCTCTGAACA AGTGCATAT GGTGACGAC GACGAGCTCA TCGAGCTCGT 150
 25 TGAGGAAGAG GTCCGTGACC TCCTCGACGA AAATGGCTTC GATCGCGATT 200
 GCCCGGTCAT CCACGTGTCC GCTTACGGCG CACTGCACGA TGACGCTCCG 250
 GACCACGAGA AGTGGGTTGA GCAGATCAAG AAGCTCATGG ACGCCGTCGA 300
 TGACTACATC CCGACCCCGG TCCACGATCT GGACAAGCCG TTCCTGATGC 350
 CGATCGAAGA TGTCTTCACC ATCTCCGGCC GTGGCACCGT GGTGACCGGC 400
 30 CGTGTGCGAGC GTGGTAAGCT CCCGGTCAAC TCCAACGTCG AGATCGTCGG 450
 CATCCGTCCG ACCCAGACCA CCACCGTCAC CTCCATCGAG ACCTTCCACA 500
 AGCAGATGGA CGAGTGCGAG GCTGGCGACA ACACCGGTCT GCTGCTCCGC 550
 GGCATCAACC GTGACCAGGT CGAGCGTGGC CAGGTTCTGG CTGCTCCGGG 600
 CTCCGTGACC CCGCACACCA AGTTCGAGGG CGAAGTCTAC GTGCTGACCA 650
 35 AGGACGAAGG CGGCCGTAC TCGCCGTTCT TCTCCAACTA CCGTCCGCAG 700
 TTCTACTTCC GTACCACCGA CGTCACCGGC GTCATCACCC TGCCGGAAGG 750
 CGTTGAGATG GTGCAGCCGG GCGATCACGC TACCTTCGGC GTTGAGCTGA 800
 TCCAGCCGAT CGCTATGGAA GAGGGCCTGA CCTTCGCAG 839

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2) INFORMATION FOR SEQ ID NO: 14

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 839 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bifidobacterium dentium*
 (B) STRAIN: ATCC 27534

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14

TGGCGCTATC CTCGTTGTGG CCGCCACCGA CGGCCCGATG GCTCAGACCC 50
 GCGAGCACGT GCTGCTCGCT CGTCAGGTGG GCGTGCCGCG TATCCTCGTC 100
 60 GCCCTGAACA AGTGCATAT GGTGACGAC GAAGAGCTCA TCGAGCTCGT 150

	TGAGGAAGAG	GTCCGTGACC	TCCTCGACGA	AAACGGCTTC	GATCGCGATT	200
	GCCCCGTGTCAT	CCACACCTCC	GCCTACGGCG	CGCTGCACGA	TGACGCTCCG	250
	GACCACGACA	AGTGGGTTGA	GTCCGTCAAG	GAATCATGA	AGGCCGTCTGA	300
	CGAGTACATC	CCGACCCCGA	CCCACGATCT	GGACAAGCCG	TTCCTGATGC	350
5	CGATCGAAGA	TGTGTTACC	ATCTCCGGCC	GTGGCACCGT	GGTTACCGGC	400
	CGTGTCGAGC	GTGGTAAGCT	CCCGGTCAAC	TCCAACGTTG	AGATCGTCGG	450
	CATCCGTCCG	ACCCAGACCA	CCACCGTCAC	CTCCATCGAG	ACCTTCCACA	500
	AGCAGATGGA	CGAGTGCGAG	GCTGGCGACA	ACACCGGTCT	GCTGCTCCGC	550
	GGCATCAACC	GTGACCAGGT	CGAGCGTGCC	CAGGTTCTGG	CTGCTCCGGG	600
10	CTCCGTGACC	CCGCACACCA	AGTTCGAGGG	CGAAGTCTAC	GTGCTGACCA	650
	AGGACGAAGG	CGGCCGTCAC	TCGCCGTTCT	TCTCCAACCTA	CCGTCCGCAG	700
	TTCTACTTCC	GTACCACCGA	CGTCACCGGC	GTCATCACCC	TGCCGGAAGG	750
	CGTTGAGATG	GTGCAGCCGG	GCGATCACGC	TACCTTCGGC	GTTGAGCTGA	800
	TCCAGCCGAT	CGCTATGGAA	GAGGGCCTGA	CCTTCGCAG		839
15						

2) INFORMATION FOR SEQ ID NO: 15

20 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 838 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

25 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Brucella abortus*
 (B) STRAIN: S2308

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15

	TGGCGCGATC	CTGGTGGTTT	CGGCTGCTGA	CGGCCCGATG	CCGCAGACCC	50
35	GCGAGCACAT	CCTGCTTGCC	CGTCAGGTTG	GCGTTCCGGC	GATCGTCGTG	100
	TTCTCAACA	AGTGCGACCA	GGTTGACGAT	GCAGAACTGC	TCGAACTGGT	150
	TGAACTGGAA	GTGCGCGAAC	TTCTGTGCGAA	GTACGAATTC	CCCGGCGACG	200
	AAATCCCGAT	CATCAAGGGC	TCGGCTCTTG	CTGCTCTGGA	AGATTCTTCC	250
	AAGGAACTGG	GCGAAGATGC	CATCCGCAAC	CTGATGGACG	CGGTTGACAG	300
40	CTACATTCCG	ACCCCGGAAC	GCCCGATCGA	CCAGCCGTTT	CTGATGCCGA	350
	TGGAAGACGT	GTTCTCGATC	TCCGGCCGTG	GTACGGTTGT	GACGGGTCGC	400
	GTGAGCGCG	GTATCGTTAA	GGTCGGTGAA	GAAGTTGAAA	TCGTGCGCAT	450
	CAAGGCGACG	ACGAAGACCA	CGGTTACCGG	CGTTGAAATG	TTCCGCAAGC	500
	TGCTCGACCA	GGGCCAGGCT	GGCGACAACA	TTGGCGCGCT	GATCCGCGGC	550
45	GTTGGCCGTG	AAGACGTTGA	ACGCGGCCAG	GTTCTCTGCA	AGCCGGGTTT	600
	TGTGAAGCCG	CACACCAAGT	TTAAGGCAGA	AGCCTATATT	CTGACCAAGG	650
	ACGAAGGTGG	CCGTCATACG	CCGTTCTTCA	CCAACTACCG	TCCGCAGTTC	700
	TACTTCCGTA	CGACGGACGT	GACGGGTGTT	GTGACGCTTC	CGGCTGGCAC	750
	GGAAATGGTC	ATGCCTGGCG	ATAACGTGCG	CATGGACGTT	ACCCTGATCG	800
50	TGCCGATCGC	CATGGAAGAG	AAGCTTCGCT	TCGCTATC		838

2) INFORMATION FOR SEQ ID NO: 16

55

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 771 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

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(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 5 (A) ORGANISM: *Burkholderia cepacia*
 (B) STRAIN: LSPQ 2217

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16

10	GGCAGCAGAC	GGCCCGATGC	CGCAAACGCG	TGAGCACATC	CTGCTGGCGC	50
	GTCAGGTTGG	CGTTCCGTAC	ATCATCGTGT	TCCTGAACAA	GTGCGACATG	100
	GTGGACGACC	CCGAAGTCT	CGAGCTGGTC	GAGATGGAAG	TTCGCGAACT	150
	CCTGTCTGAAG	TACGACTTCC	CGGGCGACGA	CACGCCGATC	GTGAAGGGTT	200
	CGGCGAAGCT	GGCGCTGGAA	GGCGACACGG	GCGAGCTGGG	CGAAGTGGCG	250
15	ATCATGAGCC	TGGCCGACGC	GCTGGACACG	TACATCCCGA	CGCCGGAGCG	300
	TGCAGTTGAC	GGCGCGTTCC	TGATGCCGGT	GGAAGACGTG	TTCTCGATCT	350
	CGGGCCGCGG	TACGGTGGTG	ACGGGTCGTG	TCGAGCGCGG	CATCGTGAAG	400
	GTCGGCGAAG	AAATCGAAAT	CGTCGGTATC	AAGCCGACGG	TGAAGACGAC	450
	CTGCACGGGC	GTTGAAATGT	TCCGCAAGCT	GCTGGACCAA	GGTCAAGCAG	500
20	GCGACAACGT	TGGTATCCTG	CTGCGCGGCA	CGAAGCGTGA	AGACGTGGAG	550
	CGTGGCCAGG	TTCTGGCGAA	GCCGGGTTCG	ATCACGCCGC	ACACGCACTT	600
	CACGGCTGAA	GTGTACGTGC	TGAGCAAGGA	CGAAGGCGGC	CGTCACACGC	650
	CGTTCTTCAA	CAACTACCGT	CCGCAGTTCT	ACTTCCGTAC	GACGGACGTG	700
	ACGGGCTCGA	TCGAGCTGCC	GAAGGACAAG	GAAATGGTGA	TGCCGGGCGA	750
25	CAACGTGTCTG	ATCACGGTGA	A			771

2) INFORMATION FOR SEQ ID NO: 17

30

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 829 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 35 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 40 (A) ORGANISM: *Cedecea davisae*
 (B) STRAIN: ATCC 33431

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17

45	GGCGCTATCC	TGGTTGTTGC	TGCGACTGAT	GGCCCAATGC	CACAGACCCG	50
	TGAGCACATC	CTGCTGGGTC	GTCAGGTTGG	CGTTCCGTAC	ATCATCGTGT	100
	TCCTGAACAA	ATGCGACATG	GTTGATGACG	AAGAGCTGCT	GGAAGTGGTA	150
	GAAATGGAAG	TTCGTGAAC	TCTGTCCCAG	TACGACTTCC	CGGGCGACGA	200
	TACTCCAATC	GTTCGTGGTT	CTGCTCTGAA	AGCGCTGGAA	GGCGAAGCAG	250
50	AGTGGGAAGC	TAAAATCGTT	GAGCTGGCTG	GCTACCTGGA	TTCTTACATC	300
	CCTGAGCCAG	AGCGTGCTAT	CGATAAGCCG	TTCCTGCTGC	CAATCGAAGA	350
	CGTATTCTCC	ATCTCCGGCC	GTGGTACCGT	TGTTACCGGT	CGTGTAGAGC	400
	GCGGTATCAT	CAAAGTTGGT	GAAGAAGTTG	AAATCGTTGG	TATCAAAGAT	450
	ACTGCGAAAT	CTACCTGTAC	CGGCGTTGAA	ATGTTCCGCA	AACTGCTGGA	500
55	CGAAGGCCGT	GCTGGTGAGA	ACGTTGGTGT	TCTGCTGCGT	GGTATCAAAC	550
	GTGAAGAAAT	CGAACGTGGT	CAGGTACTGG	CTAAGCCAGG	CTCTATCAAG	600
	CCACACACCA	AGTTCGAATC	TGAAGTGATC	ATCCTGTCCA	AAGACGAAGG	650
	CGGCCGTCAT	ACTCCGTTCT	TCAAAGGCTA	CCGTCCACAG	TTCTACTTCC	700
	GTACAACCTGA	CGTGACCGGC	ACCATCGAAT	TGCCAGAAGG	CGTTGAGATG	750
60	GTAATGCCTG	GCGACAACAT	CAAAATGGTT	GTTACCCTGA	TCCACCCAAT	800

CGCGATGGAT GACGGTCTGC GTTTCGCAA

5 2) INFORMATION FOR SEQ ID NO: 18

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 824 bases
 (B) TYPE: Nucleic acid
 10 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

15 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Cedecea neteri*
 (B) STRAIN: ATCC 33855

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18

20 CGCTATCCTG GTTGTGCTG CGACTGACGG CCCTATGCCT CAGACCCGTG 50
 AGCACATCCT GCTGGGTCGT CAGGTTGGCG TTCCTTACAT CATCGTGTTT 100
 CTGAACAAAT GTGACATGGT TGATGACGAA GAGCTGCTGG AGCTGGTTGA 150
 AATGGAAGTT CGTGAAC TTC TGTCTCAGTA CGACTTCCCG GGCGATGACA 200
 25 TTCCAATCAT CCGTGTTCT GCTCTGAAAG CGCTGCAAGG CGAAGCAGAG 250
 TGGGAAGCTA AAATYGTTGA GCTGGCTGGC TTCCTGGATT CCTACATCCC 300
 AGAACCAGTA CGTGCAATCG AYCTGCCGTT CCTGCTGCCA ATCGAAGACG 350
 TATTCTCCAT CTCCGGCCGT GGTACCGTTG TTACCGGTCG TG TAGAGCGC 400
 GGTATCGTTA AAGTGGGCGA AGAAGTAGAA ATCGTTGGTA TCAAAGATAC 450
 30 TGCGAAATCT ACCTGTACCG GCGTTGAAAT GTTCCGCAA CTGCTGGACG 500
 AAGGCCGTGC TGGTGAGAAC GTTGGTGTTT TGCTGCGTGG TATCAAACGT 550
 GAAGAAATCG AACGTGGTCA GGTCTGGCT AAGCCAGGCT CTATCAAGCC 600
 GCACACCAAG TTCGAATCTG AAGTGATACAT CCTGTCCAAA GACGAAGGCG 650
 GCCGTATAC TCCGTTCTTC AAAGGCTACC GTCCACAGTT CTA CTCTCCGT 700
 35 ACAACTGACG TGACCGGTAC CATCGAACTG CCAGAAGGCG TAGAGATGGT 750
 AATGCCAGGC GACAACATCA AAATGGTTGT TACCCTGATC CACCCAATCG 800
 CGATGGACGA CCGTCTGCGT TTCG 824

40

2) INFORMATION FOR SEQ ID NO: 19

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 827 bases
 45 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

50

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Cedecea lapagei*
 (B) STRAIN: ATCC 33432

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19

CGCTATTCTG GTTGTGCTG CAACTGACGG CCCTATGCCT CAGACCCGTG 50
 AGCACATCCT GCTGGGTCGC CAGGTTGGCG TTCCTTACAT CATCGTGTTT 100
 CTGAACAAAT GTGACATGGT TGATGACGAA GAGCTGCTGG AGCTGGTAGA 150
 60 AATGGAAGTT CGTGAAC TTC TGTCTCAGTA CGACTTCCCA GGCGATGATA 200

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      CCCC AATCAT CCGTGGTTCT GCTCTGAAAG CGCTGGAAGG CGAAGCAGAG      250
      TGGGAAGCTA AAATCGTTGA GCTGGCTGGC TTCCTGGATT CCTACATCCC      300
      AGAACCAGTA CGTGCAATCG ACCTGCCGTT CCTGCTGCCA ATCGAAGACG      350
      TATTCTCCAT CTCCGGCCGT GGTACCGTTG TKACCGGTCTG TGTAGAGCGC      400
5      GGTATCGTTA AAGTGGGCGA AGAAGTAGAA ATCGTTGGTA TCAAAGATAC      450
      TGCGAAATCT ACCTGTACTG GCGTTGAAAT GTTCCGCAAA CTGCTGGACG      500
      AAGGCCGTGC TGGTGAGAAC GTTGGTGTTC TGCTGCGTGG TATCAAACGT      550
      GAAGAAATCG AACGTGGTCA GGTTCCTGGCT AAGCCAGGCT CTATCAAGCC      600
      GCACACCAAG TTCGAATCTG AAGTGTACAT CCTGTCCAAA GACGAAGGCG      650
10     GCCGTCATAC TCCGTTCTTC AARGGCTACC GTCCACAGTT CTACTTCCGT      700
      ACCACTGACG TGACCGGTAC CATCGAACTG CCAGAAGGCG TAGAGATGGT      750
      AATGCCAGGT GACAACATCA AAATGGTTGT TACCCTGATC CACCCAATCG      800
      CGATGGACGA CGGTCTGCGT TTCGCAA      827

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15

2) INFORMATION FOR SEQ ID NO: 20

(i) SEQUENCE CHARACTERISTICS:

```

20      (A) LENGTH: 831 bases
      (B) TYPE: Nucleic acid
      (C) STRANDEDNESS: Double
      (D) TOPOLOGY: Linear

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25 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

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      (A) ORGANISM: Chlamydia pneumoniae
      (B) STRAIN: CWL 029

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30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20

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      GCGGAGCTAT CCTAGTCGTT TCAGCTACAG ACGGAGCTAT GCCACAAACT      50
      AAAGAACATA TCTTGCTAGC TCGCCAGGTT GGAGTTCCTT ATATCGTTGT      100
35     TTTCTTGAAT AAAGTAGATA TGATCTCTCA AGAAGATGCT GAACTTATTG      150
      ACCTTGTTGA GATGGAAC TTCTGCTTTG AAAGCTCTTG AAGGTGATGC      200
      GGATGCCCTA TTATCCGTGG TTCTGCTTTG AAAGCTCTTG AAGGTGATGC      250
      AAATTATATC GAAAAAGTTC GAGAACTTAT GCAAGCTGTG GATGACAACA      300
      TCCCTACACC AGAAAGAGAA ATTGATAAGC CTTTCTTAAT GCCTATCGAA      350
40     GACGTATTCT CAATCTCTGG TCGTGGTACT GTGGTTACAG GAAGAATCGA      400
      GCGTGGAATC GTTAAAGTTT CTGATAAAGT TCAGCTCGTG GGATTAGGAG      450
      AGACTAAAGA AACAATCGTT ACTGGAGTCG AAATGTTTCA GAAAGAACTT      500
      CCTGAAGGTC GTGCAGGAGA AAACGTTGGT TTA CTCTCA GAGGTATTGG      550
      AAAGAACGAT GTTGAAAGAG GTATGGTGGT TTGTCAGCCT AACAGCGTGA      600
45     AGCCTCATAC GAAATTTAAG TCAGCTGTTT ACGTTCTTCA GAAAGAAGAA      650
      GGCGGACGTC ATAAGCCTTT CTTACGCGGA TACAGACCTC AGTTCTTCTT      700
      CCGTACTACA GACGTGACAG GAGTCGTAAC TCTTCCTGAA GGAAGTGAAG      750
      TGGTAATGCC TGGAGATAAC GTTGAGCTTG ATGTTGAGCT CATTGGAACA      800
      GTTGCTCTTG AAGAAGGAAT GAGATTTGCA A      831

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50

2) INFORMATION FOR SEQ ID NO: 21

(i) SEQUENCE CHARACTERISTICS:

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55      (A) LENGTH: 826 bases
      (B) TYPE: Nucleic acid
      (C) STRANDEDNESS: Double
      (D) TOPOLOGY: Linear

```

60

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Chlamydia psittaci*

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21

	TGGAGCGATT	CTCGTTGTTT	CCGCTACTGA	CGGTGCGATG	CCTCAGACCA	50
	AAGAACATAT	TCTTTTGGCG	AGACAGGTTG	GTGTTCCCTA	CATCGTTGTT	100
10	TTCTTAACA	AAATCGATAT	GATTTCTCAA	GAAGATGCTG	AGCTCGTAGA	150
	CTTAGTTGAA	ATGGAATTGT	CCGAACCTCT	AGAAGAAAAA	GGTTATAAAG	200
	GTTGCCCAAT	TATCCGTGGT	TCTGCTTTGA	AAGCCTTAGA	AGGTGATGCA	250
	AGCTACGTTG	AAAAAATTCG	CGAGTTAATG	CAAGCAGTGG	ATGATAACAT	300
	CCCTACTCCA	GAGCGTGAAG	TTGATAAGCC	TTTCTTAATG	CCTATCGAAG	350
15	ACGTATTCTC	TATTTCTGGT	CGTGGTACTG	TGGTCACAGG	ACGTATCGAG	400
	CGTGGAATCG	TTAAAGTGGG	TGATAAAGTA	CAGATTGTTG	GTTTAAGAGA	450
	TACTAGAGAG	ACAATTGTTA	CCGGTGTGGA	AATGTTTCAG	AAAGAACTTC	500
	CAGAAGGTCA	AGCAGGGGAA	AACGTTGGTT	TGCTCCTCAG	AGGTATCGGT	550
	AAGAATGACG	TTGAACGTGG	TATGGTTATC	TGCCAACCTA	ATAGCGTGAA	600
20	ATCTCACACA	CAATTTAAAG	GTGCTGTCTA	CATTCTACAA	AAAGAAGAGG	650
	GTGGACGTCA	TAAACCTTTC	TTTACCGGAT	ACAGACCTCA	GTTCTTCTTC	700
	CGTACAACAG	ATGTTACAGG	TGTTGTAACT	CTCCCAGAAG	GTACAGAGAT	750
	GGTTATGCCA	GGCGATAACG	TTGAATTCGA	AGTTCAATTA	ATTAGCCCAG	800
25	TAGCTCTAGA	AGAAGGTATG	AGATTT			826

2) INFORMATION FOR SEQ ID NO: 22

30 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 822 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Chlamydia trachomatis*

40

(B) STRAIN: LGV 12

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22

	GGGGCTATTC	TAGTAGTTTC	TGCAACAGAC	GGAGCTATGC	CTCAAACTAA	50
45	AGAGCATATT	CTTTTGGCAA	GACAAGTTGG	GGTTCCTTAC	ATCGTTGTTT	100
	TTCTCAATAA	AATTGACATG	ATTTCCGAAG	AAGACGCTGA	ATTGGTCGAC	150
	TTGGTTGAGA	TGGAGTTGGC	TGAGCTTCTT	GAAGAGAAAG	GATACAAAGG	200
	GTGTCCAATC	ATCAGAGGTT	CTGCTCTGAA	AGCTTTGGAA	GGGGATGCTG	250
	CATACATAGA	GAAAGTTCGA	GAGCTAATGC	AAGCCGTCGA	TGATAATATC	300
50	CCTACTCCAG	AAAGAGAAAT	TGACAAGCCT	TTCTTAATGC	CCATTGAGGA	350
	CGTGTCTCTC	ATCTCCGGAC	GAGGAACTGT	AGTAACTGGA	CGTATTGAGC	400
	GTGGAATTGT	TAAAGTTTCC	GATAAAGTTC	AGTTGGTCGG	TCTTAGAGAT	450
	ACTAAAGAAA	CGATTGTTAC	TGGGGTTGAA	ATGTTTCAGAA	AAGAACTCCC	500
	AGAAGGTCGT	GCAGGAGAGA	ATGTTGGATT	GCTCCTCAGA	GGTATTGGTA	550
55	AGAACGATGT	GGAAAGAGGA	ATGGTTGTTT	GCTTGCCAAA	CAGTGTTAAA	600
	CCTCATACAC	GGTTTAAGTG	TGCTGTTTAC	GTTCTGCAAA	AAGAAGAAGG	650
	TGGACGACAT	AAGCCTTTCT	TCACAGGATA	TAGACCTCAA	TTCTTCTTCC	700
	GTACAACAGA	CGTTACAGGT	GTGGTAACTC	TGCCTGAGGG	AGTTGAGATG	750
	GTATGCGCTG	GGGATAACGT	TGAGTTTGAA	GTGCAGTTGA	TTAGCCCTGT	800
60	GGCTTTAGAA	GAAGGTATGA	GA			822

2) INFORMATION FOR SEQ ID NO: 23

5

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 835 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

10

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Chryseobacterium meningosepticum*
 (B) STRAIN: CDC B7681

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23

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20 CGGAGCTATC TTAGTATGTG CTGCTACAGA TGGTCCAATG CCTCAAACCTA      50
   GAGAACACAT CCTACTTTGC CGTCAGGTAA ACGTACCTAG AATTGTTGTG      100
   TTCATGAACA AAGTTGACAT GGTAGATGAT CCAGAATTGT TAGAGCTTGT      150
   TGAGCTTGAA CTTAGAGATC TATTATCTAC TTACGAATAT GATGGTGATA      200
   ACTCTCCAGT AATTCAAGGT TCTGCTCTTG GTGCTCTTAA CGGTGATGCT      250
25 AAGTGGGTAG CTA CTGTAGTA AGCTCTAATG GATGCTGTTG ATA CTTGGAT      300
   CGAGCAACCA GTAAGAGATT CTGATAAGCC ATTCCTTATG CCAATCGAAG      350
   ACGTATTCTC TATTACAGGT AGAGGTACTG TAGCAACTGG TAGAATCGAG      400
   GCTGGTGTA TCAACACAGG TGATCCTGTT GACATCGTAG GTATGGGTGA      450
   CGAGAAGTTA ACTTCTACTA TTACAGGTGT TGAGATGTTT AGAAAAATCC      500
30 TAGACAGAGG TGAAGCTGGT GATAACGTAG GTCTATTGTT GAGAGGTATT      550
   GAAAAGACTG ACATCAAGAG AGGTATGGTT ATCGCTAAGA AAGATTCACT      600
   TAAGCCACAC AAGAAATTCA AAGCTGAGGT TTATATCCTT TCTAAAGAAG      650
   AAGGTGGACG TCACACTCCA TTCCACAACA AATACCGTCC TCAGTTCTAT      700
   GTAAGAACTA CTGACGTTAC AGGTGAAATC TTCTTACCAG AAGGTGTAGA      750
35 AATGGTAATG CCTGGTGATA ACTTAATAT CACTGTAGAA TTGTTACAAC      800
   CAATCGCTCT TAACGAGGGT CTTAGATTCTG CGATC                      835

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40 2) INFORMATION FOR SEQ ID NO: 24

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 816 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

45

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Citrobacter amalonaticus*
 (B) STRAIN: ATCC 25405

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24

55

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CGGCGCGATC CTGGTTGTTG CTGCGACTGA CGGCCCGATG CCGCAGACTC      50
GTGAGCACAT CCTGCTGGGT CGTCAGGTAG GCGTTCCGTA CATCATCGTG      100
TTCCTGAACA AATGCGACAT GGTGATGAC GAAGAGCTGC TGGAAGTGGT      150
AGAAATGGAA GTTCGTGAAC TTCTGTCTCA GTACGATTTC CCGGCGGACG      200
60 ACACCCCGAT CGTTCGTGGT TCTGCTCTGA AAGCGCTGGA AGGCGACGCA      250

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	GAGTGGGAAG	CGAAAATCAT	CGAACTGGCC	GGCTTCCTGG	ATTCTTACAT	300
	CCCGGAACCA	GAGCGTGCGA	TTGACAAGCC	GTTCTTGCTG	CCGATCGAAG	350
	ACGTATTCTC	CATCTCCGGT	CGTGGTACCG	TTGTTACCGG	TCGTGTAGAA	400
	CGCGGTATCA	TCAAAGTGGG	CGAAGAAGTT	GAAATCGTTG	GTATCAAAGA	450
5	GACTGCCAAG	TCTACCTGTA	CTGGCGTTGA	AATGTTCCGC	AAACTGCTGG	500
	ACGAAGGCCG	TGCGGGTGAG	AACGTTGGTG	TTCTGCTGCG	TGGTATCAAA	550
	CGTGAAGAAA	TCGAACGTGG	TCAGGTACTG	GCTAAGCCGG	GCWCCATCAA	600
	GCCGCACACC	ATGTTCGAAT	CYGAAGTGTA	CATCCTGTCC	AAAGACGAAG	650
	GCGGCCGTCA	TACTCCGTTC	TTCAAAGGCT	ACCGTCCGCA	GTTCTACTTC	700
10	CGTACAACCTG	ACGTGACTGG	CACCATCGAA	CTGCCGGAAG	GCGTTGAGAT	750
	GGTAATGCCG	GGCGACAACA	TCAAATGGT	TGTTACCCTG	ATCCACCCGA	800
	TCGCGATGGA	CGACGG				816

15

2) INFORMATION FOR SEQ ID NO: 25

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 825 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

25

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Citrobacter braakii*
 (B) STRAIN: ATCC 43162

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25

	CGCGATCCTG	GTTGTTGCTG	CAACTGACGG	CCCGATGCCG	CAGACTCGTG	50
	AGCACATCCT	GCTGGGTCGY	CAGGTAGGCG	TTCCGTACAT	CATCGTGTTT	100
	CTGAACAAAT	GCGACATGGT	TGATGACGAA	GAGCTGCTGG	AACTGGTAGA	150
35	AATGGAAGTT	CGTGAAC TTC	TGTCTCAGTA	CGATTTCCCG	GGCGACGACA	200
	CGCCGATCGT	TGCTGGTTCT	GCTCTGAAAG	CGCTGGAAGG	CGAWGCAGAG	250
	TGGGAAGCGA	AAATCATCGA	ACTGGCTGGC	TTCTTGATT	CTTACATCCC	300
	GGAACCAGAG	CGTGCGATTG	ACAAGCCGTT	CCTGCTGCCT	ATCGAAGACG	350
	TATTCTCCAT	CTCTGGTCGT	GGTACCGTTG	TTACCGGTCG	TGTAGAGCGC	400
40	GGTATCATCA	AAGTTGGTGA	AGAAGTTGAA	ATCGTTGGTA	TCAARGACAC	450
	TGCTAAGTCT	ACCTGTACTG	GCGTTGAAAT	GTTCCGCAAA	CTGCTGGACG	500
	AAGGCCGTGC	TGGTGAGAAC	GTTGGTGTTT	TGCTGCGTGG	TATCAAGCGT	550
	GAAGAAATCG	AACGTGGTCA	GGTACTGGCT	AAGCCGGGCT	CTATCAAGCC	600
	GCACACCAAG	TTCGAATCTG	AAGTGATCAT	TCTGTCCAAA	GACGAAGGCG	650
45	GCCGTCATAC	TCCGTTCTTC	AARGGCTACC	GTCCGCAGTT	CTACTTCCGT	700
	ACTACTGACG	TGACTGGTAC	CATCGAACTG	CCGGAAGGCG	TTGAGATGGT	750
	AATGCCGGGC	GACAACATCA	AAATGGTTGT	TACCCTGATC	CACCCAATCG	800
	CGATGGACGA	CGGTCTGCGT	TTCGC			825

50

2) INFORMATION FOR SEQ ID NO: 26

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 830 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

60

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Citrobacter koseri*

(B) STRAIN: ATCC 27156

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 26

	CGGCGCGATC	CTGGTTGTTG	CTGCGACTGA	CGGCCCCGATG	CCGCAGACCC	50
	GTGAGCACAT	CCTGCTGGGT	CGTCAGGTAG	GCGTTCGGTA	CATCATCGTG	100
10	TTCCTGAACA	AATGCGACAT	GGTTGATGAC	GAAGAGCTGC	TGGAAGTGGT	150
	TGAGATGGAA	GTGCGTGAAC	TGCTGTCTCA	GTACGATTTC	CCGGGCGACG	200
	ACACGCCGAT	CGTTCGTGGT	TCTGCTCTGA	AAGCGCTGGA	AGGCGAMGCT	250
	GAGTGGGAAG	CGAAAATCAT	CGAACTGGCT	GGCTACCTGG	ATTCTTACAT	300
	CCCGGAACCA	GAGCGTGCGA	TTGACAAGCC	GTTCTGCTG	CCGATCGAAG	350
15	ACGTATTCTC	CATCTCCGGT	CGTGGTACCG	TTGTTACCGG	TCGTGTAGAG	400
	CGCGGTATCA	TCAAAGTGGG	CGAAGAAGTT	GAAATYGTG	GTATCAAAGA	450
	GA CTGCGAAG	TCTACCTGTA	CTGGCGTTGA	AATGTTCCGC	AACTGCTGG	500
	ACGAAGGCCG	TGCTGGTGAG	AACGTAGGTG	TTCTGCTGCG	TGGTATCAAA	550
	CGTGAAGAAA	TGAACGTGG	TCAGGTACTG	GCTAAGCCGG	GYTCCATCAA	600
20	GCCGCACACC	AAGTTCGAAT	CTGAAGTGTA	CATYCTGTCY	AAAGATGAAG	650
	GCGGCCGTCA	TACTCCGTTT	TTCAAAGGCT	ACCGTCCGCA	GTTCTACTTC	700
	CGTACAACCTG	ACGTGACTGG	CACCATCGAA	CTGCCGGAAG	GCGTAGAGAT	750
	GGTAATGCCG	GGCGACAACA	TCAAATGGT	TGTTACCCTG	ATCCACCCGA	800
	TCGCGATGGA	CGACGGTCTG	CGTTTCGCAA			830

25

2) INFORMATION FOR SEQ ID NO: 27

30 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 827 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Citrobacter farmeri*

40 (B) STRAIN: ATCC 51112

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 27

	CGCGATCCTG	GTTGTTGCTG	CGACTGACGG	CCCGATGCCG	CAGACTCGTG	50
45	AGCACATCCT	GCTGGGTCGT	CAGGTAGGCG	TTCCGTACAT	CATCGTGTTT	100
	CTGAACAAAT	GCGACATGGT	TGATGACGAA	GAGCTGCTGG	AACTGGTAGA	150
	GATGGAAGTT	CGTGAAGTGC	TGTCTCAGTA	CGATTTCCCG	GGCGACGACA	200
	CGCCGATCGT	TCGTGGTTCT	GCTCTGAAAG	CGCTGGAAGG	CGACGCAGAG	250
	TGGGAAGCGA	AAATCATCGA	ACTGGCAGGC	TTCTTGATT	CTTACATCCC	300
50	GGAACCGAG	CGTGCGATTG	ACAAGCCGTT	CCTGCTGCCG	ATCGAAGACG	350
	TATTCTCCAT	CTCTGGTCGT	GGTACCGTTG	TTACCGGTCG	TGTAGAGCGC	400
	GGTATCATCA	AAGTGGGTGA	AGAAGTTGAA	ATCGTTGGTA	TCAAAGAGAC	450
	TGCCAAGTCT	ACCTGTACTG	GCGTTGAAAT	GTTCCGCAAA	CTGCTGGACG	500
	AAGGCCGTGC	TGGTGAGAAC	GTAGGTGTTT	TGCTGCGTGG	TATCAAACGT	550
55	GAAGAAATCG	AACGTGGTCA	GGTACTGGCT	AAGCCGGGCW	CCATCAAGCC	600
	RCACACTATG	TTGCAATCTG	AAGTGTACAT	TCTGTCCAAA	GACGAAGGCG	650
	GCCGTCATAC	TCCGTTCTTC	AAAGGCTACC	GTCCGCAGTT	CTACTTCCGT	700
	ACGACTGACG	TGACTGGCAC	CATCGAAGT	CCGGAAGGTG	TTGAGATGGT	750
	TATGCCGGGC	GACAACATCA	AAATGGTTGT	TACCCTGATC	CACCCGATCG	800
60	CGATGGACGA	CGGTCTGCGT	TTCGCAA			827

2) INFORMATION FOR SEQ ID NO: 28

5

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 797 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 10 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 15 (A) ORGANISM: *Citrobacter freundii*
 (B) STRAIN: ATCC 8090

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 28

20	CCTGGTTGTT	GCTGCGACTG	ACGGCCCGAT	GCCGCAGACT	CGTGAGCACA	50
	TCCTGCTGGG	TCGTCAGGTA	GGCGTTCGGT	ACATCATCGT	GTTCTTGAAC	100
	AAATGCGACA	TGGTTGATGA	CGAAGAGCTG	CTGGAAGTGG	TAGAAATGGA	150
	AGTTCGTGAA	CTTCTGTCTC	AGTACGATTT	CCCGGGCGAC	GACACTCCGA	200
	TCGTTCTGTT	TTCTGCTCTG	AAAGCGCTGG	AAGGCGAAGC	AGAGTGGGAA	250
25	GCGAAAATCA	TCGAACTGGC	TGGCTTCCTG	GATTCTTACA	TCCCAGAACC	300
	AGAGCGTGCG	ATTGACAAGC	CGTTCCTGCT	GCCTATCGAA	GACGTATTCT	350
	CCATCTCCGG	TCGTGGTACC	GTTGTTACCG	GTCGTGTAGA	GCGCGGTATC	400
	ATCAAAGTTG	GTGAAGAAGT	TGAAATCGTT	GGTATCAAAG	AGACTGCTAA	450
	GTCTACCTGT	ACTGGCGTTG	AAATGTTCCG	CAAAGTCTG	GACGAAGGCC	500
30	GTGCTGGTGA	GAACGTTGGT	GTTCTGCTGC	GTGGTATCAA	ACGTGAAGAA	550
	ATCGAACGTG	GTCAGGTACT	GGCTAAGCCG	GGCTCTATCA	AGCCGCACAC	600
	CAAGTTCGAA	TCTGAAAGTG	ACATTCTGTC	CAAAGACGAA	GGCGGCCGTC	650
	ATACTCCGTT	CTTCAAAGGC	TACCGTCCGC	AGTTCTACTT	CCGTACTACT	700
	GACGTGACTG	GTACCATCGA	ACTGCCGGAA	GGCGTAGAGA	TGGTAATGCC	750
35	GGGCGACAAC	ATCAAAATGG	TTGTTACCCT	GATCCACCCA	ATCGCGA	797

2) INFORMATION FOR SEQ ID NO: 29

40

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 826 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 45 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 50 (A) ORGANISM: *Citrobacter sedlakii*
 (B) STRAIN: ATCC 51115

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 29

55	CGGCGCGATC	CTGGTTGTTG	CCGCGACTGA	CGGCCCGATG	CCGCAGACCC	50
	GTGAGCACAT	CCTGCTGGGT	CGTCAGGTAG	GCGTTCGGTA	CATCATCGTG	100
	TTCCTGAACA	AATGCGACAT	GGTTGATGAC	GAAGAGCTGC	TGGAAGTGGT	150
	AGAGATGGAA	GTTCGTGAAC	TGCTGTCTCA	GTACGATTTC	CCGGGCGACG	200
	ACACGCCGAT	CGTTCGTGGT	TCAGCTCTGA	AAGCGCTGGA	AGGCGACGCA	250
60	GAGTGGAAG	CGAAAATCAT	CGAACTGGCT	GGCTTCCTGG	ATTCTTACAT	300

	TCCGGAACCA	GAGCGTGCGA	TTGACAAGCC	GTTCTGCTG	CCGATCGAAG	350
	ACGTATTCTC	CATCTCCGGT	CGTGGTACCG	TTGTTACCGG	TCGTGTAGAG	400
	CGCGGTATCA	TCAAAGTGGG	CGAAGAAGTT	GAAATCGTTG	GTATCAAAGA	450
	GACTGCGAAG	TCTACCTGTA	CTGGCGTTGA	AATGTTCCGC	AACTGCTGG	500
5	ACGAAGGCCG	TGCGGGTGAG	AACGTAGGTG	TTCTGCTGCG	TGGTATCAAA	550
	CGTGAAGAAA	TCGAACGTGG	TCAGGTACTG	GCGAAGCCGG	GCACCATCAA	600
	GCCGCACACC	AAGTTCGAAT	CTGAAGTGTA	TATTCTGTCC	AAAGATGAAG	650
	GCGGCCGTCA	TACTCCGTTC	TTCAAAGGCT	ACCGTCCGCA	GTTCTACTTC	700
	CGTACAACCTG	ACGTGACTGG	CACCATCGAA	CTGCCGGAAG	GCGTAGAGAT	750
10	GGTAATGCCG	GGCGACAACA	TCAAATGGT	TGTTACCCTG	ATCCACCCGA	800
	TCGCGATGGA	CGACGGTCTG	CGTTTC			826

15 2) INFORMATION FOR SEQ ID NO: 30

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 823 bases
 (B) TYPE: Nucleic acid
 20 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

25 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Citrobacter werkmanii*
 (B) STRAIN: ATCC 51114

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 30

30	GCGATCCTGG	TTGTTGCTGC	GACTGACGGC	CCGATGCCGC	AGACTCGTGA	50
	GCACATCCTG	CTGGGTCGTC	AGGTAGGCGT	TCCGTACATC	ATCGTGTTCC	100
	TGAACAAATG	CGACATGGTT	GATGACGAAG	AGCTGCTGGA	ACTGGTAGAA	150
	ATGGAAGTTC	GTGAACTTCT	GTCTCAGTAC	GATTTCCTCG	GCGACGACAC	200
35	TCCGATCGTT	CGTGGTCTCT	CTCTGAAAGC	GCTGGAAGGC	GAAGCAGAGT	250
	GGGAAGCGAA	AATCATCGAA	CTGGCTGGCT	TTCTGGATTTC	TTACATCCCCG	300
	GAACCAGAGC	GTGCGATTGA	CAAGCCGTTT	CTGCTRCCTA	TCGAAGACGT	350
	ATTCTCCATC	TCCGGTCGTG	GTACCGTTGT	TACCGGTCGT	GTAAGACGCG	400
	GTATCATCAA	AGTTGGTGAA	GAAGTTGAAA	TCGTTGGTAT	CAAAGACACC	450
40	GCTAAGTCTA	CCTGTACCGG	CGTTGAAATG	TTCCGCAAAC	TGCTGGACGA	500
	AGGCCGTGCT	GGTGAGAACG	TTGGTGTTCT	GCTGCGTGGT	ATCAAACGTG	550
	AAGAAATCGA	ACGTGGTCAG	GTACTGGCTA	AGCCGGGCTC	TATCAAGCCG	600
	CACACCAAGT	TCGAATCTGA	AGTGATACATC	CTGTCCAAAG	ACGAAGGCGG	650
	CCGTCATACT	CCGTTCTTCA	AAGGCTACCG	TCCGCAGTTC	TACTTCCGTA	700
45	CTACTGACGT	GACTGGTACC	ATCGAACTGC	CGGAAGGCGT	AGAGATGGTA	750
	ATGCCGGGCG	ACAACATYAA	AATGGTTGTT	ACYCTGATCC	ACCCGATCGC	800
	GATGGACGAC	GGTCTGCGTT	TCG			823

50

2) INFORMATION FOR SEQ ID NO: 31

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 826 bases
 55 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

60

20

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Citrobacter youngae*
 (B) STRAIN: ATCC 29935

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 31

	GGCGCGATCC	TGGTTGTTGC	TGCGACTGAC	GGCCCGATGC	CGCAGACTCG	50
	TGAGCACATC	CTGCTGGGTC	GTCAGGTAGG	CGTTCCGTAC	ATCATCGTGT	100
	TCCTGAACAA	ATGCGACATG	GTTGATGACG	AAGAGCTGCT	GGAAGCTGGTA	150
10	GAAATGGAAG	TTCGTGAACT	TCTGTCTCAG	TACGATTTC	CGGGCGACGA	200
	TACGCCGATC	GTTCTGGTT	CTGCTCTGAA	AGCGCTGGAA	GGCGAAGCAG	250
	AGTGGGAAGC	GAAAATCATC	GAAGTGGCTG	GCTTCCTGGA	TTCTTACATC	300
	CCGGAACCAG	AACGTGCTAT	CGATAAGCCG	TTCCTGCTGC	CAATCGAAGA	350
	CGTATTCTCC	ATCTCCGGTC	GTGGTACCGT	TGTTACTGGT	CGTGTAGAAC	400
15	GCGGTATCAT	CAAAGTTGGT	GAAGAAGTTG	AAATCGTTGG	TATCAAAGAG	450
	ACTGCCAAGT	CTACCTGTAC	TGGCGTTGAA	ATGTTCCGCA	AACTGCTGGA	500
	CGAAGGCCGT	GCTGGTGAGA	ACGTTGGTGT	TCTGCTGCGT	GGTATCAAAC	550
	GTGAAGAAAT	CGAACGTGGT	CAGGTACTGG	CTAAGCCGGG	CTCTATCAAG	600
	CCGCACACCA	AGTTCGAATC	TGAAGTGATC	ATTCTGTCCA	AAGACGAAGG	650
20	CGGCCGTCAT	ACTCCGTTCT	TCAAAGGCTA	CCGTCCGCAG	TTCTACTTCC	700
	GTACTACTGA	CGTGACGGGT	ACCATCGAAC	TGCCGGAAGG	CGTAGAGATG	750
	GTAATGCCGG	GCGACAACAT	CAAAATGGTT	GTTACCCTGA	TCCACCCAAT	800
	CGCGATGGAT	GACGGTCTGC	GTTTCG			826

25

2) INFORMATION FOR SEQ ID NO: 32

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 841 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

35 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Clostridium perfringens*
 (B) STRAIN: ATCC 13124

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 32

	CGGAGCTATA	TTAGTTTGTT	CAGCAGCTGA	TGGTCCAATG	CCTCAAACAA	50
	GAGAGCACAT	CTTATTATCA	TCAAGAGTTG	GAGTTGACCA	CATCGTAGTA	100
45	TTCTTAAACA	AAGCAGATAT	GGTTGACGAC	GAAGAATTAT	TAGAATTAGT	150
	TGAAATGGAA	GTTAGAGAGT	TATTAAGCGA	GTACAACTTC	CCAGGAGACG	200
	AYATTCCAGT	AATCAARGGA	TCAGCTTTAG	TAGCATTAGA	AAACCCAACT	250
	GACGAAGCTG	CAACAGCTTG	TATCAGAGAG	TTAATGGATG	CTGTAGATAG	300
	CTACATCCCA	ACACCAGAAA	GAGCAACAGA	TAAGCCATTC	TTAATGCCAG	350
50	TAGAGGACGT	ATTCACAATC	ACTGGTAGAG	GAACAGTTGC	AACAGGAAGA	400
	GTTGAAAGAG	GAGTTCTACA	TGTAGGAGAC	GAAGTAGAAG	TAATCGGATT	450
	AACTGAAGAA	AGAAGAAAAA	CTGTTGTAAC	AGGAATCGAA	ATGTTTCAGAA	500
	AGTTATTAGA	TGAAGCACAA	GCTGGAGATA	ACATCGGAGC	ATTATTAAGA	550
	GGTATCCAAA	GAAGTAYAT	CGAAAGAGGT	CAAGTTTTCAG	CTCAAGTTGG	600
55	AACAATCAAC	CCACACAAAA	AATTCGTAGG	TCAAGTATAC	GTAAGTTAAA	650
	AAGAAGAAGG	TGGAAGACAT	ACTCCATTCT	TCGATGGATA	CAGACCACAA	700
	TTCTACTTCA	GAACAACAGA	CGTTACAGGA	TCAATCAAAT	TACCAGAAGG	750
	AAATGGAAATG	GTTATGCCTG	GAGACCACAT	CGACATGGAA	GTTGAATTAA	800
60	TCACAGAAAT	CGCTATGGAY	GAAGGATTAA	GATTCGCTAT	C	841

2) INFORMATION FOR SEQ ID NO: 33

- 5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 822 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

10

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Comamonas acidovorans*
 15 (B) STRAIN: ATCC 15668

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 33

	CGGCGCCATC	CTGGTGTGCT	CGGCCGCTGA	CGGCCCCATG	CCCCAGACCC	50
20	GCGAGCACAT	CCTGCTGGCC	CGTCAGGTGG	GCGTGCCCTA	CATCATCGTG	100
	TTCCTGAACA	AGTGCGACAT	GGTGGACGAC	GAAGAGCTGC	TGGAAGTGGT	150
	CGAAATGGAA	GTGCGCGAGC	TGCTTGCCAA	GTACGACTTC	CCCGGCGACG	200
	ACACCCCCAT	CATCCGCGGC	TCGGCCAAGC	TGGCCCTGGA	AGGCGACCAG	250
	TCCGACAAGG	GCGAACCTGC	CATCCTGCGC	CTGGCTGAAG	CACTGGACTC	300
25	CTACATCCCC	ACGCCCAGAGC	GCGCTGTGGA	CGGCGCCTTT	GCAATGCCCG	350
	TGGAAGACGT	GTTCTCGATC	TCTGGCCGTG	GCACCGTGGT	GA CTGGCCGT	400
	ATCGAGCGCG	GCATCATCAA	GGTCGGCGAA	GAAATCGAAA	TCGTGCGTAT	450
	CCGCGACACC	CAGAAGACCA	TCGTACCCGG	CGTGGAATG	TTCCGCAAGC	500
	TGCTGGACCA	AGGTCAAGCT	GGCGACAACG	TGGGTCTGCT	GCTGCGCGGC	550
30	ACCAAGCGTG	AAGACGTGGA	ACGCGGCCAA	GTGCTGTGCA	AGCCCGGCTC	600
	CATCAAGCCC	CACACCCACT	TCACGGCTGA	GGTGTACGTG	CTGTCCAAGG	650
	ACGAAGGTGG	TCGCCACACT	CCGTTCTTCA	ACA ACTACCG	TCCCCAGTTC	700
	TATTTCCGTA	CGACCGACGT	GACCGGCTCC	ATCGAGCTGC	CCGCCGACAA	750
	GGAAATGGTG	ATGCCTGGCG	ACAACGTGTC	GATCACCGTC	AAGCTGATCG	800
35	CCCCCATCGC	CATGGAAGAA	GG			822

2) INFORMATION FOR SEQ ID NO: 34

40

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 702 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 45 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 50 (A) ORGANISM: *Corynebacterium bovis*
 (B) STRAIN: ATCC 7715

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 34

55	GCCGCAGACC	CGTGAGCACG	TCCTCCTGGC	CCGTCAGGTC	GGTGTGCCCT	50
	ACATCCTCGT	CGCCCTCAAC	AAGTGCGACA	TGGTCGACGA	CGAGGACCTC	100
	ATCGAGCTCG	TCGAGATGGA	GGTCCGTGAG	CTCCTCGCCG	AGCAGGACTA	150
	CGACGAGGAC	GCCCCGATCA	TCCACATCTC	CGCCCTCAAG	GCCCTCGAGG	200
	GTGACCCGGA	GTGGACGCAG	CGCATCGTCG	ACCTCATGAA	GGCCTGCCGAC	250
60	GACGCCATCC	CGGATCCGGA	GCGCGAGACG	GACAAGCCGT	TCCTCATGCC	300

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GATCGAGGAC ATCTTCACGA TCACCGGCCG CGGCACCGTC GTCACGGGCC 350
GTGTGCGAGCG TGGCATCCTC AACGTCAACG AGGAGGTCGA GATCCTGGGT 400
ATCTGCGAGA ACTCCCAGAA GACGACCGTC ACCTCCATCG AGATGTTCAA 450
CAAGTTCCTC GACACGGCCG AGGCCGGCGA CAACGCCGCC CTGCTGCTCC 500
5 GTGGCCTGAA GCGCGAGGAC GTCGAGCGTG GCCAGATCGT GGCCAAGCCG 550
GGCGCCTACA CGCCGCACAC CGAGTTCGAG GGCTCCGTGT ACATCCTCTC 600
CAAGGACGAG GGTGGCCGCC ACACGCCGTT CTTGACAAC TACCGTCCGC 650
AGTTCTACTT CCGGACGACC GACGTCACCG GCGTCGTCAA GCTGCCGGAG 700
GG 702

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10

2) INFORMATION FOR SEQ ID NO: 35

15 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 689 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Corynebacterium cervicis*
 25 (B) STRAIN: NCTC 10604

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 35

```

GGCTCAGACC CGCGAGCACG TTCTGCTTGC TCGCCAGGTT GGC GTTCCGA 50
30 CGATCCTGGT TGCCCTCAAC AAGGCCGATA TGGTCGACGA TGAGGAAATG 100
CTGGAGCTCG TTGAGGAAGA GTGCCGCGAC CTGCTCGAGT CCCAGGACTT 150
CGATCGTGAC GCCCGGATCA TCCAGGTTTC CGCGCTGAAG GCTCTCGAAG 200
GTGATCCGCA GTGGGTGCT AAGGTCGAGG AGCTCATGGA GGCAGTGCAG 250
ACCTTCGTGC CGACTCCTGA GCGCGACATG GACAAGCCGT TCCTCATGCC 300
35 GATCGAAGAC GTCTTCACCA TCACCGGCCG TGGCACC GTT 350
GTGTTGAGCG TGGCAAGCTC CCGATCAACT CTGAGGTTGA AATCCTCGGT 400
ATCCGCGAAC TGCAGAAGAC CACCGTTACC GGTATCGAGA TGTTCCACAA 450
GTCCATGGAT GAAGCATGGG CAGGCGAGAA CTGTGGTCTC CTCCTGCGTG 500
GCACCAAGCG CGATGAGGTT GAGCGCGGTC AGGTCGTTGC CGTTCCCGGT 550
40 TCGATCACCC CGCACACCAA CTTACCGGA CAGGTCTACA TCCTCAAGAA 600
GGAAGAAGGC GGTGTCACA ACCCGTTCTT CTCGA ACTAC 650
TCTACTTCCG CACCACGGAC GTGACCGGCG TCATCACCC 689

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45

2) INFORMATION FOR SEQ ID NO: 36

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 804 bases
 50 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

55

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Corynebacterium flavescens*
 (B) STRAIN: ATCC 10340

60 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 36

	GGTTGTTGCT	GCAACCGATG	GTCCTATGCC	GCAGACCCGC	GAGCACGTTT	50
	TTCTGGCTCG	CCAGGTTGGC	GTTTCCTTACA	TCCTCGTTGC	TCTTAACAAG	100
	TGCGACATGG	TTGATGATGA	GGAAATCATC	GAGCTCGTTG	AGATGGAAAT	150
5	CCGCGAACTG	CTCGCTGAGC	AGGACTACGA	CGAGGATGCC	CCCATCATCC	200
	ACATCTCCGC	TCTCAAGGCT	CTTGAGGGTG	ACGAGAAGTG	GGTACAGGCC	250
	ATCGTCGACC	TCATGCAGGC	CTGCGATGAC	TCCATTCCGG	ATCCGGAGCG	300
	CGAGACCGAC	AAGCCCTTCC	TCATGCCTAT	CGAGGACATC	TTCACCATCA	350
	CCGGCCGCGG	TACCGTTGTT	ACCGGCCGTG	TTGAGCGTGG	CGTTTTGAAG	400
10	GTCAACGAGG	ATGTTGAGAT	CATCGGCATC	AAGGAGAAGT	CCATCTCCAC	450
	CACCGTTACC	GGTATCGAAA	TGTTCCGCAA	GATGATGGAC	TACACCGAGG	500
	CTGGCGACAA	CTGTGGTCTG	CTTCTGCGTG	GTACCAAGCG	TGAAGAGGTC	550
	GAGCGCGGCC	AGGTTGTTAT	CAAGCCGGGC	GCCTACACCC	CCCACACCAA	600
	GTTTCGAGGGT	TCCGTCTACG	TCCTCAAGAA	GGAAGAGGGC	GGCCGCCACA	650
15	CCCCGTTTCA	GGACAACCTAC	CGTCCGCAGT	TCTACTTCCG	TACCATGAC	700
	GTGACCGGCG	TTGTTACCT	GCCTGAGGGC	ACCGAGATGG	TCATGCCTGG	750
	CGACAACGTT	GATATGACCG	TTGAGCTCAT	CCAGCCCGTC	GCTAGGATGA	800
	GGGC					804

20

2) INFORMATION FOR SEQ ID NO: 37

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 692 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

30 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Corynebacterium kutscheri*
 (B) STRAIN: ATCC 15677

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 37

	TGCCTCAGAC	CCGTGAGCAC	GTTCTTCTTG	CTCGCCAGGT	TGGCGTTCCT	50
	TACATCCTCG	TTGCTCTTAA	CAAGTGCGAC	ATGGTTGACG	ATGAGGAAAT	100
40	CATCGAGCTC	GTTGAGATGG	AAGTTCGCGA	GCTTCTTGCT	GAGCAGGAGT	150
	ACGATGAAGA	GGCTCCAATC	ATCCACATCT	CTGCTTTGAA	GGCTCTTGAG	200
	GGCGACGAGA	AGTGGACTCA	GGCCATCATC	GACCTCATGC	AGGCTTGTTGA	250
	TGACTCCATC	CCAGATCCAG	AGCGTGAGAC	CGACAAGCCA	TTCTCATGC	300
	CTATCGAGGA	TATCTTCACC	ATCACCGGTC	GTGGCACCGT	TGTTACCGGT	350
45	CGTGTTGAGC	GCGGTTTCTT	GAAGGTGAAT	GAGGACGTCG	AGATCATCGG	400
	CATCAAGGAG	AAGTCCACCA	CTACTACCGT	TACCGGTATC	GAAATGTTCC	450
	GTAAGCTTCT	TGATTACACC	GAAGCTGGCG	ATAACTGTGG	TCTGCTTCTT	500
	CGTGGTATCA	AGCGCGAAGA	CGTTGAGCGT	GGTCAGGTTG	TTGTTAAGCC	550
	AGGCGCTTAC	ACACCTCACA	CCGAGTTCGA	GGGCTCTGTT	TACGTTCTTT	600
50	CCAAGGACGA	GGGCGGCCGC	CACACCCCAT	TCTTCGACAA	CTACCGTCCA	650
	CAGTTCTACT	TCCGCACCAC	TGACGTTACC	GGTGTTGTGA	AG	692

55 2) INFORMATION FOR SEQ ID NO: 38

(i) SEQUENCE CHARACTERISTICS:

- 60 (A) LENGTH: 797 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

5 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Corynebacterium minutissimum*

(B) STRAIN: ATCC 23348

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 38

10

CCTGGTTGTT	GCTGCAACCG	ATGGCCCGAT	GCCGCAGACC	CGCGAGCACG	50
TTCTTCTGGC	CCGCCAGGTT	GGCGTTCCGT	ACATCCTCGT	TGCACTGAAC	100
AAGTGTGACA	TGGTTGACGA	TGAGGAAATC	ATCGAGCTCG	TTGAGATGGA	150
GATCCGTGAG	CTGCTCGCTG	AGCAGGACTA	CGACGAGGAA	GCTCCGATCG	200
15	TTCACATCTC	CGCTCTGAAG	GCTCTTGAGG	GCGACGAGAA	250
TCCATCGTTG	ACCTGATGCA	GGCTTGCGAT	GA CTCCATCC	CGGATCCGGA	300
GCGCGAGCTG	GACAAGCCGT	TCCTGATGCC	GATCGAGGAC	ATCTTCACCA	350
TTACCGGCCG	CGGTACCGTT	GTTACCGGCC	GTGTTGAGCG	TGGCTCCCTG	400
AACGTTAACG	AGGACATCGA	GATCATCGGT	ATCAAGGACA	AGTCCATGTC	450
20	CACCACCGTT	ACCGGTATCG	AGATGTTCCG	CAAGATGATG	500
AGGCTGGCGA	CAACTGTGGT	CTGCTTCTGC	GTGGTACCAA	GCGTGAAGAG	550
GTTGAGCGTG	GCCAGGTTTG	CATCAAGCCG	GGCGCTTACA	CCCCGCACAC	600
CAAGTTCGAG	GGTTCGCTCT	ACGTCCTGAA	GAAGGAAGAG	GGCGGCCGCC	650
ACACCCCGTT	CATGGACAAC	TACCGTCCGC	AGTTCTACTT	CCGCACCACC	700
25	GACGTACCGG	GTGTCATCAA	GCTGCCGGAG	GGCACCAGAG	750
GGGCGACAAC	GTTGAGATGT	CCGTAGAGCT	GATCCAGCCG	GTCGCTA	797

30 2) INFORMATION FOR SEQ ID NO: 39

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 702 bases

(B) TYPE: Nucleic acid

35 (C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

40 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Corynebacterium mycetoides*

(B) STRAIN: ATCC 21134

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 39

45

GCCGCAGACC	CGCGAGCACG	TTCTTCTGGC	CCGCCAGGTC	GGCGTCCCCT	50
ACATCCTCGT	TGCGCTGAAC	AAGTGCGACA	TGGTTGATGA	TGAGGAGATC	100
ATCGAGCTCG	TGGAGATGGA	GGTCCGTGAG	CTGCTCGGCG	AGCAGGACTA	150
CGACGAGGAC	GCCCCCATCA	TCCACATCTC	CGCTCTGAAG	GCTCTCGAGG	200
50	GCGACGAGAA	GTGGGTTTCA	TCCGTGCTCG	ACCTCATGCA	250
GA CTCCATCC	CGGATCCGGT	CCGCGAGACC	GACCGCGACT	TCCTGATGCC	300
GATCGAGGAC	ATCTTCACCA	TCTCCGGCCG	CGGCACCGTG	GTTACCGGTC	350
GTGTGGAGCG	CGGCGTGCTC	AACCTCAACG	ACGAGGTCGA	GATCATCGGC	400
ATCCGCGACA	AGTCCCAGAA	GACCACCGTC	ACCTCCATCG	AGATGTTCAA	450
55	CAAGCTGCTC	GATACCGCTG	AGGCAGGCCA	CAACGCGGCT	500
GCGGTCTGAA	GCGCGAGGAC	GTCGAGCGTG	GCCAGGTTGT	CATCAAGCCG	550
GGCGCCTACA	CCCCGCACAC	CAAGTTCGAG	GGTTCGCTCT	ACGTCCTGTC	600
CAAGGACGAG	GGCGGCCGCC	ACACCCCGTT	CTTCGACAAC	TACCGTCCGC	650
AGTTCTACTT	CCGCACCACC	GACGTGACCG	GTGTTGTGAA	GCTGCCGGAG	700
60	GG				702

2) INFORMATION FOR SEQ ID NO: 40

5

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 674 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

10

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Corynebacterium pseudogenitalium*
 (B) STRAIN: ATCC 33038

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 40

20 GCTCGCCAGG TTGGCGTTCC TTACATCCTC GTTGGCGCTGA ACAAGTGCGA 50
 CATGGTTGAT GATGAGGAAA TCATCGAGCT CGTTGAGATG GAGATCCGTG 100
 AGCTGCTCGC AGAGCAGGAT TACGATGAGG AAGCTCCTAT CGTTCACATC 150
 TCCGCTCTGA AGGCCCTCGA GGGCGATGAC AAGTGGGTAC AGTCCGTCGT 200
 TGATCTGATG GAAGCCTGCG ACAACTCCAT CCCGGATCCG GAGCGCGCTA 250
 25 CCGACCAGCC GTTCCTGATG CCTATCGAGG ACATCTTCAC CATTACCGGC 300
 CGCGGTACCG TTGTTACCGG CCGTGTGAG CGTGGCCGTC TGAACGTCAA 350
 CGAGGACGTT GAGATCATCG GTATCCAGGA GAAGTCCCAG ACCACCACCG 400
 TTACCGGTAT CGAGATGTTT CGCAAGATGA TGGACTACAC CGAGGCTGGC 450
 GACAACTGTG GTCTGCTTCT GCGTGGTACC AAGCGTGAGG ACGTTGAGCG 500
 30 TGGCCAGGTT GTTATCAAGC CGGGCGCTTA CACCCCGCAC ACCAAGTTCTG 550
 AGGGCTCCGT CTACGTCCTG AAGAAGGAAG AGGGCGGCCG CCACACCCCG 600
 TTCATGAACA ACTACCGTCC GCAGTTCTAC TTCCGTACCA CGGACGTTAC 650
 CCGTGTGTTT CACCTGCCAG AGGG 674

35

2) INFORMATION FOR SEQ ID NO: 41

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 694 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

40

(ii) MOLECULE TYPE: Genomic DNA

45

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Corynebacterium renale*
 (B) STRAIN: ATCC 19412

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 41

TGCCTCAGAC CCGTGAGCAC GTTCTGCTTG CTCGTCAGGT CGGCGTTCCT 50
 TACATCCTCG TTGCACTGAA CAAGTGCGAC ATGGTCGACG ACGAAGAAAT 100
 55 CATCGAGCTC GTCGAGATGG AAATCCGTGA ACTGCTCGCA GAGCAGGACT 150
 ACGATGAGGA AGCTCCTATC GTTCACATCT CCGCTCTGGG CGCCCTGAAC 200
 GGCGAGCAGA AGTGGGTTGA CTCCATCGTC GAACTGATGG AAGCTTGCGA 250
 CAACTCCATC CCAGACCCAG TTCGCGACAT CGACCACCCA TTCCTGATGC 300
 CTATCGAGGA CATCTTCACC ATTACCGGTC GCGGTACCGT TGTTACCGGC 350
 60 CGTGTGAGC GTGGCCGTCT CAACGTCAAC GAAGAAGTTG AGATCATCGG 400

	TATCAAGGAC	AAGTCCCAGA	AGACCACCGT	CACCGGTATC	GAGATGTTCC	450
	GCAAGATGCT	GGACTACACC	GAAGCTGGCG	ACAACTGTGG	TCTGCTGCTC	500
	CGCGGCATCG	GCCGTGAGGA	TGTCGAGCGT	GGCCAGGTTA	TCATCAAGCC	550
	AGGCGCTTAC	ACCCCTCACT	CTGAGTTTGA	GGGCTCTGTC	TACGTCCTGT	600
5	CCAAGGACGA	GGGTGGCCGC	CACACCCCAT	TCTTCGACAA	CTACCGTCCA	650
	CAGTTCTACT	TCCGCACCAC	CGACGTGACC	GGCGTTGTGC	ACCT	694

10 2) INFORMATION FOR SEQ ID NO: 42

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 687 bases
 (B) TYPE: Nucleic acid
 15 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

20 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Corynebacterium ulcerans*
 (B) STRAIN: NCTC 8665

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 42

25	GCCGCAGACC	CGCGAGCAGC	TTCTGCTGGC	TCGCCAGGTT	GGCGTTCCKT	50
	ACATCCTSGT	TGCACTGAAC	AAGTGCGACA	TGGTTGACGA	TGAGGARCTC	100
	CTSGAGCTCG	TCGAGATGGA	GGTCCGCGAG	CTGCTGGCTG	AGCAGGACTA	150
	CGACGAGGAA	GCTCCGRTCG	TTCACATCTC	CGCWCTGAAC	GCCCTGGACG	200
30	GCGACSAGAA	GTGGGCTVAC	TCCATCCTCG	AGCTGATGCA	GGCTTGCGAC	250
	GAGTCCATCC	CGGATCCGGA	GCGCGAGACC	GACAAGCCGT	TCCTGATGCC	300
	GATTGAGGAC	ATCTTCACCA	TTACCGGTTCG	CGGYACCGTT	GTTACCGGCC	350
	GTGTTGAGCG	TGGCDTCCTG	AACGTSAAAC	ACGASGTTGA	GATCATGGGY	400
	ATCCGGGAGA	AGTCCCAGAA	GACCACCGTY	ACCKSCATCG	AGATGTTCAA	450
35	CAAGMTGMTG	GACWCCGCAG	AGGCTGGCGA	CAACGCTGSW	CTGCTGCTGC	500
	GTGTTMTSAA	GCGTGAGGAC	GTTGAGCGTG	GCCAGATCAT	CGYTAAGCCG	550
	GGCGCKTACA	CCCCGCACAC	CGAGTTCGAG	GGCTCCGTCT	ACGTCCTGTC	600
	CAAGGACGAG	GGCGGCCGCC	ACACCCCGTT	CTTCGACAAC	TACCGTCCGC	650
40	AGTTCTACTT	CCGCACCACC	GACGTSACCG	GTGTTGT		687

2) INFORMATION FOR SEQ ID NO: 43

45 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 778 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 50 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Corynebacterium urealyticum*
 55 (B) STRAIN: ATCC 43042

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 43

	CTGGTTGTTG	CTGCAACCGA	TGGCCCCGATG	CCGCAGACCC	GTGAGCACGT	50
60	TCTGCTGGCT	CGCCAGGTTG	GCGTTCCGTA	CATCCTCGTT	GCACTGAACA	100

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AGTGCGACAT GGTGACGAT GAGGAGCTCC TCGAGCTCGT CGAGATGGAG      150
GTCCGCGAGC TTCTGGCTGA GCAGGACTAC GACGAGGAGG CTCCGGTCGT      200
CCCGATCTCC GCACTGGGCG CCCTGGACGG CGATCAGAAAG TGGGTCGACT      250
CCATCCTCGA GCTCATGAAG GCTTGCGACG AGTCCATCCC GGACCCGGAG      300
5  CGCGAGACCG ACAAGCCGTT CCTGATGCCG GTTGAGGACA TCTTCACCAT      350
TACCGGTCGC GGCACCGTCG TTACCGGCCG TGTGAGCGT GGCCTCCTGA      400
ACCTGAACGA CGAGGTCGAG ATCCTGGGCA TCCGCGAGAA GTCCACCAAG      450
ACCACCGTCA CCTCCATCGA GATGTTCAAC AAGCTGCTGG ACACCGCAGA      500
GGCTGGCGAC AACGCTGCAC TGCTGCTGCG TGGTCTGAAG CGTGAGGACG      550
----- 10 ----- TCGAGCGAGG CCAGATCATC GCTAAGCCGG GCGCTTACAC CCCGCACACC      600
GAGTTCGAGG GCTCCGCTTA CGTCCTGTCC AAGGACGAGG GCGGCCGTCA      650
CACCCCGTTC TTCGACAACT ACCGTCCGCA GTTCTACTTC CGTACCACCG      700
ACGTCACCGG TGTGTTACC CTGCCAGAGG GCACCGACAT GGTTCATGCCG      750
GGCGACAACG TTGAGATGAG CGTCAAGC      778
15

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2) INFORMATION FOR SEQ ID NO: 44

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20  (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 703 bases
      (B) TYPE: Nucleic acid
      (C) STRANDEDNESS: Double
      (D) TOPOLOGY: Linear
25  (ii) MOLECULE TYPE: Genomic DNA
      (vi) ORIGINAL SOURCE:
      (A) ORGANISM: Corynebacterium xerosis
30  (B) STRAIN: ATCC 373

```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 44

```

CGCAGACCCG TGAGCACGTC CTCCTGGCCC GCCAGGTCGG CGTCCCCTAC      50
35  ATCCTCGTCG CCCTGAACAA GTGCGACATG GTCGACGATG AGGAGATCAT      100
CGAGCTCGTG GAGATGGAGG TGCCTGAGCT TCTCGCCGAG CAGGACTACG      150
ACGAGGAGGC CCCGATCGTG CACATCTCCG CCCTGGGCGC CCTCAATGGC      200
GAAGAGAAGT GGGTCGACTC CATCGTCGAG CTCATGAACG CCGTCGACGA      250
GAACGTTCCG GACCCGGTCC GCGAGACCGA CAAGCCGTTT CTGATGCCCCG      300
40  TCGAGGACAT CTTACCATC ACCGGCCGCG GCACCGTCGC CACCGGTCGC      350
GTGGAGCGCG GCACCCTGAA GGTCAACGAC GAGGTCGAGA TCCTGGGCAT      400
CCAGGAGAAG TCCAGACCA CCACCGTCAC CGGCATCGAG ATGTTCCGCA      450
AGCTGCTGGA CTCCGCCGAG GCCGGCGACA ACTGTGGCCT GCTGCTCCGC      500
GGCATCAAGC GCGAGGACAT CGAGCGCGGC CAGATCATCG CGAAGCCGGG      550
45  CGCCTACACC CCGCACACCG AGTTCGAGGG CTCCGTCTAC ATCCTGGCCA      600
AGGACGAGGG CGGCCGCCAC ACCCGTTTCT TCGACAACTA CCGTCCGCAG      650
TTCTACTTCC GCACCACCGA CGTCACCGGC GTCGTGAAGC TGCCGGAGGG      700
CAC      703
50

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2) INFORMATION FOR SEQ ID NO: 45

```

55  (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 832 bases
      (B) TYPE: Nucleic acid
      (C) STRANDEDNESS: Double
      (D) TOPOLOGY: Linear
60  (ii) MOLECULE TYPE: Genomic DNA

```

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Coxiella burnetii*

(B) STRAIN: Nine Mile phase II

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 45

	GGAGCGATAT	TGGTGGTGAG	CGCAGCGGAC	GGCCCGATGC	CGCAAACGCG	50
	GGAACACATT	GTATTGGCGA	AGCAAGTGGG	TGTTCCGAAC	ATAGTGGTTT	100
10	ACTTGAACAA	AGCGGACATG	GTGGATGACA	AAGAGCTGTT	GGAATTAGTG	150
	GAAATGGAAG	TGAGGGATT	ATTGAACAGT	TATGATTTC	CTGGGGATGA	200
	GACGCCGATA	ATAGTGGGGT	CAGCGTTAAA	GGCGTTAGAA	GGTGACAAGA	250
	GTGAGGTTGG	GGAGCCATCG	ATAATCAAAT	TAGTGGAAC	GATGGACACG	300
	TACTTCCCGC	AGCCGGAGCG	AGCGATAGAC	AAACCGTTTT	TAATGCCGAT	350
15	CGAAGATGTG	TTTTCGATAT	CGGGCCGAGG	GACGGTGGTG	ACGGGACGCG	400
	TAGAGCGAGG	GATCATCAAA	GTGGGCGACG	AGATAGAGAT	TGTGGGGATC	450
	AAGGACACGA	CGAAGACGAC	GTGCACGGGC	GTTGAGATGT	TTCGCAAATT	500
	ATTGGATGAA	GGTCAAGCGG	GTGACAACGT	AGGAATTTTA	TTGAGAGGGA	550
	CGAAACGCGA	AGAAGTGGAG	CGTGGTCAAG	TATTGGCGAA	ACCGGGATCG	600
20	ATCACGCCAC	ACAAGAAATT	TGAGGCGGAG	ATTTATGTGT	TGTCGAAGGA	650
	AGAAGGGGGA	CGCCACACAC	CGTTTTTACA	AGGCTATCGA	CCGCAATTTT	700
	ATTTCCGCAC	GACGGACGTG	ACGGGCCAGT	TATTGAGTTT	ACCGGAGGGG	750
	ATAGAGATGG	TGATGCCGGG	AGATAACGTG	AAAGTGACGG	TTGAATTGAT	800
25	TGCGCCGGTA	GCGATGGATG	AAGGGCTACG	AT		832

2) INFORMATION FOR SEQ ID NO: 46

30 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 816 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Edwardsiella hoshinae*

40

(B) STRAIN: ATCC 33379

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 46

	GGCGCTATCC	TGGTTGTTGC	TGCGACTGAC	GGCCCGATGC	CGCAGACCCG	50
45	TGAGCACATC	CTGCTGGGTC	GCCAGGTAGG	CGTTCCGTAC	ATCATCGTGT	100
	TCCTGAACAA	GTGCGACATG	GTTGATGACG	AAGAGCTGCT	GGAAGTGGTT	150
	GAGATGGAAG	TTCGCGAACT	GCTGTCTCAG	TACGATTTC	CGGGCGACGA	200
	TACGCCGGTA	ATCCGCGGTT	CTGCGCTGAA	AGCGCTGGAA	GGCGAAGCCG	250
	AGTGGGAAGC	GAAGATCATC	GAAGTGGCTG	AAACGCTGGA	CTCCTACATT	300
50	CCGGAACCTG	AGCGTGACAT	CGACAAGCCG	TTCCTGCTGC	CGATCGAAGA	350
	CGTATTCTCA	ATCTCTGGTC	GTGGTACCGT	TGTTACCGGT	CGTGTAGAGC	400
	GCGGTATCAT	CAAGGTAGGC	GACGAAGTTG	AAATCGTAGG	TATCAAGCCG	450
	ACCACCAAGA	CTACCTGTAC	TGGCGTTGAA	ATGTTCCGCA	AACTGCTGGA	500
	CGAAGGCCGT	GCTGGTGAGA	ACGTAGGTGT	TCTGCTGCGT	GGTACCAAGC	550
55	GTGACGAAAT	CGAACGTGGT	CAGGTACTGG	CTAAGCCGGG	CACCATCACT	600
	CCGCACACCA	AGTTCGAATC	AGAAGTGTAC	ATCCTGAGCA	AGGATGAAGG	650
	CGGCCGTCAT	ACTCCGTTCT	TCAAAGGTTA	CCGTCCGCAG	TTCTACTTCC	700
	GTACCACTGA	CGTGACTGGC	ACCATCGAAC	TGCCGGAAGG	CGTAGAGATG	750
	GTAATGCCGG	GCGACAACAT	CAAGATGGTT	GTTACCCTGA	TCCACCCGAT	800
60	CGCCATGGAC	GATGGT				816

2) INFORMATION FOR SEQ ID NO: 47

5

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 821 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

10

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

15

- (A) ORGANISM: *Edwardsiella tarda*
 (B) STRAIN: ATCC 15947

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 47

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20  GGCGCGATCC TGGTTGTTGC TCGACTGAC GGCCCGATGC CGCAGACCCG      50
    TGAGCACATC CTGTTGGGTC GCCAGGTAGG CGTTCCGTAC ATCATCGTGT      100
    TCCTGAACAA GTGCGACATG GTTGATGACG AAGAGCTGCT GGAAGTGGTT      150
    GAGATGGAAG TTCGCGAACT GCTGTCTCAG TACGACTTCC CGGGCGACGA      200
    CACGCCGGTA ATCCGCGGTT CTGCGCTGAA AGCGCTGGAA GGCGAAGCCG      250
25  AGTGGGAAGC GAAGATCATC GAACTGGCTG AAACCTCTGA CTCCTACATC      300
    CCGGAACCTG AGCGTGACAT CGACAAGCCG TTCCTGCTGC CGATCGAAGA      350
    CGTATTCTCT ATCTCTGGCC GTGGTACCGT TGTTACCGGT CGTGTAGAGC      400
    GCGGTATCAT CAAGGTAGGC GACGAAGTTG AAATCGTTGG TATCAAGCCG      450
    ACCACCAAGA CCACCTGTAC TGGCGTTGAA ATGTTCCGCA AACTGCTGGA      500
30  CGAAGGCCGT GCTGGTGAGA ACGTTGGTGT TCTGCTGCCG GGTACTAAGC      550
    GTGACGAAAT CGAACGTGGT CAGGTACTGG CTAAGCCGGG CACCATCACT      600
    CCGCACACCA AGTTCGAATC TGAAGTGATC ATCCTGAGCA AGGATGAAGG      650
    CGGCCGTCAT ACTCCGTTCT TCAAAGGCTA CCGTCCGCAG TTCTACTTCC      700
    GTACTACTGA CGTGACTGGT ACCATCGAAC TGCCGGAAGG CGTAGAGATG      750
35  GTAATGCCGG GCGACAACAT CAAGATGGTT GTTACCCTGA TCCACCCGAT      800
    CGCCATGGAC GATGGTCTGC G

```

40 2) INFORMATION FOR SEQ ID NO: 48

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 830 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

45

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

50

- (A) ORGANISM: *Eikenella corrodens*
 (B) STRAIN: ATCC 23834

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 48

55

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CGGTGCCATC CTGGTGGTAT CCGCTGCTGA CGGCCCCATG CCTCAGACTC      50
GCGAACACAT CCTGTTGGCT CGTCAGGTAG GTGTACCCTA CATCCTCGTA      100
TTCATGAACA AATGCGACAT GGTAGATGAT GCCGAGCTGC TTGAGTTGGT      150
TGAGATGGAA ATCCGCGACC TGCTCTCCAG CTATGACTTC CCTGGTGACG      200
60  ACTGCCCCGAT CGTACAAGGT TCCGCTCTCA AAGCCCTCGA AGGCGATGCC      250

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	GGTTACAAAG	AAAAAATCTT	CGAACTAGCT	GCTGCTTTGG	ATAGCTACAT	300
	CCCCACTCCT	CAACGTGCTG	TAGACAAACC	CTTCCTGTTG	CCGATCGAAG	350
	ACGTATTCTC	TATCTCCGGC	CGTGGTACCG	TAGTAACCGG	TCGTGTAGAG	400
	CGCGGCATCA	TCAAAGTAGG	TGAAGAGATC	GAAATCGTTG	GTCTGAAGCC	450
5	CACTCAGAAA	ACTACCTGTA	CTGGCGTGGA	AATGTTCCGC	AAACTGCTGG	500
	ACGAAGGTCA	GGCCGGTGAC	AACGTAGGCG	TACTGCTGCG	CGGTACCAAA	550
	CGTGAAGAAG	TTGAGCGTGG	TCAAGTATTG	GCTAAACCCG	GCACCATCAC	600
	TCCGCACACC	AAGTTCAAAG	CCGAAGTATA	CGTATTGAGC	AAAGAAGAAG	650
	GTGGTCGTCA	CACCCCGTTC	TTTGCCAACT	ACCGTCCACA	GTTCTACTTC	700
10	CGTACTACTG	ACGTAACCGG	TGCTGTAGAG	CTGGAGCCTG	GTGTAGAAAT	750
	GGTTATGCCT	GGTGAGAACG	TAACCATCAC	CGTAGAACTG	ATTGCTCCGA	800
	TTGCTATGGA	AGAAGGTCTG	CGCTTTGCGA			830

15

2) INFORMATION FOR SEQ ID NO: 49

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 808 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

25

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterobacter aerogenes*
 (B) STRAIN: ATCC 13048

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 49

	GGCGCGATCC	TGGTTGTTGC	TGCGACTGAC	GGCCCGATGC	CGCAGACTCG	50
	TGAGCACATC	CTGCTGGGTC	GTCAGGTAGG	CGTTCCGTAC	ATCATCGTGT	100
	TCCTGAACAA	ATGCGACATG	GTTGATGACG	AAGAGCTGCT	GGAAC TGTT	150
35	GAGATGGAAG	TTCGTGAAC	GCTGTCTCAG	TACGATTTC	CGGGCGACGA	200
	CACTCCGATC	GTTCTGTTT	CTGCTCTGAA	AGCGCTGGAA	GGCGACGCAG	250
	AGTGGGAAGC	GAAAATCATC	GAAGTGGCTG	GCTTCCTGGA	TTCTTACATC	300
	CCRGAACCAG	AGCGTGCGAT	TGACAAGCCG	TTCTGCTGCTG	CGATCGAAGA	350
	CGTATTCTCC	ATCTCCGGTC	GTGGTACCGT	TGTTACCGGT	CGTGTAGAGC	400
40	GCGGTATCAT	CAAAGTTGGT	GAAGAAGTTG	AAATCGTTGG	TATCAAAGAC	450
	ACCGCGAAAA	CCACCTGTAC	TGGCGTTGAA	ATGTTCCGCA	AACTGCTGGA	500
	CGAAGGCCGT	GCTGGTGAGA	ACGTAGGYGT	TCTGCTGCGT	GGTATCAAAC	550
	GTGAAGAAAT	CGAACGTGGT	CAGGTACTGG	CTAAGCCGGG	CAGCATCAAG	600
	CCGCACACCA	AGTTCGAATC	TGAAGTGATC	ATCCTGTCCA	AAGACGAAGG	650
45	CGGCCGTCAT	ACTCCGTTCT	TCAAAGGCTA	CCGTCCGCAG	TTCTACTTCC	700
	GTACTACTGA	CGTGACTGGT	ACCATCGAAC	TGCCGGAAGG	CGTAGAGRTG	750
	GTAATGCCGG	GCGACAACAT	CAAAATGGTT	GTTACCCTGA	TCCACCCGAT	800
	CGCGATGG					808

50

2) INFORMATION FOR SEQ ID NO: 50

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 828 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

60

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterobacter agglomerans*
 (B) STRAIN: ATCC 27989

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 50

	CGGCGCGATC	CTGGTTGTTG	CTGCGACTGA	CGGCCCGATG	CCGCAGACTC	50
	GTGAGCACAT	CCTGCTGGGT	CGTCAGGTAG	GCGTTCCTTA	CATCATCGTG	100
10	TTCCTGAACA	AATGTGACAT	GGTTGATGAC	GAAGAGCTGC	TGGAAGTGGT	150
	TGAAATGGAA	GTTCGTGAAC	TTCTGTCTCA	GTACGATTTC	CCGGGCGACG	200
	ATACTCCGAT	CGTTCGTGGT	TCTGCTCTGA	AAGCGCTGGA	AGGCGAMGCW	250
	GAGTGGGAAG	CGAAAATCAT	CGARCTGGCT	GGCCACCTGG	ATACCTATAT	300
	CCCGGAACCA	GAGCGTGCGA	TTGACAAGCC	GTTCTGCTG	CCGATCGAAG	350
15	ACGTATTCTC	CATCTCCGGT	CGCGGTACCG	TTGTTACCGG	TCGTGTAGAG	400
	CGCGGTATCA	TYAAAGTGGG	CGAAGAAGTT	GAAATCGTTG	GTATCAAAGA	450
	TACYGCGAAA	TCAACCTGTA	CCGGCGTTGA	AATGTTCCGC	AAACTGCTGG	500
	ACGAAGGCCG	TGCTGGTGAG	AACGTTGGTG	TTCTGCTGCG	TGGTATCAAA	550
	CGTGAAGAAA	TGCAACGTGG	TCAGGTACTG	GCTAAGCCCG	GCACCATCAA	600
20	GCCGCACACC	AAGTTCGAAT	CTGAAGTGTA	CATTCTGTCC	AAAGATGAAG	650
	GCGGTCGTCA	CACTCCGTTC	TTCAAAGGCT	ACCGTCCSCA	GTTCTACTTC	700
	CGTACAACCTG	ACGTGACTGG	CACCATCGAA	CTGCCGGAAG	GCGTAGAGAT	750
	GGTAATGCCG	GGCGACAACA	TCAAATGGT	TGTTACCCTG	ATCCACCCGA	800
25	TCGCGATGGA	CGACGGTCTG	CGTTCGCA			828

2) INFORMATION FOR SEQ ID NO: 51

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 825 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterobacter amnigenus*
 (B) STRAIN: ATCC 33072

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 51

	TGGCGCGATC	CTGGTTGTTG	CTGCAACTGA	TGGCCCTATG	CCACAGACGC	50
45	GTGAGCACAT	CCTGCTGGGT	CGTCAGGTAG	GCGTTCCTTA	CATCATCGTG	100
	TTCCTGAACA	AATGCGACAT	GGTTGATGAC	GAAGAGCTGC	TGGAAGTGGT	150
	AGAAATGGAA	GTTCGTGAAC	TTCTGTCTCA	GTACGATTTC	CCAGGTGATG	200
	ACACTCCAAT	CATCCGTGGT	TCTGCTCTGA	AAGCGCTGGA	AGGCGAAGCA	250
	GAGTGGGAAG	CTAAAATCGT	TGAGCTGGCT	GGCTACCTGG	ATTCTTACAT	300
50	CCCGGAACCA	GAACGTGCTA	TCGATAAGCC	ATTCCTGCTG	CCAATCGAAG	350
	ACGTATTCTC	TATCTCCGGC	CGTGGTACTG	TTGTAACCGG	TCGTGTAGAG	400
	CGCGGTATCG	TTAAAGTTGG	CGAAGAAGTT	GAAATCGTTG	GTATCAAAGA	450
	GACTGCTAAG	TCTACCTGTA	CTGGCGTTGA	AATGTTCCGC	AAACTGCTGG	500
	ACGAAGGCCG	TGCTGGTGAG	AACGTTGGTG	TTCTGCTGCG	TGGTATCAAA	550
55	CGTGAAGAAA	TCGAACGTGG	TCAGGTACTG	GCTAAGCCAG	GCTCAATCAA	600
	GCCGCACACC	AAATTCGAAT	CTGAAGTTTA	TATTCTGTCC	AAAGATGAAG	650
	GCGGCCGTCA	TACTCCGTTC	TTCAAAGGCT	ACCGTCCACA	GTTCTACTTC	700
	CGTACAACCTG	ACGTGACCGG	CACCATCGAA	CTGCCAGAAG	GCGTAGAGAT	750
	GGTAATGCCA	GGCGACAACA	TTCAGATGGT	TGTTACCCTG	ATCCACCCAA	800
60	TCGCGATGGA	TGACGGTCTG	CGTTT			825

2) INFORMATION FOR SEQ ID NO: 52

5

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 822 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

10

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterobacter asburiae*
 (B) STRAIN: ATCC 35953

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 52

20	CGGCGCGATC CTGGTTGTTG CTGCGACTGA CGGCCCAATG CCTCAGACTC	50
	GTGAGCACAT CCTGCTGGGT CGTCAGGTAG GCGTTCCTTT CATCATCGTG	100
	TTCCTGAACA AATGCGACAT GGTGATGAC GAAGAGCTGC TGGAAGTGGT	150
	AGAGATGGAA GTTCGTGAAC TGCTGTCTCA GTACGATTTC CCGGGCGACG	200
	ATACTCCAAT CGTTCGTGGT TCTGCTCTGA AAGCGCTGGA AGGCGACGCA	250
25	GAGTGGGAAG CGAAAATCAT CGAACTGGCT GGCTTCCTGG ATTCTTACAT	300
	CCCAGAACCA GAGCGTGCGA TTGACAAGCC ATTCCTGCTG CCAATCGAAG	350
	ACGTATTCTC CATCTCCGGT CGTGGTACCG TTGTTACCGG TCGTGTAGAG	400
	CGCGGTATCA TCAAAGTTGG CGAAGAAGTT GAAATCGTTG GTATCAAAGA	450
	GACTGCTAAG TCTACCTGTA CTGGCGTTGA AATGTTCCGC AAAGTCTGCTG	500
30	ACGAAGGCCG TGCTGGTGAG AACGTTGGTG TTCTGCTGCG TGGTATCAAA	550
	CGTGAAGAAA TCGAACGTGG TCAGGTTCTG GCGAAGCCAG GCTCAATCAA	600
	GCCACACACC AAGTTCGAAT CTGAAGTGTA CATCCTGTCC AAAGACGAAG	650
	GCGGCCGTCA TACTCCGTTT TTCAAAGGCT ACCGTCCACA GTTCTACTTC	700
	CGTACAACCTG ACGTGACCGG TACCATCGAA CTGCCAGAAG GCGTTGAGAT	750
35	GGTAATGCCA GCGGACAACA TCAAGATGGT TGTGACTCTG ATCCACCCAA	800
	TCGCGATGGA CGACGGTCTG CG	822

40 2) INFORMATION FOR SEQ ID NO: 53

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 826 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

45

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterobacter cancerogenus*
 (B) STRAIN: ATCC 35317

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 53

55

55	CGGCGCGATC CTGGTTGTTG CTGCGACTGA CGGCCCAATG CCTCAGACTC	50
	GTGAGCACAT CCTGCTGGGT CGTCAGGTAG GCGTTCCTTA CATCATCGTG	100
	TTCCTGAACA AGTGGACAT GGTGATGAC GAAGAGCTGC TGGAAGTGGT	150
	AGAAATGGAA GTTCGTGAAC TGCTGTCTCA GTACGATTTC CCAGGCGACG	200
60	ACACTCCAAT CGTTCGTGGT TCCGCGCTGA AAGCGCTGGA AGGCGAAGCT	250

	GAGTGGGAAG	CAAAAATCAT	CGAACTGGCT	GGCTTCCTGG	ATTCTTACAT	300
	CCCAGAACCA	GAGCGTGCGA	TTGACAAGCC	ATTCCTGCTG	CCAATCGAAG	350
	ACGTATTCTC	CATCTCCGGT	CGTGGTACCG	TTGTTACCGG	TCGTGTAGAG	400
	CGCGGTATCA	TCAAAGTTGG	TGAAGAAGTT	GAAATCGTTG	GTATCAAAGA	450
5	TACTGCKAAA	TCTACCTGTA	CTGGCGTTGA	AATGTTCCGC	AAACTGCTGG	500
	ACGAAGGCCG	TGCTGGTGAG	AACGTTGGTG	TTCTGCTGCG	TGGTATCAAA	550
	CGCGAAGAAA	TCGAACGTGG	TCAGGTTCTG	GCGAAGCCAG	GCTCAATCAA	600
	GCCACACACC	AAGTTCGAAT	CTGAAGTGTA	CATCCTGTCC	AAAGACGAAG	650
	GCGGCCGTCA	TACTCCGTTC	TTCAAAGGCT	ACCGTCCACA	GTTCTACTTC	700
10	CGTACAAC TG	ACGTGACCGG	TACCATCGAA	CTGCCAGAAG	GCGTAGAGAT	750
	GGTAATGCCA	GGCGACAACA	TCAAGATGGT	TGTGACGCTG	ATCCACCCAA	800
	TCGCGATGGA	CGACGGTCTG	CGTTTC			826

15

2) INFORMATION FOR SEQ ID NO: 54

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 806 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterobacter cloacae*
 (B) STRAIN: ATCC 13047

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 54

	GATCCTGGTA	GTAAGCTGCGA	CTGACGGCCC	AATGCCTCAG	ACTCGTGAGC	50
	ACATCCTGCT	GGGTCGTGAG	GTAGGCGTTC	CTTACATCAT	CGTGTTCTTG	100
	AACAAATGCG	ACATGGTTGA	TGACGAAGAG	CTGCTGGAAC	TGGTAGAGAT	150
35	GGAAGTTTCG	GAAGTGTGCT	CTCAGTACGA	TTTCCCAGGC	GACGATACCC	200
	CAATCGTTTCG	TGGTTCTGCT	CTGAAAGCGC	TGGAAGGCGA	CGCAGAGTGG	250
	GAAGMGAAAA	TCATCGAACT	GGCTGGCTAC	CTGGATTCTT	ACATCCCAGA	300
	ACCAGAGCGT	GCGATTGAYA	AGCCATTCTT	GCTGCCAATC	GAAGACGTAT	350
	TCTCCATCTC	CGGTCGTGGT	ACCGTTGTTA	CCGTCGTGTG	AGAGCGCGGT	400
40	ATCATCAAAG	TGGGTGAAGA	AGTTGAAATC	GTTGGTATCA	AAGAGACTGC	450
	GAAGTCTACC	TGTACTGGCG	TTGAAATGTT	CCGCAAAC TG	CTGGACGAAG	500
	GCCGTGCTGG	TGAGAACGTT	GGTGTCTCTG	TGCGTGCTAT	CAAACGTGAA	550
	GAAATCGAAC	GTGGTCAGGT	TCTGGCGAAG	CCAGGCTCAA	TCAAGCCACA	600
	CACCAAGTTC	GAATCTGAAG	TGTACATCCT	GTCCAAAGAC	GAAGGCGGCC	650
45	GTCATACTCC	GTTCTTCAAA	GGCTACCGTC	CACAGTTCTA	CTTCCGTACA	700
	ACTGACGTGA	CCGGTACCAT	CGAACTGCCA	GAAGGCGTAG	AGGTGGTAAT	750
	GCCAGGCGAC	AACATCAAGA	TGGTTGTGAC	TCTGATCCAC	CCAATCGCGA	800
	TGGACG					806

50

2) INFORMATION FOR SEQ ID NO: 55

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 826 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

60 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterobacter gergoviae*
 (B) STRAIN: ATCC 33028

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 55

	CGGCGCGATC	CTGGTTGTTG	CTGCGACTGA	CGGCCCGATG	CCGCAGACCC	50
	GTGAGCACAT	CCTGCTGGGT	CGTCAGGTAG	GCGTTCGGTA	CATCATCGTG	100
10	TTCCTGAACA	AGTGCGACAT	GGTTGATGAC	GAAGAGCTGC	TGGAACTGGT	150
	AGAGATGGAA	GTTCGTGAAC	TGCTGTCTCA	GTACGATTTC	CCGGGCGACG	200
	ACACCCCGAT	CGTTCGCGGT	TCTGCGCTGA	AAGCGCTGGA	AGGCGACGCA	250
	GAGTGGGAAG	CGAAAATCAT	CGAACTGGCT	GGCCACCTGG	ATACCTAYAT	300
	CCCGGAACCA	GAGCGTGCGA	TTGACAAGCC	GTTCCCTGCTG	CCGATCGAAG	350
15	ACGTATTCTC	CATTTCCGGT	CGTGGTACCG	TTGTTACCGG	TCGTGTAGAG	400
	CGCGGTATCA	TCAAGGTTGG	TGAAGAAGTT	GAAATCGTTG	GTATCAAAGA	450
	CACCGCGAAA	ACCACCTGTA	CTGGCGTTGA	AATGTTCCGC	AAACTGCTGG	500
	ACGAAGGCCG	TGCTGGTGAG	AACGTCGGCG	TTCTGCTGCG	TGGTATCAAG	550
	CGTGAAGAAA	TGAACGTGG	TCAGGTACTG	GCTAAGCCGG	GCTCCATCAA	600
20	GCCGCACACC	AAGTTCGAAT	CTGAAGTGTA	CATCCTGTCC	AAAGACGAAG	650
	GCGGCCGTCA	CACTCCGTTT	TTCAAAGGCT	ACCGTCCGCA	GTTCTACTTC	700
	CGTACAACCTG	ACGTGACTGG	CACCATCGAA	CTGCCGGAAG	GCGTAGAGAT	750
	GGTAATGCCG	GGCGACAACA	TCAAGATGGT	TGTTACCCTG	ATCCACCCGA	800
25	TCGCGATGGA	CGACGGTCTG	CGTTTC			826

2) INFORMATION FOR SEQ ID NO: 56

30 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 829 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterobacter hormaechei*
 40 (B) STRAIN: ATCC 49162

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 56

	GGCGCGATCC	TGGTTGTTGC	TGCGACTGAC	GGCCCTATGC	CTCAGACCCG	50
45	TGAGCACATC	CTGCTGGGTC	GTCAGGTAGG	CGTTCCTTAC	ATCATCGTGT	100
	TCCTGAACAA	ATGCGACATG	GTTGATGACG	AAGAGCTGCT	GGAAGTGGTA	150
	GAGATGGAAG	TTCGTGAACT	GCTGTCTCAG	TACGATTTC	CAGGCGACGA	200
	CACCCCAATC	GTTCTGGT	CCGCGCTGAA	AGCGCTGGAA	GGCGAMGCAG	250
	AGTGGGAAGM	GAAAATCATC	GARCTGGCTG	GCTTCCTGGA	TTCTTACATC	300
50	CCAGAACCAG	AGCGTGCGAT	TGACAAGCCA	TTCCTGCTGC	CAATCGAAGA	350
	CGTATTCTCC	ATCTCCGGTC	GTGGTACCGT	TGTTACCGGT	CGTGTWAGC	400
	GCGGTATCAT	CAAAGTAGGT	GAAGAAGTTG	AAATCGTTGG	TATCAAAGAG	450
	ACTGCGAAGT	CTACCTGTAC	TGGCGTTGAA	ATGTTCCGCA	AACTGCTGGA	500
	CGAAGGCCGT	GCTGGTGAGA	ACGTTGGTGT	TCTGCTGCGT	GGTATCAAAC	550
55	GTGAAGAAAT	CGAACGTGGT	CAGGTTCTGG	CGAAGCCAGG	CTCAATCAAG	600
	CCACACACCA	AGTTCGAATC	TGAAGTGATC	ATTCTGTCCA	AAGACGAAGG	650
	CGGCCGTCAT	ACTCCGTTCT	TCAAAGGCTA	CCGTCCACAG	TTCTACTTCC	700
	GTACAACTGA	CGTGACCGGT	ACCATCGAAC	TGCCAGAAGG	CGTAGAGATG	750
	GTAATGCCAG	GCGACAACAT	CAAGATGGTT	GTGACGCTGA	TCCACCCAAT	800
60	CGCGATGGAC	GACGGTCTGC	GTTTCGCAA			829

35

2) INFORMATION FOR SEQ ID NO: 57

5

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 831 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

10

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

15

- (A) ORGANISM: *Enterobacter sakazakii*
 (B) STRAIN: ATCC 29544

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 57

20	GGCGCTATCC TGGTTGTTGC TGC GACTGAC GGCCCGATGC CGCAGACCCG	50
	TGAGCACATC CTGCTGGGTC GTCAGGTAGG CGTTCCGTAC ATCATCGTGT	100
	TCCTGAACAA ATGCGACATG GTTGATGACG AAGAGCTGCT GGAAGTGGTT	150
	GAGATGGAAG TGCGCGAGCT GCTGTCTCAG TACGACTTCC CGGGCGACGA	200
	CACCCCGATC GTTCGTGGTT CTGCTCTGAA AGCGCTGGAA GGCGACGCTG	250
25	AGTGGGAAGC GAAAATCATC GAGCTGGCAG GTCACCTGGA TTCCTACATC	300
	CCGGAACCGG AGCGTGCGAT TGACAAGCCG TTCCTGCTGC CGATCGAAGA	350
	CGTATTCTCC ATCTCYGGTC GTGGTACCGT TGTTACCGGT CGTGTAGAGC	400
	GCGGTATCAT CAAGGTTGGT GAAGAAGTTG AAATCGTGGG CATCAAAGAC	450
	ACCGCGAAAT CCACCTGTAC CGGCGTTGAA ATGTTCCGCA AACTGCTGGA	500
30	CGAAGGCCGT GCGGGCGAGA ACGTAGGTGT TCTGCTGCGT GGTATCAAAC	550
	GTGAAGAAAT CGAACGTGGT CAGGTACTGG CTAAGCCGGG CTCCATCAAG	600
	CCGCACACCA AGTTCGAATC TGAAGTGATC ATTCTGTCCA AAGATGAAGG	650
	CGGCCGTCAC ACTCCGTTCT TCAAAGGCTA CCGTCCGCAG TTCTACTTCC	700
	GTACRACTGA CGTGACTGGC ACCATCGAAC TGCCGGAAGG CGTTGAGATG	750
35	GTAATGCCGG GCGACAACAT CAAAATGGTT GTTACCCTGA TCCACCCGAT	800
	CGCGATGGAC GACGGTCTGC GTTTCGCAAT C	831

40 2) INFORMATION FOR SEQ ID NO: 58

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 835 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

45

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

50

- (A) ORGANISM: *Enterococcus casseliflavus*
 (B) STRAIN: ATCC 25788

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 58

55

	CGGCGCGATC TTAGTAGTAT CTGCTGCTGA TGGTCCTATG CCTCAAACAC	50
	GTGAACACAT CTTGTTATCA CGTAACGTTG GTGTACCATA CATCGTTGTT	100
	TTCTTAAACA AAATGGATAT GGTGTGATGAC GAAGAATTAC TAGAATTAGT	150
	TGAAATGGAA GTTCGTGACT TATTGTCTGA ATATGACTTC CCAGGCGACG	200
60	ATGTTCTCTGT AATCGCTGGT TCTGCTTTGA AAGCTCYTGA AGGCGATGCT	250

	TCATACGAAG	AAAAAATCAT	GGAATTAATG	GCTGCAGTTG	ACGAATACGT	300
	TCCAAC TCCA	GAACGTGACA	CTGACAAACC	ATTCATGATG	CCAGTCGAAG	350
	ACGTATTCTC	AATCACTGGA	CGTGGTACTG	TTGCTACAGG	CCGTGTTGAA	400
	CGTGGACAAG	TTCGCGTTGG	TGACGAAGTT	GAAATCGTTG	GTATTGCTGA	450
5	AGAAACTGCT	AAAACAACTG	TAAGTGGTGT	TGAAATGTTC	CGTAAATTGT	500
	TAGACTATGC	TGAAGCAGGG	GATAACATTG	GTGCATTGCT	ACGTGGTGT	550
	GCTCGTGAAG	ACATCCAACG	TGGACAAGTA	TTGGCTAAAG	CTGGTACAAT	600
	CACACCTCAT	ACAAAATTTA	AAGCTGAAGT	TTACGTTTTA	ACAAAAGAAG	650
	AAGGTGGACG	TCACACACCA	TTCTTCACTA	ACTACCGTCC	TCAGTTCTAC	700
10	TTCCGTACAA	CTGACGTAAC	TGGTGTGTGT	GAATTACCAG	AAGGAACTGA	750
	AATGGTTATG	CCTGGTGATA	ACGTAACAAT	CGACGTTGAA	TTGATCCACC	800
	CAATCGCTAT	CGAAGACGGA	ACTCGTTTCT	CAATT		835

15

2) INFORMATION FOR SEQ ID NO: 59

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 826 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus cecorum*
 (B) STRAIN: ATCC 43198

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 59

	GGTGCTATCT	TAGTAGTATC	TGCTGCTGAT	GGTCCTATGC	CACAAACTCG	50
	TGAACACATT	CTTTTATCAC	GTAACGTTGG	TGTTCCATAC	ATCGTTGTTT	100
	TCTTAAACAA	AGTTGATATG	GTTGACGACG	AAGAATTATT	AGAATTAGTT	150
35	GAAATGGAAG	TACGTGACTT	ATTAAGTGAA	TACGACTTCC	CAGGAGACGA	200
	TGTTCTGTGA	ATCGCTGGTT	CTGCATTAAA	AGCTTTAGAA	GGCGACCCAT	250
	CTTACGAAGA	AAAAATCTTA	GAATTAATGG	CTGCAGTTGA	CGAATACATC	300
	CCAAC TCCAG	AACGTGACAA	CGATAAACCA	TTCATGATGC	CAGTCGAAGA	350
	CGTATTTTCA	ATCACTGGTC	GTGGTACTGT	TGCTACAGGT	CGTGTTGAAC	400
40	GTGGACAAGT	ACGTGTTGGT	GACGAAGTTG	AAATAGTTGG	TATCCATGAT	450
	GAAATTTCTA	AAACAACAGT	TACTGGTGT	GAAATGTTCC	GTAAATTATT	500
	AGATTACGCT	GAAGCTGGAG	ACAACATCGG	TGCATTATTA	CGTGGTGTGG	550
	CTCGTGAAGA	TATCCAACGT	GGTCAAGTAT	TAGCTAAACC	AGGTTCAATC	600
	ACTCCACATA	CAAAATTCAC	TGCTGAAAGT	TACGTTTTTA	CTAAAGAAGA	650
45	AGGTGGACGT	CATACTCCAT	TCTTCACTAA	CTACCGTCCA	CAATTCTACT	700
	TCCGTACAAC	TGACGTTACA	GGTGTAGTTA	ACTTACCAGA	AGGTACTGAA	750
	ATGGTTATGC	CTGGTGATAA	CGTAACTATG	GAAGTTGAAT	TAATCCACCC	800
	AATCGCTATC	GAAGACGGAA	CTCGTT			826

50

2) INFORMATION FOR SEQ ID NO: 60

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 835 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

60 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus dispar*
 (B) STRAIN: ATCC 51266

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 60

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CGGCGCGATC TTGGTAGTAT CTGCTGCTGA TGGTCCTATG CCTCAAACCTC      50
GTGAACACAT CCTATTGTCA CGTAACGTTG GTGTTCCCTTA CATCGTCGTT      100
10 TTCTTGAACA AAATGGACAT GGTTGATGAC GAAGAATTAT TAGAATTAGT      150
TGAAATGGAA GTTCGTGACT TATTGTCAGA ATACGACTTC CCAGGCGACG      200
ACACTCCAGT TATCGCAGGT TCAGCTTTGA AAGCCTTAGA AGGCGACGCT      250
TCATATGAAG AAAAAATCTT AGAATTAATG GCTGCAGTTG ACGAATATAT      300
CCCAACTCCA GTTCGTGATA CTGACAAACC ATTCATGATG CCAGTCGAAG      350
15 ATGTATTCTC AATCACTGGT CGTGGTACTG TTGCAACTGG TCGTGTGAA      400
CGTGGACAAG TTCGCGTTGG TGACGAAGTT GAAATCGTAG GTATCGCTGA      450
AGAACTGCT AAAACTACTG TAACAGGTGT TGAAATGTTC CGTAAATTGT      500
TGGATTACGC TGAAGCTGGC GACAACATTG GTGCATTATT ACGTGGTGTG      550
GCTCGTGAAG ATATCCAACG TGGTCAAGTA TTATCAAAC CAGGTTCAAT      600
20 CACTCCACAT ACAAATTTG CGGCAGAAGT TTACGTTTTA ACTAAAGAAG      650
AAGGTGGACG TCATACTCCA TTCTTCACTA ACTACCGCCC ACAATTCTAC      700
TTCCGTACAA CTGACGTAAC AGGTGTTGTT GAATTACCAG AAGGTACTGA      750
AATGGTTATG CCTGGCGATA ACGTTACTAT GGACGTTGAA TTAATCCACC      800
CAATCGCGAT CGAAGACGGT ACTCGTTTCT CAATC      835
25

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2) INFORMATION FOR SEQ ID NO: 61

30 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 835 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus durans*
 40 (B) STRAIN: ATCC 19432

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 61

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CGGAGCTATC TTAGTAGTTT CTGCTGCTGA TGGCCCTATG CCTCAAACCTC      50
45 GTGAACATAT CCTATTATCT CGTCAAGTTG GTGTTCCCTTA CATCGTYGTA      100
TTCTTGAACA AAGTAGATAT GGTTCGATGAC GAAGAATTAC TAGAATTAGT      150
TGAAATGGAA GTTCGTGACT TATTAACAGA ATACGAATTC CCTGGTGACG      200
ATGTTCCCTGT AATCGCTGGT TCAGCTTTGA AAGCTTTAGA AGGCGACGCT      250
TCATACGAAG AAAAAATCCT TGAATTAATG GCTGCAGTTG ACGAATATAT      300
50 CCCAACTCCA GAACGTGACA ACGACAAACC ATTCATGATG CCAGTTGAAG      350
ATGTATTCTC RATCACTGGT CGTGGTACTG TTGCTACAGG TCGTGTGAA      400
CGTGGACAAG TTCGCGTTGG TGACGTTGTA GATATCGTTG GTATCGCAGA      450
AGAAACAGCT CAAACAACAG TTACTGGTGT TGAAATGTTC CGTAAATTAT      500
TAGRCTACGC TGAAGCTGGA GACAACATTG GTGCTTTACT ACGTGGTGTG      550
55 GCACGTGAAG ACATCCAACG TGGACAAGTT TTAGCTAAAC CAGGTACAAT      600
CACKCCTCAT ACAAATTTCT CTGCAGAAGT ATACGTGTTG ACTAAAGAAG      650
AAGGTGGACG TCATACTCCA TTCTTCACTA ACTACCGTCC ACAATTCTAC      700
TTCCGTACAA CTGACGTAAC AGGTGTTGTT GAATTACCAG AAGGAAGTGA      750
AATGGTTATG CCTGGCGACA ACGTAACAAT GGAAGTTGAA TTAATCCACC      800
60 CAATCGCTAT CGAAAATGGT ACTAAATTCT CAATC      835

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2) INFORMATION FOR SEQ ID NO: 62

5

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 680 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

10

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus faecalis*
 (B) STRAIN: R610

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 62

```

20 AGTAGTTTCT GCTGCTGATG GTCCTATGCC TCAAACACGT GAACATATCT      50
   TATTATCACG TAACGTTGGT GTACCATACA TCGTTGTATT CTTAAACAAA      100
   ATGGATATGG TTGATGACGA AGAATTATTA GAATTAGTAG AAATGGAAGT      150
   TCGTGACTTA TTATCAGAAT ACGATTTCCC AGGCGATGAT GTTCCAGTTA      200
   TCGCAGGTTT TGCTTTGAAA GCTTTAGAAG GCGACGAGTC TTATGAAGAA      250
25 AAAATCTTAG AATTAATGGC TGCAGTTGAC GAATATATCC CAACTCCAGA      300
   ACGTGATACT GACAAACCAT TCATGATGCC AGTCGAAGAC GTATTCTCAA      350
   TCACTGGACG TGGTACTGTT GCTACAGGCC GTGTTGAACG TGGTGAAGTT      400
   CGCGTTGGTG ACGAAGTTGA AATCGTTGGT ATTAAAGACG AAACATCTAA      450
   AACAACTGTT ACAGGTGTTG AAATGTTCCG TAAATTATTA GACTACGCTG      500
30 AAGCAGGCGA CAACATCGGT GCTTTATTAC GTGGTGTAGC ACGTGAAGAT      550
   ATCGAACGTG GACAAGTATT AGCTAAACCA GCTACAATCA CTCCACACAC      600
   AAAATTCAAA GCTGAAGTAT ACGTATTATC AAAAGAAGAA GCGGACGTC      650
   ACACTCCATT CTCCTAAC TACCGTCTCT      680

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35

2) INFORMATION FOR SEQ ID NO: 63

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 680 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

40

(ii) MOLECULE TYPE: Genomic DNA

45

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus faecalis*
 (B) STRAIN: R487

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 63

```

AGTAGTTTCT GCTGCTGATG GTCCTATGCC TCAAACACGT GAACATATCT      50
TATTATCACG TAACGTTGGT GTACCATACA TCGTTGTATT CTTAAACAAA      100
55 ATGGATATGG TTGATGACGA AGAATTATTA GAATTAGTAG AAATGGAAGT      150
   TCGTGACTTA TTATCAGAAT ACGATTTCCC AGGCGATGAT GTTCCAGTTA      200
   TCGCAGGTTT TGCTTTGAAA GCTTTAGAAG GCGACGAGTC TTATGAAGAA      250
   AAAATCTTAG AATTAATGGC TGCAGTTGAC GAATATATCC CAACTCCAGA      300
   ACGTGATACT GACAAACCAT TCATGATGCC AGTCGAAGAC GTATTCTCAA      350
60 TCACTGGACG TGGTACTGTT GCTACAGGCC GTGTTGAACG TGGTGAAGTT      400

```

CGCGTTGGTG ACGAAGTTGA AATCGTTGGT ATTAAAGACG AAACATCTAA 450
 AACAACTGTT ACAGGTGTTG AAATGTTCCG TAAATTATTA GACTACGCTG 500
 AAGCAGGCGA CAACATCGGT GCTTTATTAC GTGGTGTAGC ACGTGAAGAT 550
 ATCGAACGTG GACAAGTATT AGCTAAACCA GCTACAATCA CTCCACACAC 600
 5 AAAATTCAAA GCTGAAGTAT ACGTATTATC AAAAGAAGAA GGCGGACGTC 650
 ACACTCCATT CTTCACTAAC TACCGTCCTC 680

10 2) INFORMATION FOR SEQ ID NO: 64

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 685 bases
 (B) TYPE: Nucleic acid
 15 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

20 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus faecium*
 (B) STRAIN: R482

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 64

25 AGTAGTTTCT GCTGCTGACG GCCCAATGCC TCAAACCTCGT GAACACATCC 50
 TATTGTCTCG TCAAGTTGGT GTTCCTTACA TCGTTGTATT CTTGAACAAA 100
 GTAGACATGG TTGATGACGA AGAATTACTA GAATTAGTTG AAATGGAAGT 150
 TCGTGACCTA TTAACAGAAT ACGAATTCCC TGGTGACGAT GTTCCTGTAG 200
 30 TTGCTGGATC AGCTTTGAAA GCTCTAGAAG GCGACGCTTC ATACGAAGAA 250
 AAAATTCTTG AATTAATGGC TGCAGTTGAC GAATACATCC CAACTCCAGA 300
 ACGTGACAAC GACAAACCAT TCATGATGCC AGTTGAAGAC GTGTTCTCAA 350
 TTACTGGACG TGGTACTGTT GCTACAGGTC GTGTTGAACG TGGACAAGTT 400
 CGCGTTGGTG ACGAAGTTGA AGTTGTTGGT ATTGCTGAAG AACTTCAAA 450
 35 AACACAGTT ACTGGTGTTG AAATGTTCCG TAAATTGTTA GACTACGCTG 500
 AAGCTGGAGA CAACATTGGT GCTTTACTAC GTGGTGTGTC ACGTGAAGAC 550
 ATCCAACGTG GACAAAGTTT AGCTAAACCA GGTACAATCA CACCTCATAC 600
 AAAATTCTCT GCAGAAGTAT ACGTGTGAC AAAAGAAGAA GGTGGACGTC 650
 40 ATACTCCATT CTTCACTAAC TACCGTCCTC AATTT 685

2) INFORMATION FOR SEQ ID NO: 65

45 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 825 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 50 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus flavescens*
 55 (B) STRAIN: ATCC 49996

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 65

CGGCGCGATC TTAGTAGTAT CTGCTGCTGA TGGTCCTAYG CCTCAAACAC 50
 60 GTGAACACAT CTTGTTATCA CGTAACGTTG GTGTACCATA CATCGTTGTT 100

	TTCTTAAACA	AAATGGATAT	GGTTGATGAC	GAAGAATTAC	TAGAATTAGT	150
	TGAAATGGAA	GTTTCGTGACT	TATTGTCAGA	ATATGACTTC	CCAGGCGACG	200
	ATGTTCTGT	AATCGCTGGT	TCTGCTTTGA	AAGCTCTTGA	AGGCGATGCT	250
	TCATACGAAG	AAAAAATCAT	GGAATTAATG	GCTGCAGTTG	ACGAATACGT	300
5	TCCAACCTCCA	GAACGTGACA	CTGACAAACC	ATTCATGATG	CCAGTCGAAG	350
	ACGTATTCTC	AATCACTGGA	CGTGGTACTG	TTGCTACAGG	CCGTGTTGAA	400
	CGTGGACAAG	TTCGCGTTGG	TGACGAAGTT	GAAATCGTTG	GTATTGCTGA	450
	AGAACTGCT	AAAACAACTG	TAAGTGGTGT	TGAAATGTTC	CGTAAATTGT	500
	TAGACTATGC	TGAAGCAGGG	GATAACATTG	GTGCATTGCT	ACGTGGGGTT	550
10	GCTCGTGAAG	ACATCCAACG	TGGACAAGTA	TTAGCTAAAG	CTGGTACAAT	600
	CACACCTCAT	ACAAAATTTA	AAGCTGAAGT	TTACGTTTTA	ACAAAAGAAG	650
	AAGGTGGACG	TCACACTCCA	TTCTTCACTA	ACTACCGTCC	TCAGTTCTAC	700
	TTCCGTACAA	CTGACGTAAC	TGGTGTGTGT	GAATTACCAG	AAGGAACCTGA	750
	AATGGTTATG	CCTGGTGATA	AMGTAACAAT	CGACGTTGAA	TTGATCCACC	800
15	CAATCGCTAT	CGAAGACGGA	ACTCG			825

2) INFORMATION FOR SEQ ID NO: 66

20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 636 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 25 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 30 (A) ORGANISM: *Enterococcus gallinarum*
 (B) STRAIN: R420

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 66

35	TCCTATGCCT	CAAACCTCGTG	AACACATCTT	GTTATCACGT	AACGTTGGCG	50
	TACCATACAT	CGTTGTTTTT	TTGAACAAAA	TGGATATGGT	TGATGACGAA	100
	GAATTGCTAG	AATTAGTTGA	AATGGAAGTT	CGTGACCTAT	TGTCTGAGTA	150
	TGACTTCCCA	GGCGACGATG	TTCCTGTAAT	CGCCGGTTCT	GCTTTGAAAG	200
	CTCTTGAAGG	AGATCCTTCA	TACGAAGAAA	AAATCATGGA	ATTGATGGCT	250
40	GCAGTTGACG	AATACGTTCC	AACTCCAGAA	CGTGATACTG	ACAAACCATT	300
	CATGATGCCA	GTCGAAGACG	TATTCTCAAT	CACTGGACGT	GGTACTGTTG	350
	CTACAGGCCG	TGTTGAACGT	GGACAAGTTC	GCGTTGGTGA	TGAAGTAGAA	400
	ATCGTTGGTA	TTGCTGACGA	AACTGCTAAA	ACAACTGTAA	CAGGTGTTGA	450
	AATGTTCCGT	AAATTGTTAG	ACTATGCTGA	AGCAGGGGAT	AACATTGGTG	500
45	CATTGCTACG	TGGGGTTGCT	CGTGAAGACA	TCCAACGTGG	ACAAGTATTG	550
	GCTAAAGCTG	GTACAATCAC	ACCTCATACA	AAATTCAAAG	CTGAAGTTTA	600
	TGTTTTGACA	AAAGAAGAAG	GTGGACGTCA	CACTCC		636

50

2) INFORMATION FOR SEQ ID NO: 67

(i) SEQUENCE CHARACTERISTICS:

- 55 (A) LENGTH: 835 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

60

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus hirae*
 (B) STRAIN: ATCC 8043

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 67

	CGGAGCTATC	TTAGTAGTTT	CTGCTGCTGA	TGGTCCTATG	CCTCAAACCTC	50
	GTGAACATAT	CCTAYTATCT	CGTCAAGTTG	GTGTTCCATA	CATCGTTGTA	100
	TTCTTTGAACA	AAGTAGATAT	GGTTGACGAC	GAAGAATTAC	TAGAATTAGT	150
10	TGAAATGGAA	GTTCGTGACT	TATTAACAGA	ATACGAATTC	CCTGGTGACG	200
	ATGTTCTGT	AGTTGCTGGT	YCAGCTTTGA	AAGCTTTAGA	AGGCGACGCT	250
	TCATACGAAG	AAAAAATCCT	TGAATTGATG	GCTGCAGTTG	ACGAATATAT	300
	CCCAACTCCA	GAACGTGACA	ACGACAAACC	ATTCATGATG	CCAGTCGAAG	350
	ACGTATTCTC	AATCACTGGT	CGTGGTACTG	TTGCTACAGG	TCGTGTTGAA	400
15	CGTGGACAAG	TTCGCGTTGG	TGACGTTGTA	GATATCGTTG	GTATCGCAGA	450
	AGAAACAGCT	CAAACAACAG	TTACTGGTGT	TGAAATGTTC	CGTAAATTAT	500
	TAGACTACGC	TGAAGCTGGA	GACAACATTG	GTGCTTTACT	ACGTGGTGT	550
	GCACGTGAAG	ACATCCAACG	TGGACAAGTT	TTAGCTAAAC	CAGGTACAAT	600
	CACACCTCAT	ACAAAATTCT	CTGCAGAAGT	ATACGTGTTG	ACAAAAGAAG	650
20	AAGGTGGACG	TCATACTCCA	TTCTTCACTA	ACTACCGTCC	ACAATTCTAC	700
	TTCCGTACRA	CTGACGTAAC	AGGTGTTGTT	GAATTACCAG	AAGGAACTGA	750
	AATGGTTATG	CCTGGCGACA	ACGTAACAAT	GGAAGTTGAA	TTAATCCACC	800
	CAATCGCTAT	CGAAAACGGT	ACTAAATTCT	CAATC		835

25

2) INFORMATION FOR SEQ ID NO: 68

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 835 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

35 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus mundtii*
 (B) STRAIN: ATCC 43186

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 68

	CGGAGCAATC	TTAGTTGTTT	CTGCTGCTGA	CGGCCCTATG	CCTCAAACCTC	50
	GTGAACACAT	CCTATTATCT	CGTCAAGTTG	GTGTACCATA	CATCGTTGTA	100
45	TTCTTTGAACA	AAGTAGATAT	GGTTGATGAC	GAAGAATTAC	TTGAATTAGT	150
	TGAAATGGAA	GTTCGTGACC	TATTAACAGA	ATACGAATTC	CCTGGTGACG	200
	ATGTTCTGT	AATCGCTGGT	TCAGCTTTAA	GAGCTTTAGA	AGGCGACGCT	250
	KCATACGAAG	AAAAAATTCT	TGAATTGATG	GCTGCAGTTG	ACGAATATAT	300
	CCCAACTCCA	GAACGTGATA	ACGACAAACC	ATTCATGATG	CCAGTTGAGG	350
50	ACGTATTCTC	AATCACTGGT	CGTGGTACTG	TTGCTACAGG	ACGTGTTGAA	400
	CGTGGACAAG	YTCGTGTTGG	TGACGTTATC	GATATCGTTG	GTATCGCAGA	450
	AGAAACAGCT	CAAACAACCTG	TAAGTGGTGT	TGAAATGTTC	CGTAAATTAT	500
	TAGACTACGC	TGAAGCAGGC	GATAACATTG	GTGCGTTACT	ACGTGGTGT	550
	TCACGTGAAG	ACATCCAACG	TGGTCAAGTT	TTAGCTAAAC	CAGGTACAAT	600
55	CACACCTCAT	ACAAAATTCT	CTGCAGAAGT	ATACGTGTTG	ACTAAAGAAG	650
	AAGGTGGACG	TCATACTCCA	TTCTTCACTA	ACTACCGTCC	ACAATTCTAC	700
	TTYCYTACGA	CTGACGTAAC	TRGTGTTGTY	GAATTACCAG	AAGGAACTGA	750
	AATGGTTATG	CCTGGCGACA	ACGTAACAAT	GGAAGTTGAA	TTAATCCACC	800
	CAATCGCTAT	CGAAAATGGT	ACTAAATTCT	CAATC		835

60

2) INFORMATION FOR SEQ ID NO: 69

5 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 836 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

10

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus pseudoavium*
 15 (B) STRAIN: ATCC 49372

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 69

```

CGGAGCTATC TTAGTAGTAT CTGCTGCTGA TGGCCCTATG CCTCAAACAC      50
20 GTGAACACAT CTTGTTATCT CGTAACGTTG GTGTTTCCTTA CATCGYTGTG      100
TTCTTAAACA AAATGGATAT GGTGATGAC GAAGAATTAC TAGAATTAGT      150
TGAAATGGAA GTTCGTGACT TATTGTCAGA ATACGATTTC CCAGGCGACG      200
ACACTCYAGT TATCGCTGGT TCAGCYTTGA AAGCTTTAGA AGGCGACCCCT      250
TCATACRAAG AAAAAATCTT AGAATTAATG SCTGCTGTTG ACCAATACAT      300
25 CCCAACACCA GTTCGTGATA CTGACAAACC ATTCATGATG CCAGTCGAAG      350
ACGTATTCTC AATCACTGGT CGTGGTACTG TTGCAACTGG TCGTGTTGAA      400
CGTGGACAAG TTCGCGTTGG TGACGAAGTT GAAATCGTAG GTATCGCTGA      450
AGAACTGCT AAAACAACCTG TTACAGGTGT TGAAATGTTC CGTAAATTGT      500
TAGACTACGC TGAAGCAGGC GATAACATCG GTGCATTATT ACGTGGTGT      550
30 GCACGTGAAG ACATCCAACG TGGACAAGTA TTGGCTAAAC CAGCTTCAAT      600
CACTCCACAT ACAAATTTCT CTGCAGAAGT TTACGTTTTA ACTAAAGAAG      650
AAGGCGGGCG TCACACTCCG TTCTTCACTA ACTACCGTCC TCAGTTCTAC      700
TTCCGTACAA CTGACGTAAC TGGTGTGTGT GATCTACCAG AAGGTACTGA      750
AATGGTAATG CCTGGTGATA ACGTAACTAT GGAAGTTGAA TTAATCCACC      800
35 CAATCGCGAT CGAAGACGGA ACTCGTTTCT CTATTC      836

```

2) INFORMATION FOR SEQ ID NO: 70

40

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 835 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 45 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus raffinosus*
 50 (B) STRAIN: ATCC 49427

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 70

```

CGGAGCTRTC TTAGTAGTAT CTGCTGCTGA TGGCCCTATG CCTCAAACCTC      50
GTGAACACAT CTTGTTATCT CGTAACGTTG GTGTTTCCTTA CATCGTTGTA      100
TTCTTAAACA AAATGGATAT GGTGACGAT GAAGAATTAC TAGAATTAGT      150
TGAAATGGAA GTTCGTGACT TATTAACCTGA ATACGACTTC CCAGGCGACG      200
ACACTCCAGT TATCGCAGGT TCAGCTTTGA AAGCCTTAGA AGGCGACGCT      250
60 TCATACGAAG AAAAAATCTT AGAATTAATG GCTGCTGTTG ATGAATACAT      300

```

	CCCAACACCA	GTTCTGTGATA	CTGACAAACC	ATTTCATGATG	CCAGYGGGAAG	350
	ACGTAYTCTC	AATCACTGGT	CGTGGAAGT	TTGCAACTGG	TCGTGTTGAA	400
	CGTGGACAAG	TTCGCGTTGG	TGACGAAGTT	GAAATCGTAG	GTATTGCTGA	450
	AGAACTGCT	AAAACAACTG	TTACAGGTGT	TGAAATGTTC	CGTAAATTGT	500
5	TGGATTACGC	TGAAGCGGGC	GACAACATTG	GTGCATTATT	ACGTGGTGT	550
	GCACGTGAAG	ACATCCAACG	TGGACAAGTA	TTGGCTAAAC	CAGCTTCAAT	600
	CACTCCACAT	ACAAAATTCT	CTGCAGAAGT	TTACGTTTTA	ACTAAAGAAG	650
	AAGGCGGACG	TCATACTCCA	TTCTTCACTA	ACTACCGTCC	TCAGTTCTAC	700
	TTCCGTACAA	CTGACGTAAC	TGGTGTAAGT	GATCTACCAG	AAGGTACTGA	750
10	AATGGTAATG	CCTGGTGATA	ACGTAACAT	GGAAGTTGAA	TTAATCCACC	800
	CAATCGCGAT	CGAAGACGGA	ACTCGTTTCT	CTATT		835

15 2) INFORMATION FOR SEQ ID NO: 71

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 835 bases
 (B) TYPE: Nucleic acid
 20 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

25 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus saccharolyticus*
 (B) STRAIN: ATCC 43076

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 71

30	CGGCGCGATC	TTAGTAGTAT	CTGCTGCTGA	TGGTCCTATG	CCTCAAACCTC	50
	GTGAACACAT	CTTGTTATCT	CGTAACGTAG	GTGTTCCCTTA	CATCGTTGTA	100
	TTCTTAAACA	AAATGGATAT	GGTTGATGAC	GAAGAATTAT	TAGAATTAGT	150
	AGAAATGGAA	GTTCTGTACT	TATTATCAGA	ATACGATTTC	CCAGGCGATG	200
35	ACACTCCAGT	TATTGCAGGT	TCTGCTTTGA	AAGCTTTAGA	AGGCGATCCA	250
	GTTTACGAAG	AAAAAATCTT	CGAATTAATG	GCTGCAGTTG	ACGAATATAT	300
	CCCAACTCCA	GAACGTGATA	CTGAAAAACC	ATTTCATGATG	CCAGTTGAGG	350
	ATGTATTCTC	AATCACTGGT	CGTGGTACTG	TTGCTACAGG	TCGTGTTGAA	400
	CGTGGACAAG	TTCGCGTTGG	TGACGTTGTA	GAAATCGTTG	GTATCGACGA	450
40	AGAAACAGCT	CAAACACTG	TAACAGGTGT	TGAAATGTTC	CGTAAATTAT	500
	TAGACTACGC	TGAAGCAGGC	GATAACATCG	GTGCTTTATT	ACGTGGGGTT	550
	GCTCGTGAAG	ACATCCAACG	TGGACAAGTA	TTAGCTAAAC	CAGGAACAAT	600
	CACTCCTCAT	ACAAAATTCT	TAGCTGAAGT	TTACGTTTTA	ACTAAAGAAG	650
	AAGGTGGACG	TCATACTCCA	TTCTTCACTA	ACTACCGTCC	TCAATTCTAC	700
45	TTCCGTACAA	CTGACGTAAC	TGGTGTTGTA	GAATTACGCG	AAGGTACTGA	750
	AATGGTAATG	CCTGGTGACA	ACGTAACAT	CGACGTTGAA	TTAATCCACC	800
	CAATCGCTAT	CGAAGACGGA	ACTCGTTTCT	CTATT		835

50

2) INFORMATION FOR SEQ ID NO: 72

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 823 bases
 55 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

60

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus solitarius*
 (B) STRAIN: ATCC 49428

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 72

	GAGCTATCTT	GGTAGTTTCT	GCAGCTGATG	GCCCAATGCC	ACAAACTCGT	50
	GAACATATTT	TGTTGTCACG	TAATGTAGGT	GTACCTTACA	TCGTTGTGTT	100
	CTTGAACAAA	ATGGATATGG	TTGATGACGA	AGAATTACTT	GAGTTAGTTG	150
10	AAATGGAAGT	ACGTGATCTA	TTATCTGAAT	ACGACTTCCC	AGGAGATGAT	200
	ACTCCAGTTA	TTTCCGGTTC	AGCTTTGAAA	GCTTTAGAAG	GCGACGAAGA	250
	ATATGAACAA	AAAATTATGG	ACTTAATGGA	TGCAGTTGAT	GACTACATTC	300
	CAACTCCTGA	ACGTGACCAT	GACAAACCAT	TCATGATGCC	AATTGAAGAT	350
	GTATTTTCAA	TTACAGGCCG	TGGTACTGTT	GCTACAGGAC	GTGTTGAACG	400
15	CGGGACTATC	AAAGTCGGCG	ATGAAGTTGA	CATTATTGGT	ATTTCATGAAG	450
	ACGTTAAAAA	GACAACAGTT	ACTGGTGTAG	AAATGTTCCG	TAAATTGTTG	500
	GACTACGCTG	AAGCAGGCCA	TAACATTGGT	ACTTTGTTAC	GTGGTGTTC	550
	TCGTGATGAT	ATCGAACGTG	GTCAAGTATT	AGCTAAACCA	GGTTCAATCA	600
	CACCACATAC	AAGATTCTCT	GCTGAAGTTT	ATGTTTTGAC	TAAAGAAGAA	650
20	GGCGGACGTC	ATACTCCATT	CTTCTCAAAC	TATCGTCCTC	AATTCTACTT	700
	CCGTACAAC	GATATCACTG	GTGTCATTGA	ATTGCCAGAA	GGTACTGAAA	750
	TGGTAATGCC	AGGTGATAAT	GTAACAATGG	ATGTTGAATT	AATCCACCCA	800
	GTCGCTATCG	AAGAAGGAAC	TCG			823

25

2) INFORMATION FOR SEQ ID NO: 73

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 835 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

35 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus casseliflavus*
 (B) STRAIN: ATCC 25788

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 73

	CGGTGCAATC	TTGGTCGTAT	CAGCGACAGA	TGGCCCAATG	CCACAAACAC	50
	GGGAGCATAT	TTTGCTTTCT	CGTCAAGTGG	GTGTGAAACA	TTTGATCGTC	100
45	TTTTTGAATA	AGACGGACCT	TGTCGATGAT	GACGAGTTGA	TCGATTTAGT	150
	TGAAATGGAA	GTCAGAGAAT	TGCTGACTGA	ATATGATTTT	CCTGGCGACG	200
	ACATTCCTGT	GATCAAGGGC	TCTGCGTTAA	AAGCCTTGGA	AGGGGACCCA	250
	GATGCTGAAG	CAGCGATCTT	AACGCTGATG	GATACAGTAG	ATGAATATAT	300
	CCCAACGCCA	GAACGTGATA	CTGACAAACC	ATTGTTGTTA	CCGATCGAAG	350
50	ATGTCTTTTC	GATCACAGGA	CGGGGGACCG	TTGCTTCTGG	TCGGATCGAT	400
	CGCGGCATGG	TAAAAGTCGG	GGATGAAGTA	GAAATCGTCG	GAATCAAACC	450
	TGAAACACAA	AAAGCAGTCG	TGACAGGGGT	AGAAATGTTT	CGCAAAACGA	500
	TGGACTTCGG	AGAAGCTGGC	GATAACGTAG	GGGTATTGTT	ACGGGGCATC	550
	ACCCGTGATG	AAATTGAACG	TGGCCAAGTG	TTAGCAAAAC	CAGGTTCTAT	600
55	CACACCGCAT	ACGAAATTCC	AAGCGGAAGT	CTATGTGTTG	ACAAAAGAAG	650
	AAGGCGGTCT	CCATACCCCA	TTCTTTAATA	ATTATCGCCC	ACAATTTTAC	700
	TTCCGTACAA	CGGACGTAAC	TGGGAATATC	GTTTTACCAG	AAGGAACGGA	750
	AATGGTGATG	CCTGGTGACA	ACGTAACGAT	CGATGTGGAA	TTGATCCATC	800
60	CGATCGCTGT	AGAAAATGGA	ACGACCTTCT	CGATT		835

45

2) INFORMATION FOR SEQ ID NO: 74

5 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 380 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

10

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus saprophyticus*
 15 (B) STRAIN: ATCC 15305

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 74

20	TAACGGGCGT CTCGATAGAA AAACACGTGA AAATCCCAAT GATTATAAAC	50
	AATCAATATA CGATTTTGCT GAAGCTGTAA CAAAAGGTAT TAAGGAACAA	100
	ACAAATAAAA ATTAATAGGC AACTTAACCA GAATCGTTAA AACTATATGA	150
	AGATTCTGGT TTTTAAATT CAAAAAGTTT TCTAAAAAAT TTACTTGCTT	200
	TTTTAAGTAT AGGTATAAAA TACGATTGAT TAAACAGTA AAGGAAATGA	250
	ATCATGAAAC AATTAATAA GCCTTTATAC TTTTACCTAT TACTTTTAT	300
25	TACAACAACG CTGATTGGCG CGTTACTATT ATATTGCCA ATCACAGGTA	350
	AACATCCTAT TGATTTTGTG GACGCCCGTT	380

30 2) INFORMATION FOR SEQ ID NO: 75

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 666 bases
 (B) TYPE: Nucleic acid
 35 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

40 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus flavescens*
 (B) STRAIN: ATCC 49996

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 75

45	GCAATCTTGG TCGTATCAGC GACAGATGGC CCAATGCCAC AAACACGGGA	50
	GCATATTTTG CTTTCTCGTC AAGTGGGTGT GAAACATTTG ATCGTCTTTT	100
	TGAATAAGAC GGACCTTGTC GATGATGACG AGTTGATCGA TTTAGTTGAA	150
	ATGGAAGTCA GAGAATTGCT GACTGAATAT GATTTTCCTG GCGACGACAT	200
50	TCCTGTGATC AAGGGCTCTG CGTTAAAAGC CTTGGAAGGG GACCCAGATG	250
	CTGAAGCAGC GATCTTAACG CTGATGGATA CGGTAGATGA ATATATCCCA	300
	ACGCCAGAAC GTGATACTGA CAAACCATG TTGTTACCGA TCGAAGATGT	350
	CTTTTCGATC ACAGGACGGG GGACCGTTGC TTCTGGTCGG ATCGATCGCG	400
	GCATGGTAAA AGTCGGGGAT GAAGTAGAAA TCGTCGGAAT CAAACCTGAA	450
55	ACACAAAAAG CAGTCGTGAC AGGGGTAGAA ATGTTCCGCA AAACGATGGA	500
	CTTCGGAGAA GCTGGCGATA ACGTAGGGGT ATTGTTACGG GGCATCACCC	550
	GTGATGAAAT TGAACGTGGC CAAGTGTTAG CAAAACCAGG TTCTATCACA	600
	CCGCATACGA AATTCCAAGC GGAAGTCTAT GTGTTGACAA AAGAAGAAGG	650
	CGGTCGCCAT ACCCCA	666

60

2) INFORMATION FOR SEQ ID NO: 76

5 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 751 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

10

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus gallinarum*
 15 (B) STRAIN: ATCC 49573

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 76

```

20 TGGTGCGATT TTAGTTGTAT CCGCAACAGA TGGTCCAATG CCTCAAACCC      50
   GGGAACATAT CTTGCTTTCG AGACAAGTTG GTGTGAAACA TCTGATTGTT      100
   TTCTTGAACA AAATCGATTT AGTCGATGAC GAAGAATTGA TTGATTTAGT      150
   AGAAATGGAA GTAAGAGAAC TGCTATCTGA ATATAATTTT CCAGGGGATG      200
   ACATTCCCTGT TATCAAAGGT TCGGCATTAA AAGCGTTGGA AGGAGACCCT      250
   GATGCAGAAG CTGCCATCAT GGAATTAATG GATACAGTAG ACAGCTATAT      300
25 CCCAACACCT GAGCGTGATA CAGACAAACC ATTACTCTTG CCAGTTGAAG      350
   ATGTCTTTTC GATTACTGGA CGAGGAACAG TTGCTTCCGG ACGGATCGAT      400
   CGGGGAACAG TTCGGGTAGG CGATGAAGTA GAAATCGTCG GTATCAAACC      450
   TGAAACCCAA AAAGCTGTAG TGACAGGCGT CGAAATGTTC CGCAAGACGA      500
   TGGACTTTGG GGAAGCCGGT GACAATGTAG GTGTCTTGCT GAGAGGGATC      550
30 ACTCGTGACG AAATTGAACG AGGACAAAGT TTGGCTAAAC CAGGTTTCGAT      600
   CACACCACAT ACAAATTC AAGCAGAACT TTATGTATTG ACGAAAGAAG      650
   AAGGTGGTCG TCATACACCA TTCTTCAACA ACTATCGTCC ACAATTTTAT      700
   TTCCGTACAA CGGATGTGAC AGGGAACATT ACATTGCCTG AAGGAACAGA      750
   A                                                                751
35

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2) INFORMATION FOR SEQ ID NO: 77

40 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 834 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

45

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Ehrlichia canis*
 50 (B) STRAIN: Florida

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 77

```

55 TGCAGCAATA TTAGTAGTGT CTGCAACTGA TGGAGCAATG CCACAAACAA      50
   GAGAACATAT ATTATTAGCA AAGCAAGTAG GTGTAAAAGA TATAGTAGTG      100
   TGGATGAATA AGTGTGATGT TGTAAGATGAT GAAGAAATGT TGTCATTAGT      150
   TGAAATGGAA ATAAGGGAAT TGTTATCAAA ATATGGGTAT CCTGGGGATG      200
   ATATAGATGT AGTTAGAGGA TCTGCAGTTA AAGCATTAGA AGAAGAAACA      250
   GGCTCAGGTG TGTGGAGTGA AAAAATAATG GAATTGATGA ATGCTTTAGA      300
60 AAAAATAAGT TTACCAGTAA GAGAAAAAGA TAAGCCATTT TTAATGTCAA      350

```

	TAGAAGATGT	GTTTTCAATA	CCTGGAAGAG	GTACAGTAGT	AACAGGAAGA	400
	ATAGAAAGAG	GAGTAATTAG	AGTAGGGGAT	AAAATAGAGA	TAGTAGGATT	450
	GCGTGAGATA	CAAAGTACAG	TATGTACAGG	TGTTGAAATG	TTTCATAAAG	500
	CATTAGATGC	AGGAGAAGCA	GGGGATAATG	CTGGAATATT	GTTAAGAGGG	550
5	ATAAAAAAAG	AAGATGTAGA	AAGAGGGCAA	GTATTGAGTG	CACCTGGACA	600
	GATACATTCA	TATAAGAGAT	TTAAGGCAGA	GGTATATATA	TTGAAAAAAG	650
	AAGAAGGAGG	AAGACATACT	CCATTTTCT	CAAATTACCA	GCCGCAATTT	700
	TATGTTAGAA	CAACAGATGT	AACAGGGAAT	ATAAAGTTAC	CAGAAGGAGT	750
	AGAAATGGTA	ATGCCAGGGG	ATAATATAAA	TATCGAAGTG	AGTTTGGATA	800
10	AGCCTGTTGC	TATTGATCAA	GGATTGAGAT	TTGC		834

2) INFORMATION FOR SEQ ID NO: 78

15

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 817 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 20 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 25 (A) ORGANISM: *Escherichia coli*
 (B) STRAIN: ATCC 23511

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 78

30	CGGCGCGATC	CTGGTAGTTG	CTGCGACTGA	CGGCCCGATG	CCGCAGACTC	50
	GTGAGCACAT	CCTGCTGGGT	CGTCAGGTAG	GCGTCCGTA	CATCATCGTG	100
	TTCTTGAACA	AATGCGACAT	GGTTGATGAC	GAAGAGCTGC	TGGAACGGT	150
	TGAAATGGAA	GTTCGTGAAC	TTCTGTCTCA	GTACGACTTC	CCGGGCGACG	200
	ACACTCCGAT	CGTTCGTGGT	TCTGCTCTGA	AAGCGCTGGA	AGGCGACGCA	250
35	GAGTGGGAAG	CGAAAATCCT	GGAACCTGGCT	GGCTTCCTGG	ATTCTTAYAT	300
	TCCGGAACCA	GAGCGTGCGA	TTGACAAGCC	GTTCCTGCTG	CCGATCGAAG	350
	ACGTATTCTC	CATCTCCGGT	CGTGGTACCG	TTGTTACCGG	TCGTGTAGAA	400
	CGCGGTATCA	TCAAAGTTGG	TGAAGAAGTT	GAAATCGTTG	GTATCAAAGA	450
	GACTCAGAAG	TCTACCTGTA	CTGGCGTTGA	AATGTTCCGC	AAACTGCTGG	500
40	ACGAAGGCCG	TGCTGGTGAG	AACGTAGGTG	TTCTGCTGCG	TGGTATCAAA	550
	CGTGAAGAAA	TCGAACGTGG	TCAGGTACTG	GCTAAGCCGG	GCACCATCAA	600
	GCCGCACACC	AAGTTCGAAT	CTGAAGTGTA	CATTCTGTCC	AAAGATGAAG	650
	GCGGCCGTCA	TACTCCGTTT	TTCAAAGGCT	ACCGTCCGCA	GTTCTACTTC	700
	CGTACTACTG	ACGTGACTGG	TACCATCGAA	CTGCCGGAAG	GCGTAGAGAT	750
45	GGTAATGCCG	GGCGACAACA	TCAAATGGT	TGTTACCCTG	ATCCACCCGA	800
	TCGCGATGGA	CGACGGT				817

50 2) INFORMATION FOR SEQ ID NO: 79

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 825 bases
 (B) TYPE: Nucleic acid
 55 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

60 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Escherichia fergusonii*
 (B) STRAIN: ATCC 35469

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 79

```

5      CGATCCTGGT AGTTGCTGCG ACTGACGGCC CGATGCCGCA GACTCGTGAG      50
      CACATCCTGC TGGGTCGTCA GGTAGGCGTT CCGTACATCA TCGTGTTTCCT      100
      GAACAAGTGC GACATGGTTG ATGACGAAGA GCTGCTGGAA CTGGTTGAAA      150
      TGGAAGTTTC TGAACCTCTG TCTCAGTACG ACTTCCCGGG CGACGACACT      200
----- 10  CCGATCGTTC GTGGTTCCTG TCTGAAAGCG CTGGAAGGCG ACGCAGAGTG      250
      GGAAGCGAAA ATCCTGGAAC TGGCTGGCTT CCTGGATTCT TACATTCCGG      300
      AACCAGAGCG TGCATTGAC AAGCCGTTCC TGCTGCCGAT CGAAGACGTG      350
      TTCTCCATCT CCGGTCGTGG TACCGTTGTT ACCGGTCGTG TAGAACGCGG      400
      TATCATCAA GTTGGTGAAG AAGTTGAAAT CGTTGGTATC AAAGAGACTC      450
      15  AGAAGTCTAC CTGTACTGGC GTTGAAATGT TCCGCAAAC GCTGGACGAA      500
      GGCCGTGCTG GTGAGAACGT AGGTGTTCTG CTGCGTGGTA TCAAACGTGA      550
      AGAAATCGAA CGTGGTCAGG TACTGGCTAA GCCGGGCACC ATCAAGCCGC      600
      ACACCAAGTT CGAATCTGAA GTGTACATTC TGTCAAAGA TGAAGGCGGT      650
      CGTCATACTC CGTTCTTCAA AGGCTACCGT CCGCAGTTCT ACTTCCGTAC      700
      20  TACTGACGTG ACTGGTACCA TCGAACTGCC GGAAGGCGTA GAGATGGTAA      750
      TGCCGGGCGA CAACATCAA ATGGTTGTTA CCCTGATCCA CCCGATCGCG      800
      ATGGACGACG GTCTGCGTTT CGCAA      825
  
```

25

2) INFORMATION FOR SEQ ID NO: 80

(i) SEQUENCE CHARACTERISTICS:

```

      (A) LENGTH: 829 bases
      (B) TYPE: Nucleic acid
      (C) STRANDEDNESS: Double
      (D) TOPOLOGY: Linear
  
```

(ii) MOLECULE TYPE: Genomic DNA

35

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Escherichia hermannii*
 (B) STRAIN: ATCC 33650

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 80

```

      GGCGCGATCC TGGTTGTTGC TGCGACTGAC GGCCCGATGC CGCAGACCCG      50
      TGAGCACATC CTGCTGGGTC GTCAGGTAGG CGTTCCGTAC ATCATCGTGT      100
      TCCTGAACAA ATGCGACATG GTTGATGACG AAGAGCTGCT GGAAGTGGTT      150
      45  GAGATGGAAG TTCGCGAACT GCTGTCCCAG TACGATTTCC CGGGCGACGA      200
      CACCCCGATC GTTCGTGGTT CCGCGCTGAA AGCGCTGGAA GGCGAAGCAG      250
      AGTGGGAAGA GAAAATCATC GAACTGGCTG GCTACCTGGA TTCCTATATC      300
      CCGGAACCAG AGCGTGCGAT TGACAAGCCG TTCCTGCTGC CTATCGAAGA      350
      CGTATTCTCC ATCTCCGGCC GTGGTACCGT TGTTACCGGT CGTGTAAGC      400
      50  GCGGTATCAT CAAAGTGGGT GAAGAAGTTG AAATCGTGGG TATCAAAGAT      450
      ACTGCGAAAT CAACCTGTAC CGGCGTTGAA ATGTTCCGCA AACTGTGGA      500
      CGAAGGCCGT GCGGGCGAGA ACGTGGGTGT TCTGCTGCGT GGTATCAAAC      550
      GTGAAGAAAT CGAACGTGGT CAGGTACTGG CTAAGCCGGG TTCCATCAAG      600
      CCKCACACCA AGTTCAATC TGAAGTGATC ATTCTGTCCA AAGACGAAGG      650
      55  CGGCCGTCAC ACTCCGTTCT TCAAAGGCTA CCGTCCGCAG TTCTACTTCC      700
      GTACAAGTGA CGTGAAGTGC ACCATCGAAC TGCCGGAAGG CGTTGAGATG      750
      GTAATGCCGG GCGACAACAT CAAAATGGTT GTTACCCTGA TCCACCCGAT      800
      CGCGATGGAC GACGGTCTGC GTTTCGCAA      829
  
```

60

2) INFORMATION FOR SEQ ID NO: 81

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 816 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

10 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Escherichia vulneris*
 (B) STRAIN: ATCC 33821

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 81

CGGCGCGATC CTGGTTGTTG CTGCGACTGA CGGCCCCGATG CCGCAGACCC 50
 GTGAGCACAT CCTGCTGGGT CGTCAGGTAG GCGTTCCGTA CATCATCGTG 100
 20 TTCCTGAACA AATGCGACAT GGTGTGATGAC GAAGAGCTGC TGGAACTGGT 150
 TGAGATGGAA GTGCGTGAAC TTCTGTCCCA GTACGACTTC CCGGGCGACG 200
 ACACCCCGAT CATTCGTGGT TCTGCGCTGA AAGCGCTGGA AGGCGAAGCT 250
 GAGTGGGAAG AGAAAATCGT TGAGCTGGCT GGCTACCTGG ATTCTACAT 300
 CCCGGAACCA GAGCGTGCGA TTGACAAGCC GTTCCTGCTG CCGATCGAAG 350
 25 ACGTATTCTC CATCTCCGGT CGTGGTACCG TTGTTACCGG TCGGTGATAG 400
 CGCGGTATCA TCAARGTKGG TGAAGAAGTT GAAATCGTGG GTATCAAAGA 450
 TACTGCGAAA TCTACCTGTA CCGGCGTTGA AATGTTCCGC AAAGTCTGG 500
 ACGAAGGTCG TGCAGGCGAG AACTGCGGCG TTCTGCTGCG TGGTATCAAG 550
 CGTGAAGAGA TCCAGCGTGG CCAGGTTCTG GCTAAGCCGG GCTCAATCAA 600
 30 GCCGCACACC AAGTTCGAAT CCGAAGTGTA CATCCTGTCC AAAGACGAAG 650
 GCGGCCGTCA CACTCCGTTT TTCAAAGGCT ACCGTCCGCA GTTCTACTTC 700
 CGTACAACCTG ACGTGACTGG CACCATCGAA CTGCCGGAAG GCGTAGAGAT 750
 GGTAATGCCG GGCGACAACA TCAAATGGT TGTTACCCTG ATCCATCCGA 800
 TCGCGATGGA CGACGG 816

35

2) INFORMATION FOR SEQ ID NO: 82

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 828 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

45

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Eubacterium lentum*
 50 (B) STRAIN: ATCC 43055

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 82

CGGCGCCTCC TCGTTATCGC CGCCACCGAC GGCCCGATGG CCCAGACCCG 50
 55 CGAGCACATC CTGCTCGCCC GTCAGGTCGG CGTGCCCTAC ATCGTGGTCT 100
 TCCTGAACAA GTGCGACATG GTCGACGACG AGGAGCTCCT CGAGCTCGTC 150
 GAGATGGAAG TTCGCGAGCT GCTCGACTCT TACGAGTTCC CCGGCGACGA 200
 CACCCCGATC ATCCGCGGCT CCGCTTTGAA GGCCCTCGAG GCGGACAAAG 250
 AGTGGCAGGA GAAGGTCTGG GAGCTCATGG ACGCCGTCGA CTCCTACATC 300
 60 CCGACGCCGG AGCGCATGGT CGACAAGCCG TTCCTGATGG CCGTCGAGGA 350

50

	CACGATGACC	ATCACCGGCC	GCGGCACCGT	TGCCACCGGT	CGTGTGGAGC	400
	GTGGTACGCT	GCATGTCAAC	GACCCGCTGG	AGATCGTCGG	TATCAAGGAG	450
	ACCCAGAACA	CGGTCTGCAC	CGGTATCGAG	ATGTTCCGCA	AGCTGCTCGA	500
	CGAGGCTCAG	GCCGGCGACA	ACATCGGCTG	CCTGCTCCGC	GGTGTCAAGC	550
5	GCGAGGAGAT	CGTTCGCGGC	CAGGTTCTCT	GCAAGCCCCG	TAGCGTGACC	600
	CCGCACACCG	AGTTCGAGGG	TCAGGTCTAC	ATCCTGACGA	AGGAAGAGGG	650
	CGGCCGCCAC	ACGCCGTTCT	TCGACGGCTA	CCGTCCGCAG	TTCTACTTCC	700
	GCACGACGGA	CGTGACGGGT	GTTGCCCCACC	TTCCCCGAGG	CACCGAGATG	750
	GTCATGCCGG	GCGACAACGT	GGAGATCAAG	GGCGAGCTCA	TTCACCCGAT	800
10	CGCCAGGAAG	AGGGCTGCGT	TCGCTAAC			828

2) INFORMATION FOR SEQ ID NO: 83

15

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 835 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Eubacterium nodatum*
 (B) STRAIN: ATCC 33099

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 83

30	GGAGCAATTC	TGGTTTGTGC	AGCAACKGAC	GGACCAATGC	CTCAGACAAG	50
	AGAACATATC	CTTTTGTCAA	GGCAGGTAGG	AGTGCCATAT	ATCATCGTAT	100
	TCCTGAATAA	ATGTGACATG	GTGGATGAYG	AAGAGCTTCT	GGACTTGGTA	150
	GAGATGGAAG	TAAGAGAACT	TCTCAGTGAG	TATGAATTCC	CGGGAGATGA	200
	TACCCCGATA	GTAAGAGGTT	CAGCCCTGAA	GGCACTGGAA	GAACCCAATG	250
35	GAGAAATGGGC	AGACAAGATT	GTAAGAGCTGA	TGGAGGAAGT	AGATAAATAC	300
	ATTCTCTGAAC	CAAAGAGAGA	TAACGACAAA	CCGTTCTCTGA	TGCCTGTAGA	350
	GGACGTATTC	TCAATAACAG	GAAGAGGAAC	AGTAGCGACA	GGAAGRGTTG	400
	AAAGAGGAAT	CCTGAAGGTC	GGTGATGAAG	TAGAAATCGT	GGAATGAGC	450
	GAAGAGAGAA	GAAAGGTAGT	AGTAACGGGA	GTTGAAATGT	TCAGAAAGCT	500
40	TCTGGATGAA	GCAGAGACAG	GAGACAACAT	CGGAGCACTG	CTGAGAGGAG	550
	TTCAGAGAAC	RGAGATCCAG	AGAGGTCAGG	TATTGGCRGC	ACCTGGAACG	600
	ATCAACCCAC	ATACAAAGTT	CAAGGGTCAG	GTATATGTAC	TGAAGAAGGA	650
	AGAAGGAGGA	AGGCATACGC	CGTTCTTCAA	YGGATACAGW	CCACAGTTCT	700
	ACTTCAGAAC	AACAGACGTA	ACAGGAGATT	TGCAGCTGCC	GGAAGGARCA	750
45	GAGATGTGCA	TGCCGGGAGA	TAATGTGGTA	ATGAACRTCA	GCCTGATCAC	800
	TCCGATTGCT	ATAGAAGAGG	GWCTGAGATT	TGCCA		835

50 2) INFORMATION FOR SEQ ID NO: 84

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 826 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

55

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

60

(A) ORGANISM: *Ewingella americana*
 (B) STRAIN: ATCC 33852

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 84

```

5      GCGATCCTGG TTGTTGCTGC AACTGATGGC CCTATGCCAC AGACTCGTGA      50
      GCACATCCTG TTGGGTCGYC AGGTTGGCGT TCCATTCATG ATCGTATTCA      100
      TGAACAAATG CGACATGGTT GATGACGAAG AGCTGCTGGA ACTGGTAGAA      150
      ATGGAAGTTC GYGAATTCT GTCTGCTTAC GATTTCCCAG GCGACGACAT      200
10     CCCAGTTGTT AAAGGTTTCA CGCTGAAAGC ACTGGAAGGC GAAGCAGAGT      250
      GGGAAAGCTAA GATCATCGAG CTGGCTGGCC ACCTGGATAG CTACATCCCA      300
      GAACCAAGAGC GTGCGATTGA CAAGCCATTG CTGCTGCCAA TCGAAGACGT      350
      ATTCTCCATC TCCGGTCGTG GTACCGTTGT TACCGGTCGT GTAGAGCGCG      400
      GTATCATCAA AGTTGGCGAA GAAGTTGAAA TCGTTGGTAT CAAGGACACT      450
15     GTTAAGTCTA CTTGTACTGG CGTTGAAATG TTCCGCAAAC TGCTGGACGA      500
      AGGCCGTGCT GGTGAGAACG TTGGTGTCTT GCTGCGTGGT ATCAAGCGTG      550
      AAGACATCGA ACGTGGTCAG GTTCTGGCTA AACCAGGTTC AATCAAACCA      600
      CACACCACWT TYGACTCAGA AGTTTATATC CTGAGCAAAG ATGAAGGCGG      650
      CCGTCATACT CCGTTCTTCA AAGGCTACCG TCCACAGTTC TACTTCCGTA      700
20     CAACTGACGT GACCGGTACC ATCGAACTGC CAGAAGGCGT AGAGATGGTA      750
      ATGCCAGGTG ACAACATCAA CATGRTAGTT ACCCTGATCC ACCCAATCGC      800
      GATGGATGAC GGTCTGCGTT TCGCAA      826
  
```

25 2) INFORMATION FOR SEQ ID NO: 85

(i) SEQUENCE CHARACTERISTICS:

```

30     (A) LENGTH: 828 bases
      (B) TYPE: Nucleic acid
      (C) STRANDEDNESS: Double
      (D) TOPOLOGY: Linear
  
```

(ii) MOLECULE TYPE: Genomic DNA

35

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Francisella tularensis*
 (B) STRAIN: LVS

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 85

```

      TGGTGCTATT CTAGTATGTT CTGCTGCGGA TGGTCCTATG CCACAAACTC      50
      GTGAGCACAT TCTGCTTTCT CGTCAAGTTG GTGTACCAA AATCGTTGTT      100
      TTCTTAAACA AGTGTGACAT GGTGATGAT GAAGAGTTAT TAGAGCTAGT      150
45     TGAGATGGAA GTTCGTGAGC TTTTAGATCA GTATGAGTTC CCAGGTGATG      200
      ACACTCCAGT TATTATGGGT TCAGCTCTTA GAGCTATTGA AGGTGACGAA      250
      GCTTACGTTG AGAAAATTGT TGAGCTAGTT CAAGCTATGG ATGACTATAT      300
      TCCTGCTCCT GAGCGTGATA CTGAGAAGCC ATTTATTCTT CCGATCGAAG      350
      ATGTATTCTT AATTTCAAGT CGTGGTACTG TTGTAAGTGG TCGTATTGAG      400
50     CGCGGTGTAG TTAACGTTGG TGATGAAGTT GAAGTTGTTG GTATTTCGTCC      450
      AACTCAAAAA ACTACAGTAA CTGGTGTGGA AATGTTCCGT AAGCTTTTAG      500
      ATAGAGGGGA AGCTGGTGAT AACGTTGGTA TCCTAGTTCG TGGACTTAAG      550
      AGAGATGATG TTGAGCGTGG ACAAGTATTA TGTAAGCCAG GTTCAATTAA      600
      GCCACATACT AAGTTTGAAG CTGAGGTTTA TGTATTATCT AAAGAAGAGG      650
55     GTGGTAGACA TACTCCATTC TTCAAGGGAT ATAGACCACA ATTCTACTTC      700
      CGTACTACAG ACATTACTGG AGCTGTTGAG CTTCCAGAGG GTGTAGAAAT      750
      GGTATGCCTT GGTGATAACG TTAAGATGAC TATCACTCTA ATTAACCCAA      800
      TCGCTAGGAT GAAGGGTTAC GTTTTGCA      828
  
```

60

2) INFORMATION FOR SEQ ID NO: 86

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 829 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

10 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Fusobacterium nucleatum* subsp. *polymorphum*
 (B) STRAIN: ATCC 10953

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 86

CGGTGCTATC ATCGTAGKTG CTGCTACTGA TGGTCCGATG CCTCARACTC 50
 GTGAGCAYAT CYTGCTGGCT CGTCAGGTAA ACGTWCKAG ACTGGTTGTA 100
 20 TTCATGAACA AGTGYGACAT GGTCAGACGAC GCTGAAATGY TGGAACCTCGT 150
 TGAAATGGAA ATGCGTGAAC TGCTTTTCAGC YTACGAATTC GAYGGYGACA 200
 AACTCCKTT CATTCAGGGT TCTGCTCTTG GTGCRTTGAA YGGCGTTGAA 250
 AAGTGGGAAG AGAAGGTTAT GGANCTGATG GATGCTTGCG AACTTTGGAT 300
 TCCTTTGCCT CCGCGTGATA TTGAYAAACC GTTCTTGATG CCGGTTGAAG 350
 25 ACGTATTCTC AATCACTGGT CGTGCTACTG TAGCTACTGG TCGTATCGAA 400
 GCTGGTGTTA TCCATGTAGG TGACGAAGTT GAAATCCTCG GTTTGGGTGA 450
 AGACAAGAAG TCTGTTGTAA CTGGTGTTGA AATGTTCCGC AAGTTGCTGG 500
 ATCAAGGTGA AGCTGGTGAC AACGTAGGTY TGTGCTCCG TGGTATCGAC 550
 AAGAACGAAA TCAAACGTGG TATGTTCTT TGTAAGCCCG GTCAGATTAA 600
 30 ACCTCACTCT AAGTTCAAAG CTTCTATCTA CGTTTTGAAG AAAGAAGAAG 650
 GTGGTCGTCA CACTCCGTTT CACAACAAAT ACCGTCCTCA GTTCTATCTG 700
 CGTACTATGG ACTGTACAGG TGAAATCWCT CTTCCGGAAG GAACTGAAAT 750
 GGTAATGCCT GGTGATAACG TAGAAATCAC TGTAGAACTG ATCTACCCGG 800
 TAGCATTGAA CGTAGGTTTG CGTTTCGCT 829

35

2) INFORMATION FOR SEQ ID NO: 87

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 828 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

45

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Gemella haemolysans*
 50 (B) STRAIN: ATCC 10379

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 87

CTATCTTAGT AATCGCTGCT ACAGATGGAC CAATGGCTCA AACTCGTGAG 50
 55 CACATCCTAT TATCTCGTAA CGTTGGAGTA CCAAAAATCG TTGTATTCTT 100
 AAACAAATGT GATATGGTTG ATGACGAAGA GTTATTAGAA TTAGTTGAAA 150
 TGGAAGTTCG TGAAGTATTA TCTGAATACG GATTCGACGG AGATGAACTA 200
 CCAGTAATCA AAGGTTCTGC TCTTAAAGCT CTTGAAGGAG ATGCAGATGC 250
 AGAAAAAGCT ATCATCGAAT TAATGGAAAC AGTTGACGAA TACATCCCAA 300
 60 CTCCAGAACG TGATAACGCT AAACCATTCA TGATGCCAGT TGAGGACGTA 350

	TTCTCAATCA	CAGGTCGTGG	TACAGTTGCT	ACTGGACGTG	TTGAACGTGG	400
	ACAAGTTAAA	GTTGAGACG	TAGTAGAAAT	CGTTGGATTA	ACTGAAGAAC	450
	CAGCTTCAAC	TACTGTAACA	GGTGTGAAA	TGTTCCGTAA	ATTATTAGAT	500
	TACGCTGAAG	CAGGAGATAA	CATCGGTGCA	TTATTACGTG	GTGTTGCTCG	550
5	TGAAGACATC	GAACGTGGAC	AAGTTTTAGC	AGCTCCTAAA	ACAATCACTC	600
	CACACACTCA	ATTCGTAGCT	GACGTGTACG	TATTATCTAA	AGAAGAAGGT	650
	GGACGTCACA	CTCCATTCTT	CACAACTAC	CGTCCTCAAT	TCTACTTCCG	700
	TACTACTGAC	GTAAGTGGTG	TAGTTACTTT	ACCAGAAGGT	ACTGAAATGG	750
	TAATGCCTGG	GGATAACGTA	TCAATCAACG	TAGAACTTAT	TTCTCCAATC	800
10	GCGATCGAAG	AAGGAACTCG	TTTCTCAA			828

2) INFORMATION FOR SEQ ID NO: 88

15

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 823 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 20 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 25 (A) ORGANISM: *Gemella morbillorum*
 (B) STRAIN: ATCC 27824

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 88

30	TCTTAGTAAT	CGCTGCTACA	GATGGTCCTA	TGGCTCAAAC	TCGTGAACAC	50
	ATCCTATTAT	CTCGTAACGT	TGGAGTACCT	AAAATTGTTG	TATTCTTAAA	100
	CAAATGTGAT	ATGGTTGATG	ACGAAGAGTT	ATTAGAATTA	GTAAGAAATGG	150
	AAGTTCGTGA	ACTATTATCT	GAATACGGAT	TTGATGGAGA	TGAAGTACCA	200
	GTAATCAAAG	GTTGAGCTCT	TAAAGCTCTT	GAAGGAGATG	CAGATGCTGA	250
35	AAAAGCTATC	ATCGAATTAA	TGGAAACAGT	TGACGAGTAC	ATCCCAACTC	300
	CAGAACGTGA	TAACGCTAAA	CCATTTATGA	TGCCAGTTGA	GGACGTGTTC	350
	TCAATCACAG	GTCGTGGTAC	AGTTGCTACT	GGACGTGTTG	AACGTGGACA	400
	AGTTAAAGTT	GGTGACGTAG	TAGAAATCGT	TGGATTAACT	GAAGAACCAG	450
	CTTCAACTAC	TGTAACAGGT	GTTGAAATGT	TCCGTAAATT	ATTAGATTAC	500
40	GCTGAAGCAG	GAGATAACAT	CGGTGCATTA	TTACGTGGTG	TTGCTCGTGA	550
	AGATATCGAA	CGTGGACAAG	TTTTAGCAGC	TCCTAAAACA	ATCACTCCAC	600
	ATACTCAATT	CGTAGCTGAT	GTGTACGTAT	TATCTAAAGA	AGAAGGTGGA	650
	CGTCACACTC	CATTCTTCAC	AACTACCGT	CCACAATTCT	ACTTCCGTAC	700
	TACTGACGTA	ACTGGTGTAG	TTACTTTACC	AGAAGGTACT	GAAATGGTAA	750
45	TGCCTGGGGA	CAACGTATCA	ATCAACGTAG	AACCTATTTC	TCCAATCGCT	800
	ATCGAAGAAG	GAACCTCGTTT	CTC			823

50 2) INFORMATION FOR SEQ ID NO: 89

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 829 bases
 (B) TYPE: Nucleic acid
 55 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

60 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Haemophilus actinomycetemcomitans*
 (B) STRAIN: ATCC 33384

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 89

```

5      GCTATCTTAG TAGTAGCAGC AACCGACGGT CCTATGCCAC AAACCTCGTGA      50
      GCACATCTTA TTAGGTCGCC AAGTAGGTGT TCCTTACATC ATCGTATTCT      100
      TAAACAAATG CGACATGGTA GATGACGAAG AGTTATTAGA ATTAGTTGAA      150
      ATGGAAGTTC GTGAACTTCT TTCTCAATAT GACTTCCCGG GCGATGACAC      200
10     CCCAATCGTA CGCGGTTCTG CATTAAAAGC GCTTGAAGGC GATGCCGCAT      250
      GGGGAAGAAAA AATCCTTGAA TTAGCAAAGC ATTTAGATAC TTACATCCCG
      GAACCTGAGC GTGCTATCGA CCAACCGTTC CTTCTTCCAA TTGAAGATGT      350
      GTTCTCTATC TCCGGTCGTG GTACCGTAGT AACGGGTCGT GTTGAGCGCG      400
      GTATCATCCG TACCGGTGAT GAAGTTGAAA TCGTGGGTAT CAAACCGACT      450
15     GCAAAAACCA CCGTAACCGG TGTTGAAATG TTCCGTAAAT TACTTGACGA      500
      AGGTCGTGCG GGTGAAAACA TCGGTGCATT ATTGCGTGGT ACTAAACGTG      550
      AAGAAATCGA ACGTGGTCAG GTATTGGCGA AACCGGGGTC AATCACCCCG      600
      CACACTGACT TCGAATCTGA AGTGTACGTA TTGTCCAAAG AAGAAGGTGG      650
      TCGTCATACT CCATTCTTCA AAGGTTACCG TCCACAATTC TATTTCCGTA      700
20     CAACTGACGT AACCGGTACT ATCGAGTTAC CTGAAGGCGT GGAAATGGTT      750
      ATGCCTGGCG ATAACATCAA AATGACCGTA TCCTTAATTC ACCCAATTGC      800
      GATGGACCAA GGTTTACGTT TCGCTATCG      829
  
```

25

2) INFORMATION FOR SEQ ID NO: 90

(i) SEQUENCE CHARACTERISTICS:

```

      (A) LENGTH: 833 bases
30     (B) TYPE: Nucleic acid
      (C) STRANDEDNESS: Double
      (D) TOPOLOGY: Linear
  
```

(ii) MOLECULE TYPE: Genomic DNA

35

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Haemophilus aphrophilus*
 (B) STRAIN: ATCC 33389

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 90

```

      TGGTGCTATC TTAGTAGTAG CAGCAACTGA TGGTCCCTATG CCACAAACTC      50
      GTGAGCACAT CTTATTAGGT CGCCAAGTAG GTGTTCTTCA CATCATCGTA      100
      TTCTTAAACA AATGCGACAT GGTAGATGAC GAAGAGTTAT TAGAATTAGT      150
45     TGAAATGGAA GTTCGTGAAC TTCTTTCTCA ATATGACTTC CCGGGTGATG      200
      ATACACCAAT CGTACGTGGT TCTGCATTAC AAGCGTTAAA CGGCGTTGCA      250
      GAATGGGAAG AAAAAATCCT TGAATTAGCA AACCACCTAG ATACTTACAT      300
      TCCTGAGCCA CAACGTGCTA TCGACCAACC GTTCCTTCTT CCAATTGAAG      350
      ACGTGTTCTC TATCTCCGGT CGTGGTACTG TAGTAACAGG TCGTGTTGAG      400
50     CGTGGTATCA TCCGTACCGG TGATGAAGTT GAAATCGTAG GTATCAAACC      450
      GACTGCGAAA ACTACCGTAA CCGGTGTTGA AATGTTCCGT AAATTACTTG      500
      ACGAAGGTCG TGCAGGTGAA AACATCGGTG CATTATTACG TGGCACTAAA      550
      CGTGAAGAAA TCGAACGTGG TCAAGTATTG GCTAAACCGG GCTCAATCAC      600
      TCCGCACACT GATTTCTGAAT CTGAAGTGTA CGTATTATCC AAAGAAGAAG      650
55     GTGGTCGTCA TACTCCATTG TTCAAAGGTT ACCGTCCACA ATTCTATTTT      700
      CGTACAACCTG ACGTAACCGG TACTATCGAG TTACCGGAAG GCGTGGAAT      750
      GGTTATGCCT GGCGATAACA TCAAAATGAC TGTATCCTTA ATCCACCCAA      800
      TCGCGATGGA CCAAGGTTTA CGTTTCGCTA TCG      833
  
```

60

55

2) INFORMATION FOR SEQ ID NO: 91

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 815 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

10 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Haemophilus ducreyi*
 (B) STRAIN: DSM 8925

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 91

CGGCGCTATC TTAGTTGTAG CAGCAACTGA TGGTCCTATG CCTCAAACCTC 50
 GTGAACACAT CTTATTAGGC CGCCAAGTTG GTGTTCTTA CATCATCGTA 100
 20 TTCTTAAATA AATGCGATAT GGTAGATGAT GAAGAATTAT TAGAATTAGT 150
 TGAAATGGAA GTTCGTGAAC TTCTTTCTCA ATATGATTTC CCAGGTGACG 200
 ATACTCCTAT CGTTCGTGGT TCAGCATTAC AAGCATTAAA TGGTGTGCCT 250
 GAGTGGGAAG AAAAAATCAT TGAATTAGCA CAACACTTAG ATTCTTATAT 300
 CCCTGAGCCT GAGCGTGCGA TTGATAAACC TTTCTTATTA CCAATCGAAG 350
 25 ACGTATTCTC AATTTCAGGT CGTGGTACAG TAGTAACCGG TCGTGTGAG 400
 CGTGGTATCA TCAAATCAGG TGAAGAAGTT GAAATCGTAG GGATTAAAGA 450
 AACGACAAAA ACAACAGTAA CCGGTGTTGA GATGTTCCGT AAACATTAG 500
 ACGAAGGTCG TCGGGGTGAA AACGTAGGTG CCTTATTACG TGGTACTAAA 550
 CGTGAAGAAA TCGAACGTGG TCAAGTATTA GCGAAACCAG GTACAATTAC 600
 30 ACCACACACT GATTTTGAAT CAGAAGTTTA TGTATTATCA AAAGAAGAAG 650
 GTGGTCGTCA TACTCCATTC TTCAAAGGTT ATCGTCCTCA GTTCTACTTC 700
 CGYACAACGG ACGTAACAGG AACGATTGAA TTACCTGAAG ATGTTGAGAT 750
 GGTAATGCCT GGTGATAATA TCAAGATGAC AGTAAGCTTA ATTCACCCTA 800
 TCGCGATGGA CGAAG 815
 35

2) INFORMATION FOR SEQ ID NO: 92

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 830 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

45

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 50 (A) ORGANISM: *Haemophilus haemolyticus*
 (B) STRAIN: ATCC 33390

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 92

TGGTGCTATC TTAGTAGTAG CAGCAACTGA TGGTCCAATG CCACAAACTC 50
 55 GTGAGCACAT CTTATTAGGT CGCCAAGTAG GTGTTCCATA CATCATCGTA 100
 TTCTTAAACA AATGCGACAT GGTAGATGAC GAAGAGTTAT TAGAATTAGT 150
 AGAAATGGAA GTTCGTGAAC TTCTTTCTCA ATATGACTTC CCAGGTGACG 200
 ATACACCAAT CGTACGTGGT TCTGCATTAC AAGCATTAAA TGGCGTAGCA 250
 GAATGGGAAG AAAAAATCCT TGAGTTAGCA AACCCTTAG ATACTTACAT 300
 60 CCCAGAACCA GAGCGTGCAA TTGACCAACC GTTCCTTCTT CCAATCGAAG 350

	ATGTGTTCTC	AATCTCAGGT	CGTGGTACAG	TAGTAACTGG	TCGTGTAGAA	400
	CGTGGTATCA	TCCGTACTGG	TGATGAAGTA	GAAATCGTAG	GTATCAAAGA	450
	TACAGCAAAA	ACTACTGTAA	CGGGTGTGTA	AATGTTCCGT	AAATTACTTG	500
	ACGAAGGTCG	TGCAGGTGAA	AACATCGGTG	CATTATTACG	TGGTACCAAA	550
5	CGTGAAGAAA	TCGAACGTGG	TCAAGTATTA	GCGAAACCAG	GTTCAATCAC	600
	GCCACACACT	GACTTCGAAT	CAGAAGTTTA	TGTATTATCA	AAAGAAGAAG	650
	GTGGTCGTCA	TACTCCATTC	TTCAAAGGTT	ACCGTCCACA	ATTCTATTTT	700
	CGTACAACCTG	ACGTAACCTG	TACTATCGAG	TTACCAGAAG	GCGTAGAAAT	750
	GGTAATGCCA	GGCGATAACA	TCAAGATGAC	AGTAAGCTTA	ATCCACCCAA	800
10	TCGCGATGGA	CCAAGGTTTA	CGTTTCGCAA			830

2) INFORMATION FOR SEQ ID NO: 93

15

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 824 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 20 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 25 (A) ORGANISM: *Haemophilus parahaemolyticus*
 (B) STRAIN: ATCC 10014

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 93

30	TCTTAGTAGT	AGCAGCAACA	GACGGTCCAA	TGCCACAAAC	TCGTGAGCAC	50
	ATCTTATTAG	GTCGCCAAGT	AGGTGTTCCA	TACATCATCG	TATTCTTAAA	100
	CAAATGCGAT	ATGGTTGACG	ATGAAGAATT	ATTAGAATTA	GTTGAAATGG	150
	AAGTGCGTGA	ACTTCTTTCA	CAATATGACT	TCCCAGGTGA	TGACACGCCA	200
	GTAGTACGTG	GTTTCAGCGTT	ACAAGCGTTA	AACGGCGTAG	CAGAGTGGGA	250
35	AGAAAAAATT	CTTGAATTAG	CAAACCACTT	AGATACATAC	ATCCCAGAGC	300
	CAGAGCGTGC	GATTGATAAA	CCATTCTTAT	TACCAATCGA	AGACGTATTC	350
	TCAATCTCAG	GTCGTGGTAC	AGTAGTAACA	GGTCGTGTTG	AGCGTGGTAT	400
	CATCAAAGCG	GGTGAAGAAG	TTGAAATCGT	AGGTATCAAA	GACACTGCGA	450
	AAACAACAGT	AACTGGCGTG	GAAATGTTCC	GTAAATTATT	AGACGAAGGT	500
40	CGTGCGGGTG	AAAACGTTGG	TGCATTATTA	CGTGGTACAA	AACGTGAAGA	550
	AATCGAACGT	GGTCAAGTGT	TAGCGAAACC	AGGTACAATT	ACACCACACA	600
	CAGACTTCGA	ATCAGAAGTG	TACGTATTAT	CAAAAGAAGA	AGGTGGTCGT	650
	CACACTCCAT	TCTTCAAAGG	TTACCGTCCA	CAATTCTACT	TCCGTACAAC	700
	TGACGTAAC	GGTACTATTG	AATTACCAGA	AGGCGTAGAA	ATGGTAATGC	750
45	CAGGCGATAA	CATCAAAATG	ACAGTATCAT	TAATCCACCC	AATCGCGATG	800
	GACGAAGGTT	TACGTTTTGC	GATT			824

50 2) INFORMATION FOR SEQ ID NO: 94

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 833 bases
 (B) TYPE: Nucleic acid
 55 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

60 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Haemophilus parainfluenzae*
 (B) STRAIN: ATCC 7901

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 94

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5      TGGTGCTATC TTAGTAGTAG CAGCAACTGA TGGTCCTATG CCACAAACTC      50
      GTGAGCACAT CTTATTAGGT CGCCAAGTAG GTGTTCCCTTA CATCATCGTG      100
      TTCTTAAACA AATGCGACAT GGTAGATGAC GAAGAGTTAT TAGAATTAGT      150
      TGAAATGGAA GTTCGTGAAC TTCTTTCTCA ATATGACTTC CCGGGTGACG      200
10     ATACACCAAT CGTACGTGGT TCTGCATTAC AAGCGTTAAA CGGCGTWGCA      250
      GAATGGGAAG AAAAAATCCT TGAATTAGCT AGCCACTTAG ATTCTTACAT      300
      TCCTGAGCCT CAACGTGCTA TCGACCAACC GTTCCTTCTT CCAATCGAAG      350
      ACGTGTTCTC TATCTCCGGT CGTGGTACAG TAGTAACAGG TCGTGTTGAG      400
      CGTGGTATCA TCCGTACCGG TGATGAAGTT GAAATCGTAG GTATCAAACC      450
15     GACTGCGAAA ACTACCGTAA CCGGTGTTGA AATGTTCCGT AAATTACTTG      500
      ACGAAGGTCG TGCAGGTGAA AACATCGGTG CATTATTACG TGGTACYAAA      550
      CGTGAAGAAA TCGAACGTGG TCAAGTATTG GCTAAACCGG GTTCAATCAC      600
      TCCACACACT GATTTTCAAT CTGAAGTGTA CGTATTATCC AAAGAAGAAG      650
      GTGGTCGTCA TACTCCATTG TTCAAAGGTT ACCGTCCACA ATTCTATTTT      700
20     CGTACAACCTG ACGTAACCGG AACTATCGAA TTACCGGAAG GCGTGGAAT      750
      GGTTATGCCT GGTGATAACA TCAAATGAC TGTATCCTTA ATCCACCCAA      800
      TCGCGATGGA CCAAGGTTTA CGTTTCGCTA TCG      833
  
```

25

2) INFORMATION FOR SEQ ID NO: 95

(i) SEQUENCE CHARACTERISTICS:

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30     (A) LENGTH: 824 bases
      (B) TYPE: Nucleic acid
      (C) STRANDEDNESS: Double
      (D) TOPOLOGY: Linear
  
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(ii) MOLECULE TYPE: Genomic DNA

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(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Haemophilus paraphrophilus*
 (B) STRAIN: ATCC 29241

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 95

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      TGGTGCTATC TTAGTAGTAG CAGCAACTGA TGGTCCTATG CCACAAACTC      50
      GTGAGCACAT CTTATTAGGT CGCCAAGTAG GTGTTCCCTTA CATCATCGTA      100
      TTCTTAAACA AATGCGACAT GGTAGATGAC GAAGAGTTAT TAGAATTAGT      150
45     TGAAATGGAA GTTCGTGAAC TTCTTTCTCA ATATGACTTC CCGGGTGACG      200
      ATACGCCAAT CGTACGTGGT TCTGCATTAC AAGCGTTAAA CGGCGTTGCA      250
      GAATGGGAAG AAAAAATCCT TGAATTAGCA AACCCTTGG ATACTTACAT      300
      TCCTGAGCCA CAACGTGCTA TCGACCAACC GTTCCTTCTT CCAATCGAAG      350
      ACGTGTTCTC TATCTCCGGT CGTGGTACAG TAGTAACAGG TCGTGTTGAG      400
50     CGTGGTATCA TCCGTACCGG TGATGAAGTT GAAATCGTAG GTATCAAACC      450
      GACTGCGAAA ACTACCGTAA CCGGTGTTGA AATGTTCCGT AAATTACTTG      500
      ACGAAGGTCG TGCAGGTGAA AACATCGGTG CATTATTACG TGGTACCAA      550
      CGTGAAGAAA TCGAACGTGG TCAAGTATTG GCTAAACCGG GTTCAATCAC      600
      TCCACACACT GATTTTCAAT CTGAAGTGTA CGTATTATCC AAAGAAGAAG      650
55     GTGGTCGTCA TACTCCATTG TTCAAAGGTT ACCGTCCACA ATTCTATTTT      700
      CGTACAACCTG ACGTAACCGG TACTATCGAG TTACCGGAAG GTGTGGAAT      750
      GGTAAATGCCT GGCGATAACA TCAAATGAC CGTATCCTTA ATCCACCCAA      800
      TCGCGATGGA CCAAGGTTTA CGTT      824
  
```

60

2) INFORMATION FOR SEQ ID NO: 96

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 818 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

10 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Haemophilus segnis*
 (B) STRAIN: ATCC 33393

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 96

GCTATCTTAG TAGTAGCAGC AACTGATGGT CCTATGCCAC AAACCTCGTGA 50
 GCACATCTTA TTAGGTCGCC AAGTAGGTGT TCCTTACATC ATCGTATTCT 100
 20 TAAACAAATG CGACATGGTA GATGACGAAG AGTTATTAGA ATTAGTTGAA 150
 ATGGAAGTTC GTGAACTTCT TTCTCAATAT GACTTCCCAG GTGATGATAC 200
 TCCAATCATT CGTGGTTCTG CATTACAAGC GTTAAACGGC GTAGCAGAAT 250
 GGGAAGAAAA AATCCTTGAA TTAGCTCAAG CATTAGATAC TTACATTCTT 300
 GAACCTGAGC GTGCAATCGA CCAACCGTTC CTTCTTCCAA TTGAAGACGT 350
 25 GTTCTCAATC TCTGGTCGTG GTACTGTAGT AACAGGTCGT GTAGAGCGTG 400
 GTATCATCCG TACCGGTGAT GAAGTTGAAA TCGTTGGTAT CAAACCAACT 450
 GCGAAAACAA CCGTAACCGG TGTGAAATG TTCCGTAAAT TACTTGACGA 500
 AGGTCGTGCA GGTGAAAACA TCGGTGCATT ATTACGTGGT ACTAAACGTG 550
 AAGAAATCGA ACGTGGTCAA GTATTAGCGA AACCGGGTTC AATCACTCCA 600
 30 CACACTGACT TCGAATCTGA AGTGTACGTA TTATCTAAAG AAGAAGGTGG 650
 TCGTCATACT CCATTCTTCA AAGGTTACCG TCCACAATTC TATTTCCGTA 700
 CAACTGACGT AACCGGTACT ATCGAGTTAC CGGAAGGCGT GGAAATGGTT 750
 ATGCCTGGCG ATAACATCAA AATGACCGTA TCCTTAATCC ACCCAATCGC 800
 GATGGACCAA GGTTTACG 818

35

2) INFORMATION FOR SEQ ID NO: 97

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 763 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

45

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 50 (A) ORGANISM: *Hafnia alvei*
 (B) STRAIN: ATCC 13337

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 97

CGGCGCTATC CTGGTTGTTG CTGCGACTGA CGGCCCTATG CCTCAGACTC 50
 55 GTGAGCACAT CCTGCTGGGT CGTCAGGTTG GCGTTCCTTW CATCATCGTR 100
 TTCCTGAACA AATGCGACAT GGTGATGAT GAAGAGCTGC TGGAAGTGGT 150
 AGAAATGGAA GTTCGTGAAC TTCTGTCTCA GTACGACTTC CCWGGYGATG 200
 ATACTCCAAT CATCCGTGGT TCTGCTCTGA AAGCGCTGGA AGGYGMACCT 250
 GAGTGGGAAG CTAAGATCGT AGAACTGGCT GAAACTCTGG ATTCTTACAT 300
 60 YCCACARCCA GAACGTGCTA TCGAYAAGCC ATTCTGCTG CCAATCGAAG 350

ACGTATTCTC TATCTCTGGC CGTGGTACWG TTGTTACCGG TCGTGTAGAG 400
 CGCGGTATCG TTAAAGTTGG TGAAGAAGTT GARATCGTTG GTATCAAAGA 450
 TACCGTTAAA TCAACTTGTA CCGGCGTTGA AATGTTCCGT AAAGTGTCTGG 500
 ACGAAGGTCG TGCAGGCGAG AACGTTGGTG TTCTGCTGCG TGGTATCAAG 550
 5 CGTGAAGACA TCGAACGTGG TCAGGTTCTG GCTAAACCAG GYTCYATCAA 600
 GCCACACACC AAGTTCGAAT CAGAAGTTTA TATTCTGAGC AAAGATGAAG 650
 GCGGYCGTCA TACTCCGTTT TTCAAAGGCT ACCGTCCACA GTTCTACTTC 700
 CGTACAAC TGACGTGACCGG TACCATCGAA TTGCCAGAAG GCGTGGAAT 750
 GGTAATGCCA GGC 763
 10

2) INFORMATION FOR SEQ ID NO: 98

15 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 828 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

20 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Kingella kingae*
 25 (B) STRAIN: ATCC 23330

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 98

CGGCGCAATC TTGGTATGTT CAGCAGCTGA CGGTCCTATG CCACAAACTC 50
 30 GCGAACACAT CTTGTTGGCT CGCCAAGTAG GTGTACCTTA TATCATCGTA 100
 TTCATGAACA AATGCGACAT GGTGATGAT GCTGAGTTGT TGAATTGGT 150
 TGAAATGGAA ATCCGTGACT TGTGCTGCTA CTACGATTTT CCAGGCGACG 200
 ATTGCCCAAT CGTTCAAGGT TCTGCATTGC GYGCAATTGGA AGGCGACGCT 250
 GCATACAAAG AAAAAATCTT TGAATTGGCT GCTGCTTTGG ATAGCTACAT 300
 35 TCCTACTCCA GAACGTGCTG TTGATAAACC ATTCTTGTTG CCAATCGAAG 350
 ATGTATTCTC TATCTCTGGT CGTGGTACAG TAGTTACTGG TCGTGTAGAG 400
 CGCGGTATCA TCAAAGTAGG CGAAGAGATT GAAATCGTTG GTTTGAAAGA 450
 CACGCAAAAA ACCACTTGTA CTGGCGTGGA AATGTTCCGC AAATTGTTGG 500
 ACGAAGGTCA AGCTGGTGAT AACGTTGGTG TATTATTGCG TGGTACGAAG 550
 40 CGTGAAGACG TTGAACGTGG TCAGGTATTG GCTAAACCAG GTTCTATCAC 600
 TCCGCACACT AAATTTGAAG CTGAAGTGTA TGTGTTGAGC AAAGAAGAAG 650
 TGGGCCGTCA TACGCCATTG TTCGCTAACT ACCGCCACA ATTCTACTTC 700
 CGTACGACTG ACGTAACTGG TGCAGTTACT TTGTCTGAGG GTGTGGAAAT 750
 GGTTATGCCA GGCGAAAACG TGAAAATCAC TGTGAGTTG ATTGCACCTA 800
 45 TCGCTAGGAA AACGGTTTGC GTTTTGCG 828

2) INFORMATION FOR SEQ ID NO: 99

50 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 828 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 55 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 60 (A) ORGANISM: *Klebsiella ornithinolytica*

(B) STRAIN: ATCC 31898

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 99

5	GGCGCGATCC	TGGTTGTTGC	TGCGACTGAC	GGCCCCGATGC	CGCAGACTCG	50
	TGAGCACATC	CTGCTGGGTC	GTCAGGTAGG	CGTTCCGTAC	ATCATCGTGT	100
	TCCTGAACAA	ATGCGACATG	GTTGATGACG	AAGAGCTGCT	GGAGCTGGTT	150
	GAAATGGAAG	TCCGTGAGCT	GCTGTCTCAG	TACGACTTCC	CGGGCGACGA	200
	CACGCCGATC	GTTCTGTGGT	CCGCTCTGAA	AGCGCTGGAA	GGCGAAGCAG	250
10	ACTGGGAAGC	GAAAATCATC	GAAC TGGCTG	GCTACCTGGA	TTCTTACATC	300
	CCGGAACCAG	AGCGTGCGAT	TGACAAGCCG	TTCTTGCTGC	CGATCGAAGA	350
	CGTATTCTCC	ATCTCCGGTC	GTGGTACCGT	TGTTACCGGT	CGTGTAGAGC	400
	GCGGTATCAT	CAAAGTGGGC	GAAGAAGTTG	AAATCGTTGG	TATCAAAGAG	450
	ACTGCGAAGT	CTACCTGTAC	TGGCGTTGAA	ATGTTCCGCA	AACTGCTGGA	500
15	CGAAGGCCGT	GCTGGTGAGA	ACGTTGGTGT	TCTGCTGCGT	GGTATCAAAC	550
	GTGAAGAAAT	CGAACGTGGT	CAGGTACTGG	CTAAGCCGGG	CTCTATCAAG	600
	CCGCACACCA	AGTTCGAATC	TGAAGTGATC	ATTCTGTCCA	AAGACGAAGG	650
	CGGCCGTCAT	ACTCCGTTCT	TCAAAGGCTA	CCGTCCGCAG	TTCTACTTCC	700
	GTACAACTGA	CGTGA CTGGC	ACCATCGAAC	TGCCGGAAGG	CGTAGAGATG	750
20	GTCATGCCGG	GCGACAACAT	CAAAATGGTT	GTTACCCTGA	TTCACCCGAT	800
	CGCGATGGAC	GATGGTCTGC	GTTTCGCA			828

25 2) INFORMATION FOR SEQ ID NO: 100

(i) SEQUENCE CHARACTERISTICS:

	(A)	LENGTH: 749 bases
	(B)	TYPE: Nucleic acid
30	(C)	STRANDEDNESS: Double
	(D)	TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

35 (vi) ORIGINAL SOURCE:

	(A)	ORGANISM: <i>Klebsiella oxytoca</i>
	(B)	STRAIN: ATCC 33496

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 100

40	GATGCCGCAG	ACTCGTGAGC	ACATCCTGCT	GGGTCGTCAG	GTAGGCGTTC	50
	CGTACATCAT	CGTGTTCTCTG	AACAAGTGCG	ACATGGTTGA	TGACGAAGAG	100
	CTGCTGGAAC	TGGTTGAAAT	GGAAGTTCGT	GAAC TTCTGT	CTCAGTACGA	150
	TTTCCCGGGC	GACGACACTC	CGATCGTTCTG	TGGTTCTGCT	CTGAAAGCGC	200
45	TGGAAGGCGA	CGCWGAGTGG	GAAKCKAAAA	TCATCGAACT	GGCTGGCTTC	250
	CTGGATTCTT	ACATTCCGGA	ACCAGAGCGT	GCGATTGACA	AGCCGTTCTT	300
	GCTGCCGATC	GAAGACGTAT	TCTCCATCTC	CGGTCGTGGT	ACCGTTGTTA	350
	CCGGTCGTGT	AGAGCGCGGT	ATCATCAAAG	TTGGCGAAGA	AGTTGAAATY	400
	GTTGGTATYA	AAGACACTGC	TAAGTCTACC	TGTA CTGGCG	TTGAAATGTT	450
50	CCGCAAACTG	CTGGACGAAG	GCCGYGCTGG	TGAGAACGTT	GGTGTTCTGC	500
	TGCGTGGTAT	CAAACGTGAA	GAAATCGAAC	GTGGTCAGGT	ACTGGCTAAG	550
	CCGGGCTCTA	TCAAGCCGCA	CACCAAGTTC	GAATCTGAAG	TTTATATCCT	600
	GTCCAAAGAC	GAAGGCGGCC	GTCACACTCC	GTTCTTCAAA	GGCTACCGTC	650
	CGCAGTTCTA	CTTCCGTACA	ACTGACGTGA	CTGGCACCAT	CGAACTGCCG	700
55	GAAGGCCGTAG	AGATGGTTAT	GCCGGGCGAC	AACATCAAAA	TGGTTGTTA	749

2) INFORMATION FOR SEQ ID NO: 101

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61

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 830 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 5 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 10 (A) ORGANISM: *Klebsiella planticola*
 (B) STRAIN: ATCC 33531

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 101

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15  TGGCGCGATC CTGGTTGTTG CTGCGACTGA CGGCCCGATG CCGCAGACTC      50
    GTGAGCACAT CCTGCTGGGT CGTCAGGTAG GCGTTCGGTA CATCATCGTG      100
    TTCCTGAACA AATGCGACAT GGTGATGAC GAAGAGCTGC TGGAACTGGT      150
    TGAAATGGAA GTTCGTGAGC TGCTGTCTCA GTACGACTTC CCGGGCGACG      200
    ACACTCCGAT CGTTCGTGGT TCCGCTCTGA AAGCGCTGGA AGGCGAAGCA      250
20  GACTGGGAAG CGAAAATCAT CGAACTGGCT GGCTACCTGG ATTCTTACAT      300
    CCCGGAACCA GAGCGTGCGA TTGACAAGCC GTTCCTGCTG CCTATCGAAG      350
    ACGTATTCTC CATCTCCGGT CGTGGTACCG TTGTTACCGG TCGTGTAGAG      400
    CGCGGTATCA TCAAAGTGGG CGAAGAAGTT GAAATCGTTG GTATCAAAGA      450
    TACTGCTAAR TCWACCTGTA CYGGCGTTGA AATGTTCCGC AAAGTGTCTG      500
25  ACGAAGGCCG TGCTGGTGAG AACGTTGGTG TTCTGCTGCG TGGTATCAAA      550
    CGTGAAGAAA TCGAACGTGG TCAGGTACTG GCTAAGCCGG GCTCTATCAA      600
    GCCGCACACC AAGTTCGAAT CTGAAGTGTA CATTCTGTCC AAAGACGAAG      650
    GCGGCCGTCA TACTCCGTTT TTCAAAGGCT ACCGTCCGCA GTTCTACTTC      700
    CGTACAACCTG ACGTGACTGG CACCATCGAA CTGCCGGAAG GCGTAGAGAT      750
30  GGTAATGCCG GCGGACAACA TCAAATGGT TGTTACCCTG ATTCACCCRA      800
    TCGCGATGGA CGACGGTCTG CGTTTCGCAA      830
  
```

35 2) INFORMATION FOR SEQ ID NO: 102

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 806 bases
 (B) TYPE: Nucleic acid
 40 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 45 (A) ORGANISM: *Klebsiella pneumoniae* subsp. *ozaenae*
 (B) STRAIN: ATCC 11296

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 102

```

50  CCTGGTTGTT GCTGCGACTG ACGGCCCGAT GCCGCAGACT CGTGAGCACA      50
    TCCTGCTGGG TCGTCAGGTA GCGTTCGGT ACATCATCGT GTTCCTGAAC      100
    AAATGCGACA TGGTTGATGA CGAAGAGCTG CTGGAAGTGG TTGAGATGGA      150
    AGTTCGTGAA CTGCTGTCTC AGTACGATTT CCCGGGCGAC GACACCCCGA      200
55  TCGTTCGTGG TTCTGCTCTG AAAGCGCTGG AAGGCGACGC AGAGTGGGAA      250
    GCGAAAATCA TCGAACTGGC TGGCCACCTG GATACCTATA TCCCGGAACC      300
    AGAGCGTGCG ATTGACAAGC CGTTCCTGCT GCCGATCGAA GACGTATTCT      350
    CCATCTCCGG TCGTGGTACC GTTGTTACCG GTCGTGTAGA GCGCGGTATC      400
    ATCAAAGTAG GTGAAGAAGT TGAATCGTT GGTATCAAAG AAACCGCGAA      450
60  AACCACCTGT ACTGGCGTTG AAATGTTCCG CAAACTGCTG GACGAAGGCC      500
  
```

GTGCTGGTGA GAACGTAGGT GTTCTGCTGC GTGGTATCAA ACGTGAAGAA 550
 ATCGAACGTG GTCAGGTACT GGCTAAGCCG GGCACCATCA ACCCGCACAC 600
 CAAGTTCGAA TCTGAAGTGT ACATCCTGTC CAAAGACGAA GGCGGCCGTC 650
 ATRACTCGTT CTTCAAAGGC TACCGTCCGC AGTTCTACTT CCGTACTACT 700
 5 GACGTGACTG GCACCATCGA ACTGCCGGAA GGCGTAGAGA TGGTAATGCC 750
 GGGCGACAAC ATCAAAATGG TTGTTACCCT GATCCACCCG ATCGCGATGG 800
 ACGACG 806

10

2)-INFORMATION FOR SEQ ID NO: 103

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 743 bases
 15 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

20

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Klebsiella pneumoniae* subsp. *pneumoniae*
 (B) STRAIN: ATCC 13883

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 103

GCAGACTCGT GAGCACATCC TGCTGGGTCG TCAGGTAGGC GTTCCGTACA 50
 TCATCGTGTT CCTGAACAAA TGCGACATGG TTGATGACGA AGAGCTGCTG 100
 GAACTGGTTG AGATGGAAGT TCGTGAAGTC CTGTCTCAGT ACGATTTCCC 150
 30 GGGCGACGAC ACTCCGATCG TTCGTGGTTC TGCTCTGAAA GCGCTGGAAG 200
 GCGACGCAGA GTGGGAAGCG AAAATCATCG AACTGGCTGG CCACCTGGAT 250
 ACCTATATCC CGGAACCAGA GCGTGCGATT GACAAGCCGT TCCTGCTGCC 300
 GATCGAAGAC GTATTCTCCA TCTCCGGTCG TGGTACCGTT GTTACCGGTC 350
 GTGTAGAGCG CGGTATCATC AAAGTAGGTG AAGAAGTTGA AATCGTTGGT 400
 35 ATCAAAGAAA CCGCGAAAAC CACCTGTACT GGCGTTGAAA TGTTCCGCAA 450
 ACTGCTGGAC GAAGGCCGTG CTGGTGAGAA CGTAGGTGTT CTGCTGCGTG 500
 GTATCAAACG TGAAGAAATC GAACGTGGTC AGGTACTGGC TAAGCCGGGC 550
 ACCATCAACC CGCACACCAA GTTCGAATCT GAAGTGTA TAAGCCGGGC 600
 AGACGAAGGC GGCCGTCACA CTCCGTTCTT CAAAGGCTAC CGTCCGCAGT 650
 40 TCTACTTCCG TACTACTGAC GTGACTGGCA CCATCGAACT GCCGGAAGGC 700
 GTAGAGATGG TAATGCCGGG CGACAACATC AAAATGGTTG TTA 743

45 2) INFORMATION FOR SEQ ID NO: 104

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 819 bases
 (B) TYPE: Nucleic acid
 50 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

55

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Klebsiella pneumoniae* subsp.
rhinoscleromatis
 (B) STRAIN: ATCC 13884

60

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 104

```

      TGGTTGTTGC TGC GACTGAC GGCCCGATGC CGCAGACTCG TGAGCACATC      50
      CTGCTGGGTC GTCAGGTAGG CGTTCCGTAC ATCATCGTGT TCCTGAACAA      100
      ATGCGACATG GTTGATGACG AAGAGCTGCT GGAAGTGGTT GAGATGGAAG      150
5     TTCGTGAAC TCTGTCTCAG TACGATTTCC CGGGCGACGA CACCCCGATC      200
      GTTCGTGGTT CTGCTCTGAA AGCGCTGGAA GGC GACGCAG AGTGGGAAGC      250
      GAAAATCATC GAACTGGCTG GCCACCTGGA TACCTATATC CCGGAACCAG      300
      AGCGTGCGAT TGACAAGCCG TTCCTGCTGC CGATCGAAGA CGTATTCTCC      350
      ATCTCCGGTC GTGGTACCGT TGT TACCGGT CGTGTAGAGC GCGGTATCAT      400
10    CAAAGTAGGT GAAGAAGTTG AAATCGTTGG TATCAAAGAA ACCGCGAAAA      450
      CCACCTGTAC TGGCGTTGAA ATGTTCCGCA AACTGCTGGA CGAAGGCCGT      500
      GCTGGTGAGA ACGTAGGTGT TCTGCTGCGT GGTATCAAAC GTGAAGAAAT      550
      CGAACGTGGT CAGGTACTGG CTAAGCCGGG CACCATCAAC CCGCACACCA      600
      AGTTCGAATC TGAAGTGTA ATCCTGTCCA AAGACGAAGG CGGCCGTCAC      650
15    ACTCCGTTCT TCAAAGGCTA CCGTCCGAG TTCTACTTCC GTACTACTGA      700
      CGT GACTGGC ACCATCGAAC TGCCGGAAGG CGTAGAGATG GTAATGCCGG      750
      GCGACAACAT CAAAATGGTT GTTACCCTGA TCCATCCGAT CGCGATGGAC      800
      GACGGTCTGC GTTTCGCAA      819

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20

2) INFORMATION FOR SEQ ID NO: 105

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 832 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

30 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Kluyvera ascorbata*
 (B) STRAIN: ATCC 33433

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 105

```

      CGGCGCGATC CTGGTTGTTG CTGCGACTGA TGGCCCTATG CCACAGACTC      50
      GTGAGCACAT CCTGCTGGGT CGTCAGGTAG GCGTTCCTTA CATCATCGTG      100
40    TTCCTGAACA AATGYGACAT GGTGATGAC GAAGAGCTGC TGGAAGTGGT      150
      TGAAATGGAA GTTCGTGAAC TTCTGTCTCA GTACGATTTC CCAGGCGACG      200
      ATACTCCAAT CATCCGTGGT TCTGCTCTGA AAGCGCTGGA AGGCGATGCA      250
      GAGTGGGAAG CGAAAATCAT CGAACTGGCT GGCTTCCTGG ATTCTTACAT      300
      CCCAGAACCA GAACGTGCTA TCGATAAGCC GTTCCTGCTG CCAATCGAAG      350
45    ACGTATTCTC CATCTCCGGT CGTGGTACCG TTGTTACCGG TCGGTAGAG      400
      CGCGGTATCA TCAAAGTTGG YGAAGAAGTT GAAATCGTTG GTATCAAAGA      450
      CACCGCTAAG TCTACCTGTA CCGGCGTTGA AATGTTCCGC AAATGCTGG      500
      ACGAAGGCCG TGCTGGTGAG AACGTTGGTG TTCTGCTGCG TGGTATCAA      550
      CGTGAAGAAA TCGAACGTGG TCAGGTTCTG GCTAAGCCAG GCTCTATCAA      600
50    GCCGCACACC AAGTTCGAAT CTGAAGTGTA CATTCTGTCC AAAGACGAAG      650
      GCGGCCGTCA TACTCCGTTT TTCAAAGGCT ACCGTCCACA GTTCTACTTC      700
      CGTACTACTG ACGTGACCGG TACCATCGAA CTGCCAGAAG GCGTTGAGAT      750
      GGTAATGCCA GCGACAACA TCAAGATGGT TGTGACTCTG ATCCACCCAA      800
      TCGCGATGGA CGACGGCCTG CGTTTCGCAA CC      832

```

55

2) INFORMATION FOR SEQ ID NO: 106

60 (i) SEQUENCE CHARACTERISTICS:

64

(A) LENGTH: 830 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

5

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Kluyvera cryocrescens*
 (B) STRAIN: ATCC 33435

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 106

	TGGCGCGATC	CTGGTTGTTG	CTGCAACTGA	TGGCCCTATG	CCACAGACTC	50
15	GTGAGCACAT	CCTGCTGGGT	CGTCAGGTAG	GCGTTCCTTA	CATCATCGTG	100
	TTCCTGAACA	AATGTGACAT	GGTTGATGAC	GAAGAGCTGC	TGGAAGTGGT	150
	TGAAATGGAA	GTTCGTGAAC	TTCTGTCTCA	GTACGATTTC	CCAGGCGACG	200
	ACACTCCTAT	CGTTCGTGGT	TCCGCGCTGA	AAGCGCTGGA	AGGCGACGCT	250
	GAGTGGGAAG	CAAAAATCAT	CGAACTGGCT	GGCTTCCTGG	ATTCTTACAT	300
20	CCCAGAACCA	GAGCGTGCGA	TTGATAAGCC	GTTCTGCTG	CCAATCGAAG	350
	ACGTATTCTC	CATCTCCGGT	CGTGGTACCG	TTGTTACCGG	TCGTGTAGAG	400
	CGCGGTATCA	TCAAAGTTGG	TGAAGAAGTT	GAAATCGTGG	GTATCAAAGA	450
	CACCTGTAAAG	TCTACCTGTA	CCGGCGTTGA	AATGTTCCGC	AAACTGCTGG	500
	ACGAAGGCCG	TGCTGGTGAG	AACGTTGGTG	TTCTGCTGCG	TGGTATCAAA	550
25	CGTGAAGAAA	TCGAACGTGG	TCAGGTTCTG	GCTAAGCCAG	GCTCCATCAA	600
	GCCGCACACC	AAATTCGAAT	CTGAAGTTTA	CATCCTGTCC	AAAGACGAAG	650
	GCGGCCGTCA	TACTCCGTTT	TTCAAAGGCT	ACCGTCCACA	GTTCTACTTC	700
	CGTACTACTG	ACGTGACTGG	TACCATCGAA	CTGCCAGAAG	GCGTAGAGAT	750
	GGTAATGCCG	GGCGACAACA	TCAAATGGT	TGTTACCCTG	ATCCACCCAA	800
30	TCGCGATGGA	CGACGGTCTG	CGTTTCGCAA			830

2) INFORMATION FOR SEQ ID NO: 107

35

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 826 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

40

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Kluyvera georgiana*
 (B) STRAIN: ATCC 51603

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 107

50	CGCGATCCTG	GTTGTTGCTG	CGACTGACGG	CCCGATGCCG	CAGACTCGTG	50
	AGCACATCCT	GCTGGGTCGT	CAGGTTGGCG	TTCCGTACAT	CATCGTGTTC	100
	CTGAACAAAT	GCGACATGGT	TGATGACGAA	GAGCTGCTGG	AACTGGTTGA	150
	AATGGAAGTT	CGTGAAC TTC	TGTCTCAGTA	CGACTTCCCG	GGCGACGACA	200
	CGCCGATCGT	TCGTGGTTCT	GCTCTGAAAG	CGCTGGAAGG	CGACGCTGAG	250
55	TGGGAAGCGA	AAATCATCGA	ACTGGCGGGC	TTCTTGGATT	CTTACATCCC	300
	GGAACCAGAG	CGTGCGATTG	ACAAGCCGTT	CCTGCTGCCG	ATCGAAGACG	350
	TATTCTCCAT	CTCCGGTCGT	GGTACCGTTG	TTACCGGTG	TGTAGAACGC	400
	GGTATCATCA	AAGTTGGCGA	AGAAGTTGAA	ATCGTTGGTA	TCAAAGACAC	450
	CGCTAAGTCT	ACCTGTACTG	GCGTTGAAAT	GTTCCGCAA	CTGCTGGACG	500
60	AAGGCCGTGC	TGGTGAGAAC	GTTGGTGTTC	TGCTGCGTGG	TATCAAACGT	550

```

GAAGAAATCG AACGTGGTCA GGTACTGGCT AAGCCGGGTT CTATCAAGCC      600
GCACACCAAG TTCGAATCTG AAGTGTACAT TCTGTCCAAA GACGAAGGCG      650
GCCGTCATAC TCCGTTCTTC AAAGGCTACC GTCCGCAGTT CTACTTCCGT      700
ACTACTGACG TGACTGGCAC CATCGAACTG CCGGAAGGCG TTGAGATGGT      750
5  AATGCCGGGC GACAACATCA AAATGGTTGT TACCCTGATC CACCCGATCG      800
   CGAAGGACGA AGGTCTGCGT TTCGCA                               826

```

10 2) INFORMATION FOR SEQ ID NO: 108

(i) SEQUENCE CHARACTERISTICS:

```

15  (A) LENGTH: 803 bases
    (B) TYPE: Nucleic acid
    (C) STRANDEDNESS: Double
    (D) TOPOLOGY: Linear

```

(ii) MOLECULE TYPE: Genomic DNA

20 (vi) ORIGINAL SOURCE:

```

    (A) ORGANISM: Lactobacillus casei subsp. casei
    (B) STRAIN: ATCC 393

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 108

```

25  GCTGCTGATG GCCCAATGCC ACAAACTCGT GAACATATCT TACTTTCACG      50
    TCAAGTTGGT GTTCCATACA TCGTTGTATT CATGAACAAA TGTGACATGG      100
    TTGACGATGA AGAATTACTA GAATTAGTTG AAATGGAAAT TCGTGATCTA      150
    TTAAGTGAAT ATGAATTCCT TGGCGATGAC ATTCCTGTAA TCAAAGGTTT      200
30  AGCTCTTAAA GCACTTCAAG GTGAAGCTGA CTGGGAAGCT AAAATTGACG      250
    AGTTAATGGA AGCTGTAGAT TCTTACATTC CAACTCCAGA ACGTGATACT      300
    GACAAACCAT TCATGATGCC AGTTGAGGAT GTATTCTCAA TCACTGGTCG      350
    TGGAACAGTT GCAACTGGAC GTGTTGAACG TGGACAAGTT AAAGTTGGTG      400
    ACCAAGTAGA AGTTATCGGT ATTGAAGAAG AGAGCAAAAA AGTAGTAGTA      450
35  ACTGGAGTAG AAATGTTCCG TAAATYACTA GATTACGCTG AAGCTGGCGA      500
    CAACATTGGC GCACTTCTAC GTGGTGTTGC TCGTGAAGAT ATCCAACGTG      550
    GTCAAGTATT AGCTAAACCA GGTTCGATTA CTCCACACAC TAACTTCAAA      600
    GCTGAAACTT ATGTTTTAAC TAAAGAAGAA GGTGGACGTC ACACTCCATT      650
    CTTCAACAAC TACCGCCAC AATTCTATTT CCGTACTACT GACGTAAGT      700
40  GTATTGTTAC ACTTCCAGAA GGTACTGAAA TGGTAATGCC TGGTGATAAC      750
    ATTGAGCTTG CAGTTGANCT AATTGCACCA ATCGCTATCG AAGACGGTAC      800
TAA~                               803

```

45

2) INFORMATION FOR SEQ ID NO: 109

(i) SEQUENCE CHARACTERISTICS:

```

50  (A) LENGTH: 825 bases
    (B) TYPE: Nucleic acid
    (C) STRANDEDNESS: Double
    (D) TOPOLOGY: Linear

```

(ii) MOLECULE TYPE: Genomic DNA

55

(vi) ORIGINAL SOURCE:

```

    (A) ORGANISM: Lactococcus lactis subsp. lactis
    (B) STRAIN: ATCC 19435

```

60 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 109

66

	CGGTGCAATC	CTCGTTGTTG	CTGCAACTGA	TGGACCAATG	CCACAAACTC	50
	GTGAACACAT	CTTGCTTTCA	CGTCAAGTTG	GTGTTAAATA	CCTTATCGTC	100
	TTCTTAACA	AGGCTGACCT	TGTTGATGAT	GAAGAATTGA	TGGAACCTCGT	150
5	TGAAATGGAA	GTTCGTGACC	TCTTGAGCGA	ATACGACTTC	CCAGGTGACG	200
	ATATTCTGT	AATCGCTGGT	TCAGCACTTG	GTGCTTTGAA	CGGTGAACCA	250
	CAATGGGTTG	CTAAAGTTGA	AGAATTGATG	GACATCGTTG	ATGAATACAT	300
	CCCAACTCCA	GAACGCGACA	CTGACAAACC	ACTCCTTCTT	CCAGTCGAAG	350
	ACGTATTCTC	TATCACTGGT	CGTGGTACAG	TTGCTTCAGG	ACGTATCGAA	400
10	CGTGGTACTG	TTAAAGTTGG	TGACGAAGTT	GAAATCGTTG	GTATCAAAGA	450
	AGAAACTAAA	AAAGCTGTTG	TTACTGGTAT	CGAAATGTTT	CGTAAAACAC	500
	TTACTGAAGG	TCTTGCTGGT	GATAACGTCG	GTGCACTTCT	CCGTGGTATC	550
	CAACGTGACG	AAATCGAACG	TGGTCAAGTT	ATTGCTAAAC	CAGGTTCAAT	600
	CACTCCACAC	AACTTTTTCG	AAGGTGAAGT	TTACGTATTG	AGCAAAGAAG	650
15	AAGGCGGACG	TCACACTCCA	TTCTTCGACA	ACTACCGTCC	TCAATTCTAC	700
	TTCCACACAA	CTGACGTTAC	TGGTTCAGTT	AACTTCCAG	AAGGAACTGA	750
	AATGGTAATG	CCTGGTGACA	ACGTGCATAT	CGACGTTGAA	TTGATCCACC	800
	CAGTTGCGAT	CGAACAAGGT	ACTAC			825

20

2) INFORMATION FOR SEQ ID NO: 110

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 824 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

30 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Leclercia adecarboxylata*
 (B) STRAIN: ATCC 23216

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 110

	GGCGCGATCC	TGGTTGTTGC	TGCGACTGAC	GGCCCAATGC	CTCAGACCCG	50
	TGAGCACATC	CTGCTGGGTC	GTCAGGTAGG	CGTTCCTTTC	ATCATCGTGT	100
40	TCCTGAACAA	ATGCGACATG	GTTGATGACG	AAGAGCTGCT	GGAAGTGGTT	150
	GAGATGGAAG	TTCGTGAACT	YCTGTCCCAG	TACGACTTCC	CGGGCGACGA	200
	CACCCCAATC	GTTCTGTGTT	CTGCGCTGAA	AGCGCTGGAA	GGCGAAGCAG	250
	AGTGGAAGA	GAAATCATC	GARCTGGCTG	GCTACCTGGA	TTCCTACATC	300
	CCAGAGCCAG	AGCGTGCGAT	TGACAAGCCG	TTCCTGCTGC	CTATCGAAGA	350
45	CGTATTCTCC	ATCTCCGGTC	GTGGTACCGT	TGTTACCGGT	CGTGTAGAGC	400
	GCGGTATCAT	CAARGTTGGC	GAAGAAGTTG	AAATCGTTGG	TATCAAGGAC	450
	ACTGCTAAGT	CTACCTGTAC	CGGCGTTGAA	ATGTTCCGCA	AACTGCTGGA	500
	CGAAGGCCGT	GCCGGTGAGA	ACGTTGGTGT	TCTGCTGCGT	GGTATCAAAC	550
	GTGAAGAAAT	CGAACGTGGT	CAGGTTCTGG	CTAAGCCAGG	CTCYATCAAG	600
50	CCGCACACCA	AGTTTCAATC	TGAAGTGTAC	ATCCTGTCYA	AAGACGAAGG	650
	CGGCCGTCAT	ACTCCGTTCT	TCAAAGGCTA	CCGTCCACAG	TTCTACTTCC	700
	GTACKACTGA	CGTGACCGGT	ACCATCGARC	TGCCAGAAGG	CGTTGAGATG	750
	GTAATGCCAG	GCGACAACAT	CAAATGGTT	GTTACCCTGA	TCCACCCAAT	800
	CGCAATGGAC	GATGGTCTGC	GTTC			824

55

2) INFORMATION FOR SEQ ID NO: 111

60 (i) SEQUENCE CHARACTERISTICS:

67

- (A) LENGTH: 838 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

5

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Legionella micdadei*
- (B) STRAIN: ATCC 33218

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 111

	CGGAGCGATA	TTAGTAGTAT	CAGCAGCGGA	TGGCCCAATG	CCTCAAACGA	50
15	GAGAGCACAT	ACTYTTATCC	CGSCAGGTAG	GTGTTCCCTA	TATAGTAGTG	100
	TTCTTAAACA	AAGCTGACAT	GGTGGATGAT	GCGGAGTTAT	TAGAATTAGT	150
	TGAAATGGAA	GTACGCGAYT	TGTTGAGCAG	CTATGAATTT	CCAGGAGATG	200
	AGATCCCGAT	TGTAGTTGGT	TCAGCATTAA	AAGCATTGGA	AGGCGATACG	250
	AGTGATATAG	GTGTACCAGC	GATTGAGAAG	TTAGTTGAGA	CGATGGATTTC	300
20	TTATATACCT	GAGCCGGTAA	GAAACATCGA	TAAAAGTTTC	TTGTTACCGA	350
	TCGAAGACGT	GTTCTCAATA	TCTGGACGAG	GAACAGTAGT	AACAGGACGT	400
	ATCGAAAGCG	GGATCATCAA	AGTTGGTGAG	GAAGTCGAGA	TTGTTGGTAT	450
	ACGTGACACT	CAAAAGACGA	CATGCACAGG	CGTTGAAATG	TTCCGTAAAT	500
	TACTTGACGA	AGGTCGAGCT	GGAGACAACG	TTGGTATATT	GCTACGTGGT	550
25	ACGAAGCGGG	ATGAAGTTGA	ACGCGGACAA	GTATTAGCTA	AGCCGGGAAG	600
	CATTAAACCG	CATACTAAAT	TTGAAGCTGA	AGTGTATGTG	TTGTCAAAAAG	650
	ATGAAGGTGG	ACGTCATACC	CCATTCTTTA	ACGGATATCG	GCCTCAATTT	700
	TACTTCAGGA	CCACAGACGT	AACTGGTTCT	TGTGATTTAC	CTGARGGTAT	750
	AGAAATGGTA	ATGCCAGGTG	ATAACGTCAA	GCTGATTGTT	AGCTTACACT	800
30	CACCGATTGC	TATGGACGAA	GGTTTGC GTT	TTGCAATC		838

2) INFORMATION FOR SEQ ID NO: 112

35

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 838 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

40

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Legionella pneumophila* subsp. *pneumophila*
- (B) STRAIN: ATCC 33152

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 112

50	CGGAGCGATA	CTGGTTGTAT	CAGCAGCTGA	TGGTCCTATG	CCACAAACGA	50
	GGGAACACAT	TCTATTGTCT	CGCCAGGTAG	GTGTTCCATA	TATTGTTGTG	100
	TTCATGAACA	AAGCGGATAT	GGTTGATGAC	CCTGAGTTAT	TAGAGTTAGT	150
	GGAAATGGAA	GTGCGAGATT	TATTAAGCAG	TTACGATTTC	CCAGGGGATG	200
	ACATACCTAT	TGTTGTTGGT	TCAGCTTTGA	AAGCATTGGA	AGGTGAAGAC	250
55	AGTGATATAG	GCGTTAAGGC	TATTGAGAAA	TTGGTTGAAA	CAATGGATTTC	300
	ATACATTTCCT	GAGCCAGTTA	GAAACATAGA	CAAGCCATTTC	TTGTTGCCGA	350
	TTGAAGACGT	ATTTTCAATT	TCTGGACGCG	GAACAGTGGT	AACTGGTCGT	400
	GTAGAGAGTG	GAATTGTTAA	AGTTGGTGAG	GAAGTTGAAA	TTGTTGGAAT	450
	AAGAGACACC	CAAAAGACGA	CTTGTACGGG	TGTTGAGATG	TTCCGTAAAT	500
60	TACTTGATGA	AGGTCGAGCT	GGTGATAACG	TTGGTGTGTT	ATTACGAGGT	550

ACGAAGCGAG ATGAAGTGGG GCGTGGACAG GTATTGGCGA AGCCAGGAAC 600
 CATCAAGCCA CACACCAAGT TTGAAGCAGA AGTGTATGTA TTATCCAAGG 650
 AAGAAGGCGG ACGTCACACT CCATTCTTTA ATGGATACCG TCCACAATTC 700
 TATTTTCAGAA CCACTGACGT GACAGGTACT TGTGACTTGC CATCAGGAGT 750
 5 TGAAATGGTA ATGCCTGGAG ATAATGTGCA ATTAGTTGTT AGCTTGCATG 800
 CTCCGATTGC GATGGATGAA GGTTTAAGAT TCGCAATT 838

10 2) INFORMATION FOR SEQ ID NO: 113

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 828 bases
 (B) TYPE: Nucleic acid
 15 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

20 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Leminorella grimontii*
 (B) STRAIN: ATCC 33999

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 113

25 GTGCAATCCT GGTAGTAGCA GCGACTGACG GCGCGATGCC TCAGACTCGC 50
 GAGCACATCC TGCTGGGTCG TCAGGTAGGC GTTCCGTACA TCATCGTATT 100
 CCTGAACAAG TGCGATATGG TTGATGACGA AGAGCTGCTG GAGCTGGTTG 150
 ARATGGAAGT TCGCGAACTG CTGTCTCAGT ACGACTTCCC GGGCGACGAC 200
 30 ACTCCGGTAG TCCGCGGTTT AGCGCTGAAA GCGCTGGAAG GCGAAGCCGA 250
 GTGGGAARCG AAAATCATCG AGCTGGCAGG CCMTCTGGAT ACTTATATCC 300
 CAGAACCTGA GCGTGCGATT GACAAGCCGT TCCTGCTGCC KATCGAAGAC 350
 GTATTCTCTA TCTCCGGCCG TGGTACCGTT GTTACCGGTC GTGTAGAGCG 400
 CGGCATCATC AAAGTCGGTG AAGAAGTGA AATCGTCGGT ATCAAAGATA 450
 35 CCACCAAGAC CACCTGTACC GGCCTTGAAA TGTTCCGTAA GCTGCTGGAC 500
 GAAGGCCGTG CGGGCGAGAA CGTGGGCGTT CTGCTGCGCG GTACCAAGCG 550
 TGACGAAATC GAACGTGGTC AAGTTCTGGC CAAGCCGGGC ACCATCACTC 600
 CTCACACCCA GTTCGTGTCA GAAGTGATA TCCTGAGCAA GGATGAAGGC 650
 GGCCGTCATA CTCCGTTCTT CAAAGGCTAC CGTCCTCAGT TCTACTTCCG 700
 40 TACGACTGAC GTGACAGGCA CCATCGAAGT GCCGGAAGGC GTAGAGATGG 750
 TAATGCCAGG CGACAACATT CAGATGACCG TAAGTCTGAT TGCGCCGATC 800
 GCAATGGACG AAGGTCTGCG CTTCGCAA 828

45

2) INFORMATION FOR SEQ ID NO: 114

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 826 bases
 50 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

55

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Leminorella richardii*
 (B) STRAIN: ATCC 33998

60 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 114

```

      GCTATCCTGG TTGTTGCTGC GACTGACGGC CCAATGCCTC AGACTCGTGA      50
      GCACATCCTG CTGGGTCGCC AGGTAGGCGT TCCTTACATC ATCGTGTTCC      100
      TGAACAAGTG CGACATGGTT GATGACGAAG AGCTGCTGGA ACTGGTAGAA      150
5     ATGGAAGTTC GTGAACTTCT GTCTCAATAC GACTTCCCGG GCGACGATAC      200
      GCCGGTTGTT CGCGGTTTCAG CGCTGAAAGC GCTGGAAGGT GACGCYGAGT      250
      GGGAARCGAA AATCATTGAA CTGGCGGAAT CCTTRGATAC TTAYATTCCA      300
      GAGCCAGAGC GTGCGATTGA CAAGCCGTTT CTGCTGCCTA TCGAAGACGT      350
      TTTCTCTATC TCTGGCCGTG GTACTGTAGT CACCGGTCGT GTAGAGCGCG      400
10    GCATCATCAA AGTTGGTGAA GAAGTGGAAG TCGTGGGAAT CAAAGACACC      450
      ACCAAGACCA CCTGTACTGG CGTTGAAATG TTCCGTAAGC TGCTGGACGA      500
      AGGCCGTGCA GGTGAGAACG TTGGTGTTCT GCTGCGYGGT ACTAAGCGTG      550
      ACGAAATCGA ACGTGGTCAG GTACTGGCTA AGCCAGGCAC CATCACTCCT      600
      CACACAGAAAT TCGTGTGAGA AGTGTATATC CTGAGCAAGG ATGAAGGCGG      650
15    YCGTCATACT CCGTTCTTCA AAGGCTACCG TCCTCAGTTC TACTTCCGTA      700
      CGACTGACGT GACCGGCACC ATCGAACTGC CAGAAGGCGT AGAGATGGTA      750
      ATGCCAGGCG ATAACATCCA GATGGTAGTT ACGCTGATTG CCCCAATCGC      800
      GATGGACGAA GGTCTGCGCT TCGCAA      826

```

20

2) INFORMATION FOR SEQ ID NO: 115

- (i) SEQUENCE CHARACTERISTICS:
- 25 (A) LENGTH: 843 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear
- 30 (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Leptospira interrogans*
(B) STRAIN: ATCC 23581

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 115

```

      TGCGGCGATT CTGTAGTAT CCGCAACTGA CGGACCTATG CCACAAACAA      50
      AAGAACATAT CCTTCTTGCT CGTCAGGTAG GTGTTCCATA TGTAATTGTA      100
40    TTCATTAACA AAGCAGATAT GCTTGCTGCT GACGAAAGAG CAGAAATGAT      150
      CGAAATGGTT GAGATGGACG TTCGTGAACT TCTCAATAAG TATAGCTTCC      200
      CAGGAGATAC AACTCCTATC GTTCAATGGTT CTGCGGTAAA AGCACATTGAG      250
      GGCGATGAAT CTGAAATTGG GATGCCTGCA ATTCTCAAAT TGATGGAAGC      300
      TCTGGATACT TTCGTTCCAA ATCCAAAACG TGTAATCGAC AAACCTTTCC      350
45    TTATGCCAGT AGAAGACGTT TTCTCGATCA CTGGTCGTGG AACTGTTGCA      400
      ACTGGAAGAG TGGAACAAGG TGTTTTGAAA GTGAACGACG AAGTTGAAAT      450
      TATCGGTATC CGCCCAACAA CAAAACTGT TGTTACCGGT ATCGAAATGT      500
      TCAGAAAAC TCTCGATCAA GCGGAAGCTG GCGACAACAT CGGCGCTCTT      550
      CTTCGTGGAA CTAAAAAAGA AGAAATCGAA AGAGGGCAAG TTCTTGCGAA      600
50    GCCAGTTTCT ATCACTCCTC AAAAAAGTT TGCCGCTGAG GTGTATGTAT      650
      TAACTAAGGA TGAAGGCGGA CGTCATACTC CGTTTATCAA TAACTACCGT      700
      CCTCAGTTTT ACTTTAGAAC AACTGACGTA ACCGGAGTTT GTAACCTTCC      750
      TAATGGTGTC GAAATGGTTA TGCCTGGTGA TAACGTTTCT TTGACGGTTG      800
      AATTGATTAG CCCGATCGCA ATGACAAGG GTCTTAAGTT CGC      843

```

55

2) INFORMATION FOR SEQ ID NO: 116

- 60 (i) SEQUENCE CHARACTERISTICS:

70

(A) LENGTH: 832 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

5

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Megamonas hypermegale*
 (B) STRAIN: ATCC 25560

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 116

	CGGTGCTATC	CTCGTTGTTA	GTGCTGCTGA	TGGTCCTATG	CCTCAGACTC	50
15	GTGAACACAT	CCTTCTCGCT	CGTCAGGTTG	GTGTTCCAGC	TATCGTTGTA	100
	TTCCTCAACA	AAGCTGACCA	GGTTGATGAC	CCTGAACTTC	TCGAACTTGT	150
	TGAAATGGAA	GTTCGTGAAC	TTCTTTCCAG	CTATGACTTC	CCAGGCGATG	200
	ACGTTCCAGT	AATCACTGGT	TCCGCTCTTC	AGGCTCTCGA	AGGCGACGAA	250
	GAAGCTAAAA	AGAAAATTCT	TGAATTAATG	GATGCTGTTG	ATGATTACAT	300
20	CCCAACTCCA	ACACGTGACA	CTGATAAACC	TTTCTTAATG	CCAGTTGAAG	350
	ACGTATTAC	AATTACTGGT	CGTGGTACTG	TTGCTACAGG	CCGTGTTGAA	400
	CGTGGCGAAC	TTAAACTTGG	TGACAGCGTT	GAAATCGTTG	GTCTTTCCGA	450
	TGAAAAGAAA	TCCACTACTG	TAAGTGGTAT	CGAAATGTTC	CGCAAAATGC	500
	TTGATAGCGC	TGTTGCTGGT	GATAACATCG	GTGCACTTCT	TCGTGGTATT	550
25	GACCGTAAAG	AAATCGAACG	TGGTCAAGTT	CTTGCTAAAC	CTGGCACAAT	600
	TCATCCACAC	AAAAAATTCA	AAGCTCAGGT	TTACGTATTA	ACTAAAGAAG	650
	AAGGTGGACG	TCATACTCCA	TTCTTCTCCA	ACTATCGTCC	ACAGTTCTAT	700
	TTCCGTACTA	CTGACGTTAC	TGGTGTTGTA	ACTCTTCCAG	AAGGTACTGA	750
	AATGGTTATG	CCTGGCGATA	ACATTGAAAT	GAGCATCGAA	CTCATCACTC	800
30	CAATCGCTAT	TGAAAAAGGT	CTTCGCTTCG	CT		832

2) INFORMATION FOR SEQ ID NO: 117

35

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 820 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

40

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Mitsuokella multacida*
 (B) STRAIN: ATCC 27723

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 117

50	TGGTGCTATC	CTCGTCGTTT	CCGCTGCTGA	TGGCCCCGATG	CCGCAGACGC	50
	GTGAGCACAT	CCTGCTCGCT	CGCCAGGTCG	GTGTTCCGGC	AATCGTTGTC	100
	TTCCTCAACA	AGGTTGACCA	GGTTGACGAT	CCGGAGCTCC	TCGAGCTCGT	150
	CGAGATGGAA	GTTCGCGAGC	TGCTCTCCAG	CTACGACTTC	CCGGGCGATG	200
	ACATCCCTGT	AATCGCTGGT	TCCGCTCTGA	AGGCCCTCGA	AGGCGACGAA	250
55	GAGCAGAAGA	AGAACATCCT	CAAGCTCATG	GAAGCTGTCT	ATGAGTACAT	300
	CCCACGCCC	GTCCGCGACA	ACGCTAAGCC	GTTCTTGATG	CCGGTCGAGG	350
	ATGTCTTCAC	GATCACGGGC	CGTGGTACGG	TTGCAACGGG	CCGCGTTGAG	400
	CGTGGTGAGC	TCAAGATGAA	CGATACGGTT	GAGATCGTTG	GTCTGCAGGA	450
	CGAGCCGCGT	CAGACGGTTG	TCACGGGCAT	CGAGATGTTT	CGCAAGATGC	500
60	TTGATTTCGC	TGAGGCTGGC	GATAACATCG	GTGCTCTGCT	CCGTGGTATC	550

GACCGCAAGG AGATCGAGCG TGGCCAGGTT CTCGCAAAGC CGGGCACGAT 600
 TCATCCGCAC ACGAAGTTCA AGGCTCAGGT CTATGTCCTG ACGAAAGAAG 650
 AAGGCGGCCG TCATACGCCG TTCTTCACGA ACTATCGCCC GCAGTTCTAC 700
 TTCCGCACGA CGGACGTAAC TGGCGTAGTC AAAGTGGCCG AAGGCACGGA 750
 5 GATGGTTATG CCTGGCGATA ACGTCGAGAT GGAAGTTGAG CTCATCACCC 800
 CGATCGCTAT CGAGAAGGGC 820

10 2) INFORMATION FOR SEQ ID NO: 118

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 831 bases
 (B) TYPE: Nucleic acid
 15 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

20 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Mobiluncus curtisii* subsp. *holmesii*
 (B) STRAIN: ATCC 35242

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 118

25 CGGCGCTATC CTCGTGGTGG CTGCTACTGA CGGTCCGATG GCTCAGACCA 50
 AGGAACACAT CCTGTTGGCT AAGCAGGTTG GCGTGCCCTC CATCCTGGTC 100
 GCTCTGAACA AGTGCGATTC TTCCGATGTG GACGAAGACA TGCTCGAAAT 150
 CGTCGAGGAC GAAATCCGCG ATGACCTGGA GAAGCAGGGC TTCGATCGTG 200
 30 ACTGCCCGAT TATCCACGTT TCCGCTCTGA AGGCCCTGGA AGGCGACCCC 250
 GAGTGGACCA AGAAGATTGA AGAGCTCATG GAAGCGGTCG ATACCTACAT 300
 TCCTGAGCCT GTTCGTGACC TCGACAAGCC GTTCTTGATG CCTATCGAAG 350
 ACGTCTTCAC CATTACTGGT CGCGGTACCG TAGTGACCGG TCGTGTGGAA 400
 CGCGGCAAGC TACCGTTGAA CGCCGAAGTG GAAATCGTAG GTATTCGTCC 450
 35 TACGCAAAAG ACCACCGTTA CCGGTATCGA AATGTTCCAC AAGTCCATGG 500
 ACGAAGCCTA CGCCGCGCAG AACTGTGGTC TGTGCTGCG TGGACCAAG 550
 CGTGAGGACG TTGAGCGCGG TCAGGTTGTC TGCATTCCTG GCTCCGTGAC 600
 CCCGCACACC AAGTTCGAGG GCAAGGTCTA CATCTTGAAG AAGGACGAAG 650
 GTGGACGTCA CAAGTCGTTT TACGACGGCT ACCGCCCCGA GTTCTTCTTC 700
 40 CGCACCACCG ACGTGACCGG TGTTATTAC CTGCCCCAAG GCACCGAAAT 750
 GGTATGCCT GCGACACCA CCGAAATTAG CGTTGAGCTG ATTCAGCCTA 800
 TCGCTATGGA GGAAGGTCTC GGCTTCGCTA T 831

45

2) INFORMATION FOR SEQ ID NO: 119

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 825 bases
 50 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

55

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Moellerella wisconsensis*
 (B) STRAIN: ATCC 35017

60 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 119

	GGTGCAATTC	TGGTTGTTGC	TGCAACTGAT	GGCCCTATGC	CACAGACTCG	50
	TGAGCACATC	CTGTTAGGTC	GTCAGGTTGG	CGTTCCTATC	ATCATCGTTT	100
	TCCTGAACAA	ATGTGACATG	GTAGACGACG	AAGAGCTGTT	AGAAGCTGGT	150
5	GAAATGGAAG	TCCGTGAGCT	GCTGTCTCAG	TACGATTTCC	CAGGCGATGA	200
	CACTCCAGTA	ATCCGTGGTT	CAGCGCTGAA	AGCTCTGGAA	GGCGAAGCTG	250
	AGTGGGAAGC	TAAAATCATT	GAAGTGGCAG	AAGCACTGGA	TTCTTATATC	300
	CCAGAGCCAG	AGCGTGACAT	TGATAAGCCA	TTCCTGTTAC	CAATCGAAGA	350
	CGTATTCTCA	ATTTCAAGCC	GTGGTACAGT	TGTTACTGGT	CGTGGTTGAGC	400
10	GTGGTATCGT	TAAAGTCGGT	GAAGAAGTTG	AAATCGTTGG	TATCAAAGAT	450
	ACCGTGAAAA	CAACATGTAC	TGGCGTTGAA	ATGTTCCGTA	AACTGCTGGA	500
	CGAAGGCCGT	GCTGGTGAGA	ACGTTGGTGT	TCTGCTGCGT	GGTACTAAAC	550
	GTGATGATAT	CGAACGTGGT	CAAGTATTGG	CTAAACCAGG	TTCAATCACT	600
	CCGCATACAA	CTTTCGAATC	AGAAGTTTAC	ATCCTGAGCA	AAGATGAAGG	650
15	TGGCCGTCAT	ACTCCATTCT	TCAAAGGTTA	CCGTCCACAG	TTCTACTTCC	700
	GTACAACCTGA	CGTAACCGGT	ACTATCGAAC	TGCCAGAAGG	CGTTGAGATG	750
	GTAATGCCAG	GTGATAACAT	CAAAATGATC	GTTACTCTGA	TCCACCCAAT	800
	TGCAATGGAT	GCAGGTCTGC	GTTTT			825

20

2) INFORMATION FOR SEQ ID NO:120

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 827 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

30 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Branhamella catarrhalis*
 (B) STRAIN: ATCC 43628

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 120

	TGGTGCTATC	TTGGTTGTTT	CTGCAACTGA	TGGTCCTATG	CCACAAACTC	50
	GTGAGCATAT	CCTACTATCT	CGTCAGGTTG	GTGTACCATA	CATCATGGTA	100
40	TTCATGAACA	AGTGCGATAT	GGTTGATGAT	GAAGAGCTAC	TAGAATTGGT	150
	TGAAATGGAA	GTTCTGTAAC	TTCTATCTGA	CTATGATTTC	CCTGGTGATG	200
	ATACCCCAAT	CATCAAAGGT	TCAGCACIAG	AAGCATTGAA	TGGTTCCTGAT	250
	GGTAAATATG	GCGAGCCTGC	AGTTCTAGAA	CTGCTAGACA	CACTAGACAG	300
	CTATATCCCA	GAGCCTGAGC	GTGATATCGA	TAAGTCATTC	TTGATGCCAA	350
45	TTGAAGATGT	CTTCTCGATC	TCAGGTCGTG	GTACAGTTGT	GAATGGTCGT	400
	GTTGAATCAG	GTATTATTAA	AGTTGGTGAT	GAAATTGAAA	TCATCGGTAT	450
	CAAACCAACT	GCTAAAACCA	CCTGTACTGG	TGTTGAAATG	TTCCGTAAAC	500
	TGTTAGACGA	AGGTCGTGCA	GGTGAGAACT	GTGGTATCTT	GTTGCGTGGT	550
	ACTAAGCGTG	AAGAAGTTCA	ACGCGGTCAA	GTAAGTTGCA	AACCAAGTTC	600
50	AATCACCCTA	CATACTAAGT	TTGATGCTGA	AGTTTATGTA	CTGTCAAAAG	650
	AAGAAGGTGG	TCGTACACAC	CCATTCTTAA	ATGGCTATCG	CCCACAGTTC	700
	TACTTCCGTA	CCACAGATGT	GACTGGTGCC	ATCACTCTAC	AAGAAGGTAC	750
	CGAAATGGTT	ATGCCTGGTG	ACAATGTTGA	GATGAGTGTT	GAGCTTATCC	800
	ACCCAATCGC	CAGGATAAAG	GTCTACG			827

55

2) INFORMATION FOR SEQ ID NO: 121

60 (i) SEQUENCE CHARACTERISTICS:

73

- (A) LENGTH: 806 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

5

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Morganella morganii* subsp. *morganii*
 (B) STRAIN: ATCC 25830

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 121

```

CGGCGCTATC CTGGTTGTTG CTGCAACTGA TGGCCCTATG CCACAGACCC      50
15 GTGAGCACAT CCTGTTAGGT CGTCAGGTTG GCGTTCCTTA CATCATCGTA      100
TTCCTGAACA AATGTGACAT GGTGTGATGAT GAAGAGCTGC TGGAACTGGT      150
TGAAATGGAA GTTCGTGAAC TTCTGTCTCA GTACGATTTC CCTGGCGACG      200
ACACGCCAAT CGTTCGCGGT TCAGCGCTGA AAGCACTGGA AGGCGAGCCA      250
GAGTGGGAAG CTAARATCGT TGAAGTGGCA GGTTCCTGG ATTCTTACAT      300
20 CCCTGAGCCA GAGCGTGCAA TTGACAAGCC GTTCCTGCTG CCAATCGAAG      350
ACGTATTCTC AATCTCCGGC CGTGGTACCG TTGTTACCGG TCGTGTGAG      400
CGCGGTATCA TCAAGGTTGG TGAGGAAGTT GAAATCGTGG GTATCAAAGA      450
TACTGCGAAA ACCACCTGTA CCGGTGTTGA AATGTTCCGC AAAGTGTGAG      500
ACGAAGGCCG TCGMGGTGAG AACGTCGGTG TTCTGCTGCG TGGTACCAAG      550
25 CGTGAAGAAA TCGAACGTGG TCAGGTTCTG GCTAAACCAG GTTCAATCAA      600
ACCACAYACC AAATTTGAAT CAGAAGTTTA TATTCTGAGC AAAGATGAAG      650
GTGGTCGTCA TACTCCATTC TTCAAAGGYT ACCGTCCACA GTTCTACTTC      700
CGTACCACAG ACGTAACAGG TACTATCGAA CTGCCGGAAG GCGTTGAAAT      750
GGTAATGCCG GCGACAACA TCAAATGAT CGTCACCCTG ATCCACCCAA      800
30 TCGCAA      806

```

2) INFORMATION FOR SEQ ID NO: 122

35

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 825 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

40

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Mycobacterium tuberculosis*
 (B) STRAIN: TB 299

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 122

```

50 GGTGCGATCC TGGTGGTCGC CGCCACCGAC GGCCCGATGC CCCAGACCCG      50
CGAGCACGTT CTGCTGGCGC GTCAAGTGGG TGTGCCCTAC ATCCTGGTAG      100
CGCTGAACAA GGCCGACGCA GTGGACGACG AGGAGCTGCT CGAACTCGTC      150
GAGATGGAGG TCCGCGAGCT GCTGGCTGCC CAGGAATTCG ACGAGGACGC      200
CCCGGTTGTG CGGGTCTCGG CGCTCAAGGC GCTCGAGGGT GACGCGAAGT      250
55 GGGTTGCCTC TGTCGAGGAA CTGATGAACG CGGTCGACGA GTCGATTCCG      300
GACCCGGTCC GCGAGACCGA CAAGCCGTTT CTGATGCCGG TCGAGGACGT      350
CTTCACCATC ACCGGCCGCG GAACCGTGGT CACCGGACGT GTGGAGCGCG      400
GCGTGATCAA CGTGAACGAG GAAGTTGAGA TCGTCGGCAT TCGCCATCG      450
ACCAACAAGA CCACCGTCAC CGGTGTGGAG ATGTTCCGCA AGCTGCTCGA      500
60 CCAGGGCCAG GCGGGCGACA ACGTTGGTTT GCTGCTGCGG GCGTCAAGC      550

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	GCGAGGACGT	CGAGCGTGGC	CAGGTTGTCA	CCAAGCCCCG	CACCACCACG	600
	CCGCACACCG	AGTTCGAAGG	CCAGGTCTAC	ATCCTGTCCA	AGGACGAGGG	650
	CGGCCGGCAC	ACGCCGTTCT	TCAACAATA	CCGTCCGCAG	TTCTACTTCC	700
	GCACCACCGA	CGTGACCGGT	GTGGTGACAC	TGCCGGAGGG	CACCGAGATG	750
5	GTGATGCCCC	GTGACAACAC	CAACATCTCG	GTGAAGTTGA	TCCAGCCCCG	800
	CGCCATGGAC	GAAGGTCTGC	GTTTC			825

10 2) INFORMATION FOR SEQ ID NO: 123

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 806 bases
 (B) TYPE: Nucleic acid
 15 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

20 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Neisseria cinerea*
 (B) STRAIN: ATCC 14685

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 123

25	CGGTGCGATC	TTGGTATGTT	CCGCAGCTGA	CGGTCCTATG	CCGCAAACTC	50
	GCGAACACAT	CCTGTTGGCC	CGCCAAGTAG	GTGTACCTTA	CATCATCGTG	100
	TTCATGAACA	AATGCGACAT	GGTTGACGAT	GCCGAGCTGT	TGGAGCTGGT	150
	TGAAATGGAA	ATCCGTGACT	TGCTGTCAAG	CTACGACTTC	CCAGGTGACG	200
30	ACTGCCCCGAT	CGTACAAGGT	TCTGCACTGA	AAGCCTTGGA	AGGCGACGCA	250
	GCTTACGAAG	AAAAAATCTT	CGAATTGGCT	GCTGCATTGG	ACAGCTACAT	300
	CCCAACACCT	GAGCGTGCAG	TGGACAAACC	TTTCTTGTTG	CCTATCGAAG	350
	ACGTATTCTC	TATTTCCGGT	CGCGGTACAG	TAGTAACCGG	TCGTGTAGAG	400
	CGCGGTATCA	TCCACGTTGG	TGACGAGATC	GAAATCGTAG	GTCTGAAAGA	450
35	AACTCAAAAA	ACCACTTGTA	CCGGTGTTGA	AATGTTCCGC	AAACTGCTGG	500
	ACGAAGGTCA	AGCTGGTGAC	AACGTAGGTG	TATTGCTGCG	TGGTACTAAA	550
	CGTGAAGACG	TAGAGCGTGG	TCAAGTATTG	GCTAAACCGG	GTACTATCAC	600
	TCCTCACACC	AAGTTCAAAG	CAGAAGTATA	CGTACTGAGC	AAAGAAGAGG	650
	GTGGTCGTCA	CACTCCGTTT	TTCGCTAACT	ACCGTCCACA	ATTCTACTTC	700
40	CGTACTACCG	ACGTAACCGG	CGCGGTTACT	TTGGAAGAAG	GTGTAGAAAT	750
	GGTAATGCCG	GGTGAGAACG	TAACCATTAC	TGTAGAACTG	ATTGCGCCTA	800
	TCGCTA					806

45

2) INFORMATION FOR SEQ ID NO: 124

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 822 bases
 50 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

55

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Neisseria elongata* subsp. *elongata*
 (B) STRAIN: ATCC 25295

60

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 124

75

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CGGCGCAATC TTGGTATGTT CCGCTGCTGA CGGTCCTATG CCGCAAACCT 50
GCGAACACAT CCTGTTGGCC CGCCAAGTAG GCGTACCTTA CATCATCGTG 100
TTCATGAATA AATGCGACAT GGTGAYGAT GCCGAACTGC TGGAAGTGGT 150
5  TGAAATGGAA ATCCGTGACT TGCTGTCAAG CTACGACTTC CCAGGCGACG 200
ACTGCCCCGAT CGTACAAGGT TCCGCACTGA AAGCCTTGGG AGGCGACGCA 250
GCTTACGAAG AAAAAATCTT CGAACTGGCT GCTGCATTGG ACAGCTACAT 300
CCCCGACACCT GAGCGTGCCG TGGACAAACC GTTCCTGTTG CCTATCGAAG 350
ACGTATTCTC TATCTCCGGC CGTGGTACAG TAGTAACCGG TCGTGTAGAG 400
10 CGCGGTATCA TCCACGTCGG TGACGAGATC GAAATCGTAG GTCTGAAAGA 450
-----AACECAAAAA-AGCACTTGTA-CCGGTGTGTA-AATGTTCCGC-AAAETGCTGG-----500-----
ACGAAGGTCA AGCAGGTGAC AACGTAGGCG TATTGCTGCG CGGTACCAAA 550
CGTGAAGAAG TGGAACGCGG TCAAGTATTG GCTAAACCGG GTACCATCAC 600
TCCTCACACC AAATTCAAAG CAGAAGTTTA CGTATTGAGC AAAGAAGAGG 650
15 GTGGTCGTCA TACTCCGTTT TTCGCTAACT ACCGTCCACA ATTCTACTTC 700
CGTACTACCG ACGTAACCGG TCGCGTTACT TTGGAAGAAG GTGTAGAAAT 750
GGTTATGCCT GGTGAGAACG TGGCCATCAC TGTAGAACTG ATTGACACCTA 800
TCGCTATGGA AGAAGGTCTG CG 822

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20

2) INFORMATION FOR SEQ ID NO: 125

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25 (i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 820 bases
    (B) TYPE: Nucleic acid
    (C) STRANDEDNESS: Double
    (D) TOPOLOGY: Linear

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30 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

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    (A) ORGANISM: Neisseria flavescens
    (B) STRAIN: ATCC 13120

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35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 125

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CGGCGCGACT TGGTATGTTT CGCAGCTGAC GGTCTCTATG CGCAAACCCG 50
CGAACACATC CTGTTGGCTC GCCAAGTAGG TGTACCTTAC ATCATCGTAT 100
40 TCATGAACAA ATGCGACATG GTAGACGATG CCGAGCTGTT GGAAGTGGTT 150
GAAATGGAAA TTCGTGACTT GTTGTCAGC TACGACTTCC CAGGCGACGA 200
-----CTGCCCAATC GTACAAGGTT CTGCACTGAA AGCTTTGGAA GGTGATGCTG-----250-----
CTTACGAAGA AAAAAATCTT GAATTGGCTG CTGCCTTGGA CAGCTACATC 300
CCAACACCTG AGCGTGCTGT GGACAAACCT TTCTTGTTGC CTATCGAAGA 350
45 CGTATTCTCT ATCTCTGGTC GTGGTACAGT AGTAACCGGT CGCGTAGAGC 400
GCGGTATCAT CCACGTTGGT GACGAGATCG AAATCGTAGG TCTGAAAGAA 450
ACTCAAAAAA CCACTTGTAC CGGCGTTGAA ATGTTCCGCA AACTGCTGGA 500
CGAAGGTCAA GCAGGTGACA ACGTAGGCGT ATTGCTGCGT GGTACTAAAC 550
GTGAAGACGT AGAGCGTGGT CAAGTATTGG CTAAACCAGG TACCATCACT 600
50 CCTCACACCA AATTCAAAGC AGAAGTATAC GTACTGAGCA AAGAAGAGGG 650
TGGTCGTAC ACTCCATTTT TCGCTAACTA CCGTCCACAA TTCTACTTCC 700
GTACTACCGA CGTAACTGGT GCAGTTACTT TGGAAGAAGG CGTAGAAATG 750
GTAATGCCAG GTGAGAACGT AACCATTACT GTAGAACTGA TTGCGCCAAT 800
CGCTATGGAA GAAGTCTGCG 822

```

55

2) INFORMATION FOR SEQ ID NO: 126

60 (i) SEQUENCE CHARACTERISTICS:

76

- (A) LENGTH: 830 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

5

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Neisseria gonorrhoeae*
 (B) STRAIN: ATCC 49226

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 126

	GGTGCAATCC	TGGTATGTT	TGCTGCCGAC	GGCCCTATGC	CGCAAACCCG	50
15	CGAACACATC	CTGCTGGCCC	GTCAAGTAGG	CGTACCTTAC	ATCATCGTGT	100
	TCATGAACAA	ATGCGACATG	GTCGACGATG	CCGAGCTGTT	GGAAGTGGT	150
	GAAATGGAAA	TCCGCGACCT	GCTGTCCAGC	TACGACTTCC	CCGGCGACGA	200
	CTGCCCAGATC	GTACAAGGTT	CCGCACTGAA	AGCCTTGGA	GGCGATGCCG	250
	CTTACGAAGA	AAAAATCTTC	GAAGTGGCTA	CCGCATTGGA	CAGCTACATC	300
20	CCGACTCCCG	AGCGTGCCGT	GGACAAACCA	TTCCTGCTGC	CTATCGAAGA	350
	CGTGTTCTCC	ATTTCGGGCC	GCGGTACCGT	AGTCACCGGC	CGTGTAGAGC	400
	GAGGTATCAT	CCACGTTGGT	GACGAGATTG	AAATCGTCGG	TCTGAAAGAA	450
	ACCCAAAAAA	CCACCTGTAC	CGGCGTTGAA	ATGTTCCGCA	AACTGCTGGA	500
	CGAAGGTCAG	GCGGGCGACA	ACGTAGGCGT	ATTGCTGCGC	GGTACCAAAC	550
25	GTGAAGACGT	AGAACGCGGT	CAGGTATTGG	CCAAACCGGG	TACTATCACT	600
	CCTCACACCA	AGTTCAAAGC	AGAAGTGATC	GTATTGAGCA	AAGAAGAGGG	650
	CGGCCGCCAT	ACCCCGTTTT	TCGCCAACTA	CCGTCCCCAA	TTCTACTTCC	700
	GTACCACTGA	CGTAACCGGC	GCGGTTACTT	TGAAAAAAGG	TGTGGAAATG	750
	GTAATGCCGG	GTGAGAACGT	AACCATTACT	GTAGAACTGA	TTGCGCCTAT	800
30	CGCTATGGAA	GAAGGTCTGC	GCTTTGCGAT			830

2) INFORMATION FOR SEQ ID NO: 127

35

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 816 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

40

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Neisseria lactamica*
 (B) STRAIN: ATCC 23970

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 127

50	CGGCGCAATC	TTGGTATGTT	CCGCCGCCGA	CGGCCCTATG	CCGCAAACCC	50
	GCGAACACAT	TCTGTTGGCC	CGCCAAGTAG	GTGTACCTTA	CATCATCGTA	100
	TTCATGAACA	AATGCGATAT	GGTCGACGAT	GCCGAGCTGT	TGGAAGTGGT	150
	TGAAATGGAA	ATCCGCGACC	TGCTGTCAAG	CTACGACTTC	CCAGGCGACG	200
	ACTGCCCAAT	CGTACAAGGT	TCCGCACTGA	AAGCTTTGGA	AGGCGATGCC	250
55	GCTTACGAAG	AAAAAATCTT	CGAACTGGCT	GCCGCATTGG	ACAGCTACAT	300
	CCCGACTCCC	GAGCGTGCCG	TGGACAAACC	GTTCTGCTG	CCTATCGAAG	350
	ACGTATTCTC	CATCTCCGGC	CGCGGTACGG	TAGTAACCGG	CCGTGTAGAG	400
	CGCGGTGTCA	TCCACGTTGG	CGACGAGATC	GAAATCGTCG	GTCTGAAAGA	450
	AACCCAAAAA	ACCACCTGTA	CCGGTGTCGA	GATGTTCCGC	AAACTGCTGG	500
60	ACGAAGGTCA	GGCAGGCGAC	AACGTAGGCG	TATTGCTGCG	CGGTACCAAA	550

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      CGTGAAGAAG TGGAACGCGG TCAGGTATTA GCCAAACCGG GTACCATCAC      600
      TCCGCACACC AAGTTCAAAG CAGAAGTGTA TGTATTGAGC AAAGAAGAGG      650
      GCGGTCGTCA CACTCCGTTC TTCGCCAACT ACCGTCCGCA ATTCTACTTC      700
      CGTACCACCG ACCTAACCAG CGCGGTTACT TTGGAAGAAG GCGTGGAAT      750
5     GGTAAATGCC GGTGAGAACG TAACCATTAC TGTAGAACTG ATTGCGCCTA      800
      TCGCTATGGA AGAAGG      816

```

10 2) INFORMATION FOR SEQ ID NO: 128

(i) SEQUENCE CHARACTERISTICS:

```

      (A) LENGTH: 831 bases
      (B) TYPE: Nucleic acid
15     (C) STRANDEDNESS: Double
      (D) TOPOLOGY: Linear

```

(ii) MOLECULE TYPE: Genomic DNA

20 (vi) ORIGINAL SOURCE:

```

      (A) ORGANISM: Neisseria meningitidis
      (B) STRAIN: ATCC 13077

```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 128

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25     CCGTGCAATC CTGGTATGTT CCGCAGCCGA CCGTCCTATG CCGCAAACCC      50
      GCGAACACAT CCTGCTGGCC CGTCAAGTAG GCGTACCTTA CATCATCGTG      100
      TTCATGAACA AATGCGACAT GGTGACGAT GCCGAGCTGT TGGAAGTGGT      150
      TGAAATGGAA ATCCGCGACC TGCTGTCCAG CTACGACTTC CCCGGCGACG      200
30     ACTGCCCCGAT CGTACAAGGT TCCGCACTGA AAGCCTTGA AGGCGATGCC      250
      GCTTACGAAG AAAAAATCTT CGAATTGGCT GCTGCATTGG ACAGCTACAT      300
      CCCGACTCCC GAGCGTGCCG TGGACAAACC TTTCTTGTG CCTATCGAAG      350
      ACGTATTCTC TATTTCGGT CGTGGTACG TAGTAACCGG TCGTGTAGAG      400
      CGCGGTATCA TCCACGTCGG TGACGAGATC GAAATCGTCG GTCTGAAAGA      450
35     AACTCAAAAA ACCACTTGTA CCGGTGTTGA AATGTTCCGC AAAGTCTGG      500
      ACGAAGGTCA AGCAGGCGAC AACGTAGGCG TATTGCTGCG CGGTACCAAA      550
      CGTGAAGACG TAGAGCGTGG TCAAGTATTG GCTAAACCGG GTACAATCAC      600
      TCCTCACACC AAGTTCAAAG CAGAAGTATA CGTACTGAGC AAAGAAGAGG      650
      GCGGCCGCCA TACCCCGTTC TTCGCCAACT ACCGTCCCCA ATTCTACTTC      700
40     CGTACCACCG ACCTAACCAG CGCGGTTACT TTGGAAGAAG GTGTGGAAT      750
      GGTAAATGCC GGCAGAGAACG TAACCATTAC CTAGAACTG ATTGCGCCTA      800
      TCGCTATGGA AGAAGGTTTG CGCTTTGCGA T

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831

45

2) INFORMATION FOR SEQ ID NO: 129

(i) SEQUENCE CHARACTERISTICS:

```

      (A) LENGTH: 815 bases
50     (B) TYPE: Nucleic acid
      (C) STRANDEDNESS: Double
      (D) TOPOLOGY: Linear

```

(ii) MOLECULE TYPE: Genomic DNA

55

(vi) ORIGINAL SOURCE:

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      (A) ORGANISM: Neisseria mucosa
      (B) STRAIN: ATCC 19696

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60 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 129

78

	CGGCGCAATC	TTGGTATGTT	CTGCTGCTGA	CGGTCCTATG	CCGCAAACCC	50
	GYGAACACAT	CCTGTTGGCC	CGTCAAGTAG	GYGTACCTTA	CATCATCGTG	100
	TTCATGAACA	AATGCGACAT	GGTTGACGAT	GCCGAAYTGT	TGGAACCTGGT	150
5	TGAAATGGAA	ATCCGTGACT	TGCTGTCAAG	CTACGACTTC	CCTGGYGACG	200
	ACTGCCCCGAT	TGTACAAGGT	TCTGCACTGA	AAGCCTTGGA	AGGCGATGCC	250
	GCTTACGAAG	AAAAAATCTT	CGAACTGGCT	GCCGCATTGG	ACAGCTACAT	300
	CCCGACTCCC	GAGCGTGCCG	TAGACAAACC	GTTCTGTGTG	CCTATCGAAG	350
	ACGTATTCTC	CATCTCCGGT	CGTGGTACAG	TAGTAACCGG	CCGTGTAGAG	400
10	CGCGGTGTTA	TCCACGTTGG	TGACGAGATC	GAAATCGTAG	GTCTGAAAGA	450
	AACCCAAAAA	ACCACATGTA	CCGGTGTGTA	AATGTTCCGC	AACTGCTGG	500
	ACGAAGGTCA	AGCCGGTGAC	AACGTAGGCG	TATTGCTGCG	CGGTACCAAA	550
	CGTGAAGAAG	TGGAACGCGG	TCAAGTATTG	GCTAAACCGG	GTACCATCAC	600
	TCCGCACACC	AAATTCAAAG	CAGAAGTGTA	CGTATTGAGC	AAAGAAGAGG	650
15	GTGGTCGTCA	TACTCCGTTC	TTCGCTAACT	ACCGTCCTCA	ATTCTACTTC	700
	CGTACTACCG	ACGTAACCGG	TGCGGTTACT	TTGGAAGAAG	GTGTAGAAAT	750
	GGTTATGCCT	GGTGAGAAAG	TAGCCATYAC	TGTAGAACTG	ATTGCGCCTA	800
	TYGCTATGGA	AGAAG				815

20

2) INFORMATION FOR SEQ ID NO: 130

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 829 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

30 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Neisseria sicca*
 (B) STRAIN: ATCC 9913

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 130

	GGCGCAATCT	TGGTATGTTT	CGCTGCTGAC	GGTCCTATGC	CGCAAACCCG	50
	CGAACACATC	CTGTTGGCCC	GCCAAGTAGG	CGTACCTTAC	ATCATCGTGT	100
40	TCATGAACAA	ATGCGACATG	GTTGACGATG	CCGAGCTGTT	GGAAGTGGTT	150
	GAAATGGAAA	TCCGTGACTT	GCTGTCAAGC	TACGACTTCC	CTGGTGACGA	200
	CTGCCCCGATC	GTACAAGGTT	CTGCACTGAA	AGCCTTGGA	GGCGACGCCG	250
	CTTACGAAGA	AAAAATCTTC	GAAGTGGCTG	CTGCATTGGA	CAGCTACATC	300
	CCGACTCCTG	AGCGTGCCGT	GGACAAACCG	TTCCTGTTGC	CTATTGAAGA	350
45	CGTATTCTCC	ATCTCCGGTC	GCGGTACCGT	AGTAACCGGC	CGTGTAGAGC	400
	GCGGTGTTAT	CCACGTTGGT	GACGAGATTG	AAATCGTAGG	TCTGAAAGAA	450
	ACCCAAAAAA	CCACTTGTAC	CGGTGTTGAA	ATGTTCCGCA	AACTGCTGGA	500
	CGAAGGTCAA	GCCGGTGACA	ACGTAGGCGT	ATTGCTGCGC	GGTACCAAAC	550
	GTGAAGAAGT	GGAACGCGGT	CAAGTATTGG	CTAAACCGGG	TACCATCACT	600
50	CCTCACACTA	AATTCAAAGC	AGAAGTTTAC	GTATTGAGTA	AAGAAGAGGG	650
	TGGTCGTCAT	ACTCCGTTCT	TCGCTAACTA	CCGTCCTCAA	TTCTACTTCC	700
	GTACTACCGA	CGTAACCGGC	GCGGTTACTT	TGGAAGAAGG	TGTAGAAATG	750
	GTTATGCCTG	GTGAGAACGT	AGCCATCACT	GTAGAAGTGA	TTGCACCGAT	800
55	CGCTATGGAA	GAAGGTCTGC	GCTTTGCGA			829

2) INFORMATION FOR SEQ ID NO: 131

60 (i) SEQUENCE CHARACTERISTICS:

79

- (A) LENGTH: 814 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

5

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Neisseria subflava*
 (B) STRAIN: ATCC 14221

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 131

	CGGCGCGACT	TGGTATGTTT	CGCAGCTGAT	GGTCCTATGC	CTCAAACCTCG	50
15	CGAACACATC	CTGTTGGCTC	GCCAAGTAGG	TGTACCTTAC	ATCATCGTAT	100
	TCATGAACAA	ATGCGACATG	GTTGACGATG	CCGAGCTGTT	GGAACCTGGTT	150
	GAAATGGAAA	TCCGTGACCT	GTTGTCAAGC	TACGACTTCC	CAGGCGACGA	200
	CTGCCCAATC	GTACAAGGTT	CTGCACTGAA	AGCTTTGGAA	GGTGACGCTG	250
	GTTACGAAGA	GAAAATCTTC	GAATTGGCTG	CTGCTCTGGA	CAGCTACATC	300
20	CCAACACCTG	AGCGTGCTGT	GGACAAACCT	TTCTTGTTGC	CTATCGAAGA	350
	CGTATTCTCT	ATCTCTGGCC	GTGGTACAGT	AGTAACTGGT	CGTGTAGAGC	400
	GCGGTATCAT	CCACGTTGGT	GACGAGATCG	AAATCGTAGG	TCTGAAAGAA	450
	ACCCAAAAAA	CCACTTGTAC	CGGCGTTGAA	ATGTTCCGCA	AACTGCTGGA	500
	CGAAGGTCAA	GCTGGTGACA	ACGTAGGCGT	ATTGCTGCGT	GGTACCAAAC	550
25	GTGAAGACGT	AGAGCGTGGT	CAAGTATTGG	CTAAACCAGG	TACCATTACT	600
	CCTCACACCA	AATTCAAAGC	AGAAGTATAC	GTACTGAGCA	AAGAAGAGGG	650
	TGGTCGTCAC	ACTCCATTCT	TCGCTAACTA	CCGTCCACAA	TTCTACTTCC	700
	GTACTACTGA	CGTAACTGGT	GCAGTTACTT	TGGAAGAAGG	CGTAGAAATG	750
	GTAATGCCAG	GTGAGAACGT	AACCATTACT	GTAGAACTGA	TTGCGCCTAT	800
30	CGCTATGGAA	GAAG				814

2) INFORMATION FOR SEQ ID NO: 132

35

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 818 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

40

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Neisseria weaveri*
 (B) STRAIN: ATCC 51223

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 132

50	GCCATCTTGG	TATGTTCTGC	TGCTGACGGT	CCTATGCCGC	AAACCCGTGA	50
	GCACATCCTG	TTGGCTCGTC	AAGTAGGTGT	ACCCTACATC	ATCGTATTCA	100
	TGAACAAATG	CGATATGGTT	GATGATGCAG	AGCTGCTGGA	ATTGGTAGAA	150
	ATGGAAATCC	GTGATCTGCT	GAGCAGCTAC	GATTTCCCTG	GCGATGATTG	200
	YCCAATCGTG	CAAGGTTCTG	CTTTGAAAGC	TTTGGAAGGT	GATGCCGCTT	250
55	ACGAAGAAAA	AATCTTTGAA	TTAGCTGCTG	CATTGGATAG	CTATATTCCA	300
	ACWCTGAGC	GYGCTGTTGA	TAAACCATTC	CTGTTGCCGA	TTGAAGATGT	350
	ATTCTCAATT	TCAGGTCGTG	GTACAGTAGT	AACTGGTCGT	GTAAGACGCG	400
	GTATTATTCA	CGTAGGCGAT	GAAATTGAAA	TTGTAGGTTT	GAAAGARACY	450
	CAAAAACTA	CTTGTACCGG	CGTTGAAATG	TTCCGTAAAT	TGCTGGATSA	500
60	AGGTCAGGCT	GGTGATAACG	TAGGCGTATT	GTTGCGTGGT	ACCAAACGTG	550

80

AAGACGTTGA GCGTGCTCAA GTATTGGCTA AGCCTGGTWC TATTACTCCG 600
 CAYACCAAAT TCAAAGCAGA RGTKTATGTW TTGAGYAAGG AAGAAGGCCG 650
 TCGTCATACT CCGTTCTTCG CTAACATATCG TCCGCAATTC TATTTCCGTA 700
 CTACAGACGT TACCGGTGCK GTRACTTTAG AAGAAGGTGT GGAAATGGTA 750
 5 ATGCCTGGTG AGAAYGTTGC CATTACTGTW GARYTGATYG CTCCGATTGC 800
 KATGGAAGAA GGYTGCGT 818

10 2) INFORMATION FOR SEQ ID NO: 133

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 836 bases
 (B) TYPE: Nucleic acid
 15 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

20 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Ochrobactrum anthropi*
 (B) STRAIN: ATCC 49188

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 133

25 CGGCGCAATT CTGGTTGTTT CGGCCGCTGA CGGCCCGATG CCGCAGACCC 50
 GTGAGCACAT CCTGCTCGCT CGTCAGGTTG GCGTTCCGCGC AATCGTCGTG 100
 TTCCTGAACA AGTGCGACCA GGTTGACGAT GCAGAACTGC TCGAACTGGT 150
 TGAAGTGGAA GTTCGCGAAC TTCTGTGCGAA ATACGATTTC CCGGGCGACG 200
 30 AAGTTCCGAT CATCAAGGGC TCGGCTCTTG CTGCTCTGGA AGATTCTTCG 250
 AAGGAACTGG GCGAAGACGC CGTTCGTTTCG CTGATGGCCG CTGTTGACGA 300
 CTACATTCCG ACCCCGGAAC GTCCGATCGA CCAGCCGTTT CTGATGCCGA 350
 TCGAAGACGT TTTCTCGATC TCGGGCCGTG GTACGGTTGT GACGGGTCCG 400
 GTTGAGCGCG GTATCGTCAA GGTTGGTGAA GAAGTTGAAA TCGTCGGCAT 450
 35 CAAGGCGACG GCGAAGACGA CGGTAACCGG CGTTGAAATG TTCCGCAAGC 500
 TGCTCGAYCA GGGCCAGGCT GCGGACAACA TCGGCGCTCT GATCCGCGGC 550
 GTTGGCCGTG AAGACGTTGA ACGCGGCCAG GTTCTCTGCA AGCCGGGTTT 600
 TGTGAAGCCG CACACCAAGT TCAAGGCAGA AGCCTACATT CTGACCAAGG 650
 ACGAAGGTGG CCGTCATACG CCGTTCTTTA CGAACTACCG TCCGCAGTTC 700
 40 TACTTCCGCA CGACGGACGT GACCGGTGTT GTCACGCTGC CGGAAGGCAC 750
 GGAAATGGTT ATGCCTGGCG ACAACGTGCG TATGGACGTC ACCCTGATCG 800
 TGCCGATCGC CATGGAAGAG AAGCTCCGCT TCGCTA 836

45

2) INFORMATION FOR SEQ ID NO: 134

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 805 bases
 50 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

55

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Pantoea agglomerans*
 (B) STRAIN: ATCC 27155

60 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 134

81

	CCTGGTTGTT	GCTGCGACTG	ATGGCCCAAT	GCCACAGACC	CGTGAGCACA	50
	TCCTGCTGGG	TCGTCAGGTT	GGCGTTCCTT	ACATCATCGT	GTTCTCTGAAC	100
	AAGTGTGACA	TGGTTGATGA	TGAAGAGCTG	CTGGAAGTGG	TAGAGATGGA	150
5	AGTACGTGAC	CTGCTGTCAC	AGTACGACTT	CCCAGGCGAT	GACACCCCGA	200
	TCGTTCTGG	TTCTGCTCTG	AAAGCGCTGG	AAGGCGTTCC	TGAGTGGGAA	250
	GCAAAAATCG	TTGAGCTGGC	TGAACACCTG	GACAACTACA	TCCCGGATCC	300
	AGTCCGTGCG	ATCGACATGC	CGTTCCTGCT	GCCAATCGAA	GACGTATTCT	350
	CAATCTCTGG	CCGTGGTACC	GTTGTTACCG	GTCGTGTTGA	GCGCGGCATC	400
10	GTTAAAGTCG	GCGACGAAGT	TGAAATCGTG	GGTATCAAAG	ATACTGCGAA	450
	ATCAACCTGT	ACCGGTGTTG	AGATGTTCCG	TAAGCTGCTG	GACCAGGATC	500
	AGGCAGGCGA	AAACTGTGGT	GTTCTGCTGC	GCGGTATCAA	GCGTGAAGAC	550
	ATCCAGCGTG	GCCAGGTTCT	GGCTAAGCCA	GGCTCAATCA	AGCCGCACAC	600
	CCAGTTCGAG	TCAGAAGTTT	ACGTTCTGTC	TAAAGACGAA	GGTGGCCGCC	650
15	ATACTCCGTT	CTTCAAAGGC	TATCGTCCAC	AGTTCTACTT	CCGTACAAC	700
	GATGTAACCG	GTTCAAGTAG	GCTGCCAGAA	GGCGTTGAGA	TGGTCATGCC	750
	AGGCGACAAC	ATCAAAATGG	TTGTTACCCT	GATCCACCCA	ATCGCAATGG	800
	ACGAA					805

20

2) INFORMATION FOR SEQ ID NO: 135

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 825 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

30 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Pantoea dispersa*
 (B) STRAIN: ATCC 14589

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 135

	CGCGATCCTG	GTTGTTGCTG	CGACTGATGG	CCCAATGCCT	CAGACCCGTG	50
	AGCACATCCT	GCTGGGCCGT	CAGGTTGGCG	TTCCTTACAT	CATCGTGTTT	100
40	CTGAACAAGT	GTGACATGGT	TGATGACGAA	GAGCTGCTGG	AACTGGTTGA	150
	GATGGAAGTT	CGCGATCTGC	TGTCTCAGTA	CGACTTCCCA	GGCGACGATA	200
	CCCCAATCGT	ACGCGGTTC	GCGCTGAAAG	CGCTGGAAGG	CGACGCTGAG	250
	TGGGAAGCGA	AAGTCGTTGA	GCTGGCTGGT	CACCTGGATA	CTTACATTCC	300
	AGATCCAGTA	CGTGCTATCG	ATCTGCCGTT	CCTGCTGCCA	ATCGAAGACG	350
45	TATTCTCAAT	CTCTGGCCGT	GGTACCGTTG	TTACCGGTCG	TGTTGAGCGC	400
	GGCATCGTGA	AAGTGGGCGA	CGAAGTAGAA	ATCGTTGGTA	TCAAAGCGAC	450
	TGCCAAGTCT	ACCTGTACCG	GTGTTGAAAT	GTTCCGCAAA	CTGCTGGACC	500
	AGGGTCAGGC	AGGCGAGAAC	TGTGGTGTTC	TGCTGCGCGG	TATCAAGCGT	550
	GAAGAGATCC	AGCGTGGTCA	GTTCTGGCT	AAGCCAGGCA	CCATCAAGCC	600
50	ACACACCAAG	TTCGTATCAG	AAGTGTACGT	ACTGTCTAAA	GACGAAGGCG	650
	GCCGTCATAC	TCCGTTCTTC	AAAGGCTACC	GTCCACAGTT	CTACTTCCGT	700
	ACYACTGATG	TGACCGGCAM	CATMGAAGT	CCAGAAGGCG	TTGAGATGGT	750
	AATGCCAGGC	GACAACATCA	AAATGRCCGT	TGAGCTGATC	CACCCAATCG	800
55	CGATGGACCA	GGGTCTGCGT	TTCGC			825

2) INFORMATION FOR SEQ ID NO: 136

60 (i) SEQUENCE CHARACTERISTICS:

82

- (A) LENGTH: 762 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

5

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Pasteurella multocida*
 (B) STRAIN: NCTC 10322

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 136

15 CACAAACACG TGAGCACATC CTTTtaggTC GCCAAGTAGG CGTTCCTTAC 50
 ATCATCGTAT TCTTAAACAA ATGCGACATG GTGGATGATG AAGAATTATT 100
 AGAATTAGTT GAAATGGAAG TGC GTGAACT TCTTCTCAA TATGATTTC 150
 CAGGTGATGA TACACCAATC GTACGTGGTT CAGCGTTACA AGCGTTAAAC 200
 GGYGTAGCTG AGTGGGAAGA GAAAATTCTT GAGTTAGCCA ACCACTTAGA 250
 TACTTACATT CCAGAGCCAC AACGTGCAAT CGACCAACCG TTCCTTCTTC 300
 20 CGATTGAAGA CGTGTCTCA ATTTCTGGT GTGGTACAGT AGTAACAGGT 350
 CGTGTGAGC GTGGTATCAT CCGTACAGGT GAAGAGGTTG AAATTGTTG 400
 TATTAAAGCG ACAACGAAGA CCACAGTAAC AGGTGTTGAG ATGTTCCGTA 450
 AATTATTAGA CGAAGGTCGT GCGGGTGAGA ACGTTGGTGC TTTATTACGT 500
 GGTACTAARC GTGAAGAAAT CGAACGTGGT CAAGTGTTAG CGAAACCGGG 550
 25 TTCAATYACG CCACACACTG ATTTTGAATC AGAAGTTTAC GTGTTATCAA 600
 AAGAAGAAGG TGGTCGTCAT ACACCATTCT TCAAAGGTTA CCGTCCACAG 650
 TTCTACTTCC GTACAACGGA CGTAACAGGT ACAATCGAAT TACCGGAAGG 700
 TGTTGAGATG GTGATGCCTG GTGATAACAT CAAGATGACT GTAAGTTTGA 750
 TTCACCCAAT CG 762

30

2) INFORMATION FOR SEQ ID NO: 137

35 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 832 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

40

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Peptostreptococcus anaerobius*
 (B) STRAIN: ATCC 27337

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 137

50 TGGAGCTATC TTAGTTGTAT CAGCAGCGGA TGGACCAATG CCACAAACAA 50
 GAGAACACAT CTTATTATCA AGACAAGTAG GAGTACCATA TATCGTAGTA 100
 TATTTGAATA AAGCAGATAT GGTAGAAGAT GAAGAATTAT TAGAATTAGT 150
 AGAAATGGAA GTAAGAGAAT TACTATCTGA ATATGGATTC CCAGGAGATG 200
 AAATTCCAAT CATAACAGGA TCATCCTTAG GAGCATTAAA TGGAGAACAA 250
 AAATGGATAG ATCAAATCAT GGCATTGATG AAAGCCGTAG ATGAATATAT 300
 55 TCCAACACCG GAAAGAGCAG TAGATCAACC ATTCTTGATG CCAATCGAAG 350
 ACGTATTTAC AATTACAGGA AGAGGAACTG TAGTAACAGG AAGAGTTGAA 400
 AGAGGAGTTG TAAAGTWGG AGAAGAAGTT GAAATCGTAG GAATCAAAGC 450
 GACAACAAAG ACAACTTGTA CYGGAGTAGA AATGTTCCGA AAATTATTGG 500
 ATCAAGGACA AGCAGGAGAT AACATCGGAG CTTTATTRAG AGGAACCAAG 550
 60 AAAGAAGATG TAGAAAGAGG ACAAGTATTG GCAAAACCAAG GAACAATTCA 600

	TCCTCATACA	AACTTCAGTG	GAGAAGTATA	TGTATTGACA	AAAGAAGAAG	650
	GAGGAAGACA	TACTCCATTC	TTCTCAGGAT	ACAGACCACA	ATTTTACTTT	700
	AGAACCACAG	ATATTACAGG	AGCAGTAACA	TTACCAGAAG	GAGTAGAAAT	750
	GGTAATGCCR	GGAGATAATA	TCACAATGAC	AGTAGAATTG	ATTCACCCAA	800
5	TTGCAATGGA	AACAGGATTA	CGATTGCAA	TT		832

2) INFORMATION FOR SEQ ID NO: 138

10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 823 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 15 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 20 (A) ORGANISM: *Peptostreptococcus asaccharolyticus*
 (B) STRAIN: LSPQ 2639

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 138

25	TAGTATGTTT	AGCAGCAGAY	GGTCCAATGC	CACAAACAAG	AGAACACATT	50
	CTACTAGCAA	GACAAGTTGG	TGTACCAAAG	ATAGTAGTAT	TCCTAAACAA	100
	AGAAGACCAA	GTAGACGATC	CAGAACTAAT	TGAATTAGTA	GAGATGGAAA	150
	TCAGAGACCT	ACTATCAGAA	TATGACTTCG	AYGGAGACAA	CACACCAATC	200
	GTAGTAGGAT	CAGCATTAAA	AGCCCTAGAC	GATCCAGACG	GAGAATGGGG	250
30	AGACAAAATC	GTAAACTAA	TGGAAGMAGT	AGACGAATAC	ATCCCAACAC	300
	CAGTAAGAGA	TACAGAACAC	CCATTCTCTA	TGCCAATCGA	AGACRTATTC	350
	TCAATYACAG	GAAGAGGAAC	AGTAGCAACA	GGAAGAGTAG	AACAAGGTGT	400
	AGTAAAAGTA	GGMGACACAG	TAGAACTAGT	AGGCTTAACA	GACGAAAGCA	450
	GACAAGTAGT	AGTAACAGGT	GTAGAAATGT	TTAGAAAACA	ACTAGACCTA	500
35	GCAGAAGCMG	GAGACAACAT	TGGAGCCCTA	CTAAGAGGAG	TACAAAGAGA	550
	AGAAATCCAA	AGAGGACAAG	TACTAGCAGC	ACCAGGAACA	ATCAAACCAC	600
	ACACAAAATT	TGAAGCAGAA	GTATACGTAC	TAACAAAAGA	AGAAGGTGGA	650
	AGACACACAC	CATTCTTTAA	CGGATACAGA	CCACAATTCT	ACTTCAGAAC	700
	AACAGACGTA	ACAGGAGACA	TCCAAC TAGC	AGACGGAGTA	GAAATGGTAA	750
40	TGCCAGGAGA	CAACTCAACA	TTTACAGTAA	CACTAATCAC	ACCAATCGCA	800
	ATGGACGAAG	GACTAAGATT	CGC			823

45 2) INFORMATION FOR SEQ ID NO: 139

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 832 bases
 (B) TYPE: Nucleic acid
 50 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 55 (A) ORGANISM: *Peptostreptococcus prevotii*
 (B) STRAIN: ATCC 9321

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 139

60

CTATCATCGT AGTATCTGCA GCAGACGGTC CAATGCCCAA ACAGAGAGAA 50
 CACATCCTAC TAGCAAGACA AGTAGGCGTT CCAAAAATCG CAGTATTCCT 100
 AAACAAAGAA GACCAAGTAG ACGATCCAGA ACTAATCGAA TTAGTAGAAA 150
 TGGAAATCAG AGACCTACTT TCAGAATACG ACTTCGATGG AGACAACGCT 200
 5 CCAGTAGTAG TAGGATCTGC TCTTAAATCA CTAGAAGAAG GCGGAGAAGG 250
 CCCATGGTCA GACAAAATCC TTGACCTAAT GGCACAAGTA GACGAATACT 300
 TCGACATCCC AGAAAGAGAC AACGACCAAC CATTCCCTAAT GCCAGTAGAA 350
 GACGTAATGA CAATCTCAGG ACGTGGAACA GTAGCAACAG GAAGAGTTGA 400
 AAGAGGAACA CTAAAAGTTG GTGATACAGT AGAAATCGTA GGACTAACAG 450
 10 AAGATACAAA AGAAACAGTA GTAACCTGGAG TAGAAATGTT CCACAAATCM 500
 CTAGACCAAG CAGAATCTGG AGATAACGTA GGACTACTAG TAAGAGGAGT 550
 AACAAGAGAT CAAATCTCAA GAGGACAAGT ACTAGCAAAA CCAGGWTGAG 600
 TAAACCCACA CACAGAATTC GAAGGTCAAG TATACGTACT AACAAAAGAA 650
 GAAGGTGGAC GTCACACACC ATTCTTCAGT GGATATAGAC CACAATTCTT 700
 15 CTTTAGAACA ACAGACGTAA CAGGAGACAT CGAACTAGAA GAAGGCCTAG 750
 AAATGGTAAT GCCAGGAGAC AACGCAACAT TCAAAATCAC ACTCCAAAAA 800
 CCAATCGCTC TAGAAGAAGG ACTAAGATTC GC 832

20

2) INFORMATION FOR SEQ ID NO: 140

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 831 bases
 25 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

30

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Porphyromonas asaccharolytica*
 (B) STRAIN: ATCC 25260

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 140

CGGTGCTATC ATCGTAGTTG CTGCAACTGA TGGTCCTATG CCTCAGACGC 50
 GTGAGCACAT CCTACTAGCA CGTCAGGTCA ACGTACCTCG TCTAGTTGTC 100
 TTTATGAACA AGTGCGACCT TGTGTATGAC GAGGAGATGC TCGAGCTCGT 150
 40 AGAGATGGAT ATGCGTGAGC TACTAAGCTT CTATGACTTT GACGGCGACA 200
 ACACTCCTGT CATCCGTGGT TCTGCTCTTG GTGCTCTCAA TGGTGAGCCT 250
 AAGTGGGTAG AGAAGGTTAT GGAGCTCATG GAGGCTGTAG ACACCTGGAT 300
 CCCACTACCT GAGCGCGACA TCGACAAGCC TTTCCTAATG CCTGTAGAGG 350
 ACGTATTCTC TATCACAGGT CGTGGTACTG TCGCTACTGG TCGTATCGAG 400
 45 ACTGGTGTCT TTAAGGTCAA CGATGAGGTT CAGATCATCG GTCTAGGTGC 450
 TGAGGGTAAG AAGAGCGTCG TAACTGGCGT GGAAATGTTT CGCAAGATCC 500
 TTGATGAGGG TGAAGCTGGT GATAACGTAG GTCTCCTACT CCGTGGTATC 550
 GACAAGGACG AGATCAAGCG CGGTATGGTC CTAGCACACC CAGGTCAGGT 600
 CAAGCCTCAC GATCACTTCA AGGCTGAGGT CTATATCCTG AAGAAGGAAG 650
 50 AGGGTGGTCTG TCACACACCA TTCCACAACA AGTACCGTCC TCAGTTCTAC 700
 ATCCGTACGC TAGACGTAAAC GGGCGAGATC ACACTCCCAG AGGGTGTAGA 750
 GATGGTTATG CCTGGTGATA ACGTCACCAT CGATGTCAAG CTCATCTCTC 800
 CAGTAGCTTG TAGCGTAGGT CTACGCTTCG C 831

55

2) INFORMATION FOR SEQ ID NO: 141

(i) SEQUENCE CHARACTERISTICS:

- 60 (A) LENGTH: 818 bases

85

(B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

5 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Porphyromonas gingivalis*
 (B) STRAIN: ATCC 33277

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 141

	CGGTGCTATA ATCGTTGTAG CAGCTACAGA CGGTCCTATG CCTCAGACTC	50
	GCGAGCACAT CCTTTTGGCT CGCCAGGTAA ACGTTCCTCG TCTGGTTGTT	100
15	TTCATGAACA AATGTGACAT GGTAGACGAT GAAGAGATGC TCGAGCTTGT	150
	TGAAATGGAC ATGCGCGAAC TCCTTTCTTT CTACGATTTC GATGGTGACA	200
	ATACCCCTAT CATCCGTGGT TCTGCTCTGG GCGCTTTGAA TGGAGAGCCT	250
	CAGTGGGAAG ACAAGGTGAT GGAGCTTATG GAAGCTGTTG ACAACTGGGT	300
	TCCCCTGCCT GAGCGCGATA TCGACAAACC GTTCTTGATG CCGGTTGAAG	350
20	ACGTGTTCTC TATCACGGGT CGTGGTACGG TCGCTACAGG ACGTATCGAA	400
	ACCGGTATTG TGAAGACCGG TGACGAAGTT CAAATCATCG GCCTCGGTGC	450
	AGAAGGAATG AAGTCGGTTG TTACGGGTGT TGAAATGTTT CGTAAGATT	500
	TTGACGAAGG TCAGGCTGGT GACAACGTTG GTCTCCTCCT GCGTGGTATC	550
	GATAAGGATC AGATCAAGCG TGGTATGGTT ATCTCTCACC CGGGTAAGAT	600
25	TACTCCTCAC AAGAGATTTA AGGCCGAGGT TTATATCTTG AAGAAAGAAG	650
	AAGGTGGTCG CCACACTCCT TTCCACAACA AATATCGTCC GCAGTTCTAC	700
	ATCCGTACGC TTGACGTGAC CGGTGAAATC ACTCTTCCCG AAGGAACAGA	750
	AATGGTTATG CCCGGTGACA ACGTAACGAT CACTGTAGAA CTCATCTACC	800
	CGGTTGCATG TAATGTAG	818

30

2) INFORMATION FOR SEQ ID NO: 142

35 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 830 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

40

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Pragia fontium*
 (B) STRAIN: ATCC 49100

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 142

	CGGCGCTATT CTGGTTGTTG CTGCAACTGA TGGTCCTATG CCTCAAATC	50
50	GTGAGCACAT CCTGTTAGGY CGCCAGGTTG GCGTACCATA CATCATTGTG	100
	TTCCTGAACA AGTGTGACAT GGTTGAYGAT GAAGAGCTGT TAGAACTGGT	150
	TGAAATGGAA GTTCGTGAGC TTCTGTCTCA GTACGATTTC CCAGGTGATG	200
	ATACTCCAGT TGTTCTGTGGT TCTGCGCTGA AAGCGTTRGA AGGCGAAGCT	250
	GAGTGGGAAG CTAAAATCAT TGAATTGGCT GACTCCCTGG AYAGCTACAT	300
55	TCCACAGCCA GAGCGTGCAA TTGATAAGCC GTTCCTGCTG CCAATCGAAG	350
	ACGTTTTCTC AATCTCTGGC CGTGGTACAG TAGTAACCGG TCGTGTAGAG	400
	CGCGGTATCG TTAAAGTTGG TGAAGAAGTT GAAATCGTTG GTATCAAAGA	450
	TACTGTGAAA ACAACTTGTA CTGGCGTTGA AATGTTCCGT AARTTACTGG	500
	ATGAAGGCCG TGCGGGTGAG AACGTTGGTG TTCTGCTGCG TGGTACTAAG	550
60	CGTGATGAAA TCGAACGTGG TCAAGTATTA GCAAAACCAG GTTCAATCAA	600

CCCGCATACT AACTTCGTAT CAGAAGTTTA TATCCTGAGC AAAGATGAAG 650
 GTGGTCGTCA TACTCCATTC TTCAAAGGCT ACCGTCCACA GTTYTACTTC 700
 CGTACAACTG ACGTGACCGG TACCATCGAA CTGCCAGAAG GCGTAGAGAT 750
 GGTAATGCCA GGTGATAACA TTCAGATGAC TGTAAGTCTG ATTGCCCCAA 800
 5 TCGCGATGGA CGAAGGTTTA CGCTTCGCTA 830

2) INFORMATION FOR SEQ ID NO: 143

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(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 821 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 15 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

20 (A) ORGANISM: *Prevotella melaninogenica*
 (B) STRAIN: ATCC 25845

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 143

25 TGGTGCTATC TTGGTTGTAG CTGCTACTGA TGGTCCTATG CCTCAGACTC 50
 GTGAGCACGT ATTGCTCGCT CGTCAGGTAA ACGTACCTCG CTTGGTTGTA 100
 TTCTTGAACA AGTGTGATAT GGTGACGAT GCTGAGATGC TTGACCTCGT 150
 TGAGATGGAG GTTCGTGAGA TCCTCGAGCA GTACGGTTAT GAGGAGGATA 200
 CTCCTATTAT TCGTGGTTCT GCACTCGGTG CTTTGAACGG TGTGAGAAG 250
 30 TGGGTAGACT CTGTAATGGA GCTCATGGAT ACTGTTGACA CTTGGATTGA 300
 AGAGCCAGAG CGTGAGATTG ACAAGCCATT CTTGATGCCT GTTGAGGACG 350
 TATTCTCTAT CACAGGTCGT GGTACTGTAG CTACTGGTCG TATCGAGACT 400
 GGTATCTGTA AGGTAGGTGA TGAGGTTGAG TTGCTCGGTC TCGGTGAGGA 450
 CAAGAAGTCT GTTATCACTG GTGTTGAGAT GTTCCGTAAG AACCTTCCAA 500
 35 CAGGTCAGGC TGGTGACAAC GTAGGTCTCC TCCTTCGTGG TATCGATAAG 550
 GCTGAGGTTA AGCGTGGTAT GGTGTTGTG CACCCAGGTG CTATTACTCC 600
 TCACGATCAC TTCAAGGCAT CTATCTATGT ATTGAAGAAG GAAGAGGGTG 650
 GTCGTCATAC TCCATTTCGT AACAAGTATC GTCCACAGTT CTACCTCCGT 700
 ACAATGGACT GTACAGGTGA AATCCACCTC CCAGAGGGCG TTGAGATGGT 750
 40 TATGCCAGGT GACAACGTAG AGATTGAAGT TGTATTGATC TATAAGGTTG 800
 CTTTGAACGA GGTCTTCGT T 821

45 2) INFORMATION FOR SEQ ID NO: 144

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 827 bases
 (B) TYPE: Nucleic acid
 50 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

55 (A) ORGANISM: *Prevotella oralis*
 (B) STRAIN: ATCC 33269

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 144

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TGGTGCTATT CTTGTAGTAG CTGCTACTGA CGGTCCTATG CCTCAAACCTC      50
GTGAACACGT GCTTCTTGCT CGTCAGGTGA ACGTACCTCG TTTGGTCGTT      100
TTCTTGAACA AGTGCGATAT GGTTGACGAT GAAGAAATGC TTGAGCTCGT      150
AGAAATGGAG CTTCATGAAC TTCTCGAGCA GTATGAATAT GAGGAGGATA      200
5  CTCCTATTGT TCGTGGTTCG GCACTTGGCG CTCTGAATGG AGTAGAGAAG      250
TGGGTTGACA GCGTGATGAA GTTGATGGAT ACCGTTGATG AATGGATACA      300
GGAACCACCG CGTGATCTTG ATAAGCCTTT CTTGATGCCG GTAGAGGATG      350
TATTTTCTAT TACTGGTCGT GGAACGGTTG TTACAGGCCG TATTGAAACT      400
GGTAAGGTTA AGGTGGGCGA TGAAGTTCAA CTTCTTGGTC TCGGTGAAGA      450
10 TAAGAAGTCC GTTGTGACAG GCGTTGAGAT GTTCCGTAAG ATTCTTGACG      500
AAGGTGAAGC TGGTGATAAT GTAGGCTTGC TGCTTCGTGG TATCGATAAG      550
ACGGAAGTAA AGCGTGGTAT GGTGTGCGTA CATCCGGGGG CTATTACTCC      600
TCACGATCAT TTCAAGGCTT CAGTTTACGT ATTGAAGAAA GAAGAAGGCG      650
GTCGCCATAC TCCGTTTGGT AMCAAGTATC GTCCACAGTT CTATCTTCGT      700
15 ACCATGGACT GTACTGGTGA AATTACTCTT CCGGAAGGAG TTGAGATGGT      750
AATGCCGGGT GATAACGTCG AAATTGAAGT TAAGTTGATC TATCCGGTAG      800
CTTTGAACGA GGGACTTCGT TTCGCTA      827

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2) INFORMATION FOR SEQ ID NO: 145

(i) SEQUENCE CHARACTERISTICS:

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25 (A) LENGTH: 833 bases
    (B) TYPE: Nucleic acid
    (C) STRANDEDNESS: Double
    (D) TOPOLOGY: Linear

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(ii) MOLECULE TYPE: Genomic DNA

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(vi) ORIGINAL SOURCE:

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    (A) ORGANISM: Propionibacterium acnes
    (B) STRAIN: ATCC 6919

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35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 145

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CGGCGCCATC CTCGTGGTTG CTGCTACCGA CGGCCCGATG CCTCAGACTC      50
GCGAGCACGT TCTGCTCGCT CGTCAGGTGG GCGTGCCCGC CATCGTCGTC      100
GCCCTCAACA AGTGCGACAT GGTTGACGAT GAGGAGCTCA TTGAGCTCGT      150
40 CGAGATGGAG GTCCGCGAGC TGCTGACCTC GCAGGAGTTC GACGGCGACA      200
ACTGCCCTGT CGTTCGCATC TCCGCCTTCC AGGCCCTCCA GGGTGATGAG      250
AAGTGGAACC AGTCGATCCT CGACCTCATG GACGCCGTGG ACGAGTACAT      300
CCCGCAGCCT GAGCGCGATC TCGACAAGCC CTTCTTATG CCGATCGAGG      350
ACGTCTTCAC CATCACCGGC CGTGGCACCG TTGTCACCGG TCGTGTCGAG      400
45 CGCGGCGTCG TCAAGACTGG CGAAGAGGTC GAGATCGTCG GTATCCACGA      450
GAAGACCCAG AAGACCACCG TTACCGGTGT CGAGATGTTT CGCAAGATCC      500
TCGACGAGGG CCGCGCTGGT GAGAACGTCG GCGTTCTGCT CCGTGGCACC      550
AAGAAGGAGG ATGTCGTTCC CGGCATGGTC CTCTCCAAGC CTGGTTCCAC      600
CACCCCCCAC ACCGACTTCG AGGGCCAGGT CTACGTCCTC AAGAAGGATG      650
50 AGGGTGGCCG CCACAAGCCG TTCTTCTCCC ACTACAGCCC CCAGTTCTAC      700
TTCCGTACCA CGGACGTGAC TGGCACTGTT GAGCTCCCCG AGGGCACCGA      750
GATGGTCATG CCTGGCGACA ACACCGACAT GACTGTGCAC CTGATTACCC      800
CGGTTGCCAT GGAGGATCAG CTCAAGTTCG CTA      833

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55

2) INFORMATION FOR SEQ ID NO: 146

(i) SEQUENCE CHARACTERISTICS:

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60 (A) LENGTH: 745 bases

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(B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

5 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Proteus mirabilis*
 (B) STRAIN: ATCC 35659

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 146

	CACAAACTCG	TGAGCACATC	CTGTTAGGTC	GTCAGGTTGG	TGTTCCCTTAC	50
	ATCATCGTAT	TCCTGAACAA	ATGTGACATG	GTAGATGATG	AAGAGCTGTT	100
15	AGAATTAGTT	GAAATGGAAG	TTCGTGAACT	TCTGTCTCAA	TACGATTTC	150
	CAGGTGATGA	CACTCCAGTA	ATCCGTGGTT	CAGCGCTGAA	AGCACTGGAA	200
	GGCGAAGCAG	AGTGGGAAGC	AAAAATTGTT	GAATTAGCAG	AAGCACTGGA	250
	TTCTTATATC	CCAGAGCCAG	AGCGTGCAAT	TGACAAACCA	TTCTTGTTAC	300
	CAATCGAAGA	TGTATTCTCA	ATCTCAGGCC	GTGGTACAGT	AGTTACTGGT	350
20	CGTGTAGAGC	GTGGTATCAT	CAAAGTAGGT	GATGAAGTTG	AGATTGTTGG	400
	TATCAAAGAA	ACCGCCAAAA	CAACTTGATC	TGGCGTTGAA	ATGTTCCGTA	450
	AATTACTTGA	CGAAGGTCGT	GCAGGTGAGA	ACGTAGGTGT	TCTGCTGCGT	500
	GGTACAAAAC	GTGAAGAAAT	CGAACGTGGA	CAAGTACTGG	CRAAACCAGG	550
	CTCAATCAAC	CCACACAACA	AATTTGAATC	AGAAGTTTAT	ATTCTGAGCA	600
25	AAGATGAAGG	TGGTCGTCAC	ACTCCATTCT	TCAAAGGCTA	CCGTCCACAG	650
	TTCTACTTCC	GTACAACTGA	CGTAACTGGT	ACTATCGAAT	TACCAGAAGG	700
	CGTAGAAATG	GTAATGCCAG	GCGACAACGT	GAACATGATC	GTTGA	745

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2) INFORMATION FOR SEQ ID NO: 147

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 829 bases
 35 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

40

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Proteus penneri*
 (B) STRAIN: ATCC 33519

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 147

	GGAGCTATCC	TGGTTGTTGC	TGCGACAGAT	GGCCCAATGC	CACAAACTCG	50
	TGAGCACATC	CTGTTAGGTC	GTCAGGTTGG	TGTTCCCTTAC	ATCATCGTAT	100
	TCCTGAACAA	ATGTGACATG	GTAGATGATG	AAGAGTTACT	GGAATTAGTM	150
50	GAAATGGAAG	TTCGTGAACT	TCTGTCTCAG	TACGATTTC	CAGGTGATGA	200
	CACTCCAGTA	ATCCGTGGTT	CAGCGCTGAA	AGCACTGGAA	GGCGAAGCAG	250
	AGTGGGAAGC	AAAAATTGTT	GAATTAGCAG	AAGCACTGGA	TTCATACATC	300
	CCAGARCCAG	AGCGTGCAAT	TGACAAACCA	TTCTTGTTAC	CAATTGAAGA	350
	CGTATTCTCA	ATTTCAGGCC	GTGGTACAGT	AGTAACAGGT	CGTGTTGAGC	400
55	GTGGCGTAAT	CAAAGTTGGT	GAAGAAGTTG	AAATCGTTGG	TATTAAACCA	450
	ACAGCGAAAA	CAACTTGATC	TGGCGTTGAA	ATGTTCCGTA	AATTACTTGA	500
	CGAAGGTCGT	GCAGGTGAGA	ACGTAGGTGT	TCTTCTGCGT	GGTACTAAAC	550
	GTGAAGAAAT	CGAACGTGGA	CAAGTACTGG	CGAAACCAGG	TTCAATCAAC	600
	CCACACACTA	AATTTGAATC	AGAAGTTTAT	ATTCTGAGCA	AAGATGAAGG	650
60	TGGTCGTCAT	ACTCCATTCT	TCAAAGGCTA	CCGTCCACAG	TTCTACTTCC	700

GTACAACTGA	CGTAACTGGT	ACTATCGAAT	TACCAGAAGG	CGTAGAAATG	750
GTAATGCCAG	GTGACAACAT	CAACATGATC	GTTGAACTGA	TTCACCCAAT	800
CGCGATGGAC	GACGGTTTAC	GTTTCGCTA			829

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2) INFORMATION FOR SEQ ID NO: 148

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 824 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

15 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Proteus vulgaris*
 (B) STRAIN: ATCC 13315

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 148

	CGGAGCTATT	CTGGTTGTTG	CTGCGACTGA	TGGCCCAATG	CCACAAACTC	50
	GTGAGCACAT	CCTGTTAGGT	CGCCAGGTTG	GTGTACCTTA	CATCATCGTA	100
25	TTCCTGAACA	AATGTGACAT	GGTTGATGAT	GAAGAACTGC	TGGAATTAGT	150
	AGAAATGGAA	GTTTCGTGAAC	TTCTGTCTCA	GTACGATTTC	CCAGGTGATG	200
	ACACTCCAGT	AATCCGTGGT	TCAGCGCTGA	AAGCACTGGA	AGGCGAAGCT	250
	GAGTGGGAAG	CAAAAATTGT	TGAATTAGCA	GAAGCACTGG	ATTCTTACAT	300
	CCCAGAACCA	GAGCGTGCAA	TTGACAAACC	ATTCTTGCTG	CCTATCGAAG	350
30	ACGTATTCTC	AATCTCTGGT	CGTGGTACAG	TAGTAACAGG	CCGTGTAGAG	400
	CGTGGTGTG	TTAAAGTTGG	TGAAGAAGTT	GAGATTGTTG	GTATTAAAGA	450
	CACAGTTAAA	ACAACCTGTA	CTGGCGTTGA	AATGTTCCGT	AAATTACTTG	500
	ACGAAGGTCG	TGCAGGTGAG	AACGTAGGTG	TTCTTCTGCG	TGCTACTAAA	550
	CGTGAAGAAA	TCGAACGTGG	ACAAGTACTG	GCTAAACCAG	GTTCAATCAA	600
35	GCCACACACT	AAATTCTGAAT	CAGAAGTTTA	TATCCTGAGC	AAAGATGAAG	650
	GTGGTCGTCA	CACTCCATTC	TTCAAAGGTT	ACCGTCCACA	GTTCTACTTC	700
	CGTACAACCTG	ACGTAACTGG	TACTATCGAA	TTACCAGAAG	GCGTAGAAAT	750
	GGTAATGCCA	GGTGACAACA	TCAACATGAT	CGTTGAACTG	ATTCACCCTA	800
40	TCGCGTAGGA	CGACGGTTTA	CGTT			824

2) INFORMATION FOR SEQ ID NO: 149

(i) SEQUENCE CHARACTERISTICS:

- 45 (A) LENGTH: 745 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Providencia alcalifaciens*
 (B) STRAIN: ATCC 9886

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 149

	CACAAACTCG	TGAGCACATC	CTGTTAGGTC	GCCAAGTAGG	TGTTTCCTTAC	50
60	ATCATCGTTT	TCCTGAACAA	ATGTGACATG	GTAGACGACG	AAGAACTGTT	100

	AGAATTAGTT	GAAATGGAAG	TTCGTGAACT	TCTGTCTCAG	TACGATTTC	150
	CAGGCGATGA	CACTCCAGTT	GTTTCGCGTT	CAGCACTGAA	AGCGCTGGAA	200
	GGCAACCCAG	AGTGGGAAGC	AAAAATTGTT	GAATTAGCAG	GTTACCTGGA	250
	TTCTTACATC	CCAGAACCAG	AGCGTGCAAT	TGACAAGCCA	TTCTGTCTGC	300
5	CAATCGAAGA	CGTATTCTCA	ATCTCTGGTC	GTGGTACAGT	AGTAACAGGC	350
	CGTGTTGAGC	GTGGTATCAT	CAAAGTTGGT	GAAGAAGTTG	AAATCGTTGG	400
	TATTCAAGCG	ACTGCGAAAA	CAACTTGTA	TGGCGTTGAA	ATGTTCCGTA	450
	AACTGCTGGA	TGAAGGTCGT	GCGGGTGAGA	ACGTTGGTGT	TCTGCTGCGT	500
	GGTACTAAAC	GTGAAGAAAT	TCAACGTGGT	CAAGTACTGG	CTAAACCAGG	550
10	TTCAATCAAG	CCACACACTC	AATTCGAATC	AGAAGTATAT	ATTCTGAGCA	600
	AAGATGAAGG	TGGTCGTCAT	ACTCCATTCT	TCAAAGGCTA	CGGTCCACAG	650
	TTCTACTTCC	GTACAACTGA	CGTAACCGGT	ACTATCGAAC	TGCCAGAAGG	700
	CGTAGAGATG	GTAATGCCAG	GCGACAACAT	CAACATGATC	GTGAC	745

15

2) INFORMATION FOR SEQ ID NO: 150

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 830 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

25 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Providencia rettgeri*
 (B) STRAIN: ATCC 9250

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 150

	CGGTGCAATC	CTGTTGTTG	CTGCGACTGA	TGGCCCAATG	CCACAAACTC	50
	GTGAGCACAT	CCTGTTAGGY	CGCCAAGTAG	GTGTWCCTTA	CATCATCGTT	100
35	TTCTTGAACA	AATGTGACAT	GGTAGACGAC	GAAGAACTGT	TAGAATTAGT	150
	TGAAATGGAA	GTTTCGTGAAC	TTCTGTCTCA	ATACGATTTC	CCAGGCGACG	200
	ACACTCCAGT	TGTCCGTGGT	TCAGCTCTGA	AAGCGCTGGA	AGGCAACCCA	250
	GAGTGGGAAG	CGAAAATTGT	TGAATTAGCA	GGTCACTTGG	ATTCTTACAT	300
	CCCAGAACCA	GAGCGTGCAA	TTGACAAACC	ATTCCTGCTG	CCAATCGAAG	350
40	ACGTATTCTC	AATCTCTGGT	CGTGGTACAG	TAGTAACAGG	CCGTGTTGAG	400
	CGTGGTATCA	TCAAAGTTGG	TGAAGAAGTT	GAAATCGTTG	GTATCCAAGA	450
	CACGGTTAAA	ACAACTTGTA	CTGGCGTTGA	AATGTTCCGT	AAACTGCTGG	500
	ACGAAGGTCG	TGCGGGTGAG	AACGTTGGTG	TTCTGCTGCG	TGGTACTAAA	550
	CGTGAAGAAA	TTCAACGTGG	TCAAGTACTG	GCAAAACCAG	GTTCAATCAA	600
45	GCCACACACT	AAATTCGAAT	CAGAAGTCTA	TATTCTGAGC	AAAGATGAAG	650
	GTGGTCGTCA	CACTCCATT	TTCAAAGGTT	ACCGTCCACA	GTTCTACTTC	700
	CGTACAACTG	ACGTAACAGG	TACTATCGAA	CTGCCAGAAG	GCGTAGAGAT	750
	GGTAATGCCA	GGTGATAACA	TCAACATGAT	CGTTACCCTG	ATCCACCCAA	800
	TCGCGATGGA	CGACGGTTTA	CGTTTCGCAA			830

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2) INFORMATION FOR SEQ ID NO: 151

(i) SEQUENCE CHARACTERISTICS:

- 55 (A) LENGTH: 826 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

60

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Providencia rustigianii*
 5 (B) STRAIN: ATCC 33673

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 151

	CGGTGCAATC	CTGGTTGTTG	CTGCGACTGA	TGGCCCAATG	CCACAAACTC	50
10	GTGAGCACAT	CCTGTTAGGT	CGCCAAGTAG	GTGTCCTTA	CATCATCGTT	100
	TTCCTGAACA	AATGTGACAT	GGTTGACGAC	GAAGAACTGT	TAGAATTAGT	150
	TGAAATGGAA	GTTCTGTAAC	TTCTGTCTCA	GTACGATTTC	CCAGGCGACG	200
	ACACTCCAGT	TGTTCTGYGGT	TCAGCACTGA	AAGCGCTGGA	AGGTATCCCT	250
	GAGTGGGAAG	CGAAAATTGT	TGAATTAGCC	GGTTACCTGG	ACAGCTACAT	300
15	CCCAGAACCA	GAGCGCGCAA	TTGACCGTCC	ATTCCTGCTG	CCAATCGAAG	350
	ACGTATTCTC	AATCTCTGGT	CGTGGTACAG	TAGTAACAGG	SCGTGTTGAG	400
	CGTGGTATCG	TTAAAGTTGG	TGAAGAAGTT	GAAATCGTTG	GTATCCAAGA	450
	CACRGTTAAA	ACAACTTGTA	CTGGCGTTGA	AATGTTCCGT	AAACTGCTTG	500
	ACGAAGGTGC	TGCTGGTGAG	AACGTTGGTG	TTTTACTGCG	TGGTACTAAG	550
20	CGTGAAGAAA	TTCAACGTGG	TCAAGTACTG	GCTAAACCAG	GTTCAATCAA	600
	GCCACACACT	ACTTTTGAAT	CAGAAGTTTA	TATTCTGAGC	AAAGATGAAG	650
	GTGGTCGTCA	TACTCCATTC	TTCAAAGGCT	ACCGTCCACA	GTTCTACTTC	700
	CGTACAACCTG	ACGTAACCGG	TACTATCGAA	CTGCCAGAAG	GCGTAGAGAT	750
	GGTAATGCCA	GGCGACAACA	TCAACATGAT	CGTGACACTG	ATTCACCCAA	800
25	TCGCGATGGA	TGATGTTTA	CGTTTC			826

2) INFORMATION FOR SEQ ID NO: 152

30

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 830 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 35 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 40 (A) ORGANISM: *Providencia stuartii*
 (B) STRAIN: ATCC 33672

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 152

45	CGGTGCAATC	CTAGTTGTTG	CGGCAACAGA	TGGCCCAATG	CCACAAACTC	50
	GTGAGCACAT	CCTGTTAGGT	CGTCAGGTTG	GCGTTCCTTA	CATCATCGTG	100
	TTCCTGAACA	AATGTGACAT	GGTAGACGAC	GAAGAGCTGC	TGGAAGTGGT	150
	TGAAATGGAA	GTTCTGTAAC	TTCTGTCTCA	ATACGATTTC	CCAGGTGATG	200
	ACACTCCAGT	TATCCGTGGT	TCAGCGCTGA	AAGCGTTGGA	AGGCAACCCA	250
50	GAGTGGGAAG	CGAAAATCGT	TGAAGTAGCA	GAAGCACTGG	ACAGCTACAT	300
	CCCAGAGCCA	GAGCGTGCAA	TTGACAAGCC	ATTCCTGCTG	CCAATCGAAG	350
	ACGTATTCTC	AATCTCAGGT	CGTGGTACAG	TAGTCACAGG	CCGTGTTGAG	400
	CGTGGTATCA	TCAAAGTTGG	TGAAGAAGTT	GAAATCGTAG	GTATCAAAGA	450
	GACTGCGAAA	ACCACTTGTA	CTGGCGTTGA	AATGTTCCGT	AAACTGCTGG	500
55	ACGAAGGCCG	TGCGGGTGAG	AACGTAGGTG	TTCTGCTGCG	TGGTACTAAG	550
	CGTGAAGAAA	TCGAACGTGG	TCAAGTTCTG	GCGAAACCAG	GTTCAATCAA	600
	GCCACACACA	ACTTTTGAAT	CAGAAGTTTA	TATTCTGAGC	AAAGATGAAG	650
	TGGGTCGTCA	CACGCCATTTC	TTCAAAGGYT	ACCGTCCACA	GTTCTACTTC	700
	CGTACAACCTG	ACGTAACAGG	TACTATCGAA	CTGCCAGAAG	GCGTAGAGAT	750
60	GGTAATGCCA	GGCGACAACG	TGAACATGAA	AGTAACTCTG	ATTCACCCAA	800

TCGCGATGGA CGATGGTTTG CGTTTCGCAA

5 2) INFORMATION FOR SEQ ID NO: 153

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 827 bases
 (B) TYPE: Nucleic acid
 10 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

15 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Pseudomonas aeruginosa*
 (B) STRAIN: ATCC 35554

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 153

20 CCTGGTTTGC TCGGCTGCCG ACGGCCCAT GCCGCAGACC CGCGAGCACA 50
 TCCTGCTGTC CCGCCAGGTA GCGTTCCCT ACATCGTCGT GTTCCTGAAC 100
 AAAGCCGACA TGGTCGACGA CGCCGAGCTG CTGGAAGTGG TCGAGATGGA 150
 AGTTCGCGAT CTGCTGAACA CCTACGACTT CCCGGGCGAC GAACTCCGA 200
 25 TCATCATCGG TTCCGCGCTG ATGGCGCTGG AAGGCAAGGA TGACAACGGC 250
 ATCGGCGTAA GCGCCGTGCA GAAGCTGGTA GAGACCCTGG ACTCCTACAT 300
 TCCGGAGCCG GTTCGTGCCA TCGACCAGCC GTTCCTCATG CCGATCGAAG 350
 ACGTGTTCCT GATCTCCGGT CGCGGTACCG TGGTAACCGG TCGTGTAGAG 400
 CGCGGCATCA TCAAGGTCCA GGAAGAAGTG GAAATCGTCG GCATCAAGGC 450
 30 GACCACCAAG ACCACCTGCA CCGGCGTTGA AATGTTCCGC AAGCTGCTCG 500
 ACGAAGGTCG TGCTGGTGAG AACGTTGGTA TCCTGCTGCG TGGCACCAAG 550
 CGTGAAGACG TAGAGCGTGG CCAGGTACTG GCCAAGCCGG GCACCATCAA 600
 GCGGCACACC AAGTTCGAGT GCGAAGTGTA CGTGCTGTCC AAGGAAGAAG 650
 GTGGTCGTCA CACCCCGTTC TTCAAGGGCT ACCGTCCGCA GTTCTACTTC 700
 35 CGTACCACKG ACGTGACCGG TAMCTGCGAG CTGCCGGAAG GCGTAGAGAT 750
 GGTAATGCCG GCGACAACA TCAAGATGGT TGTCACCCTG ATCGCTCCGA 800
 TCGCCATGGA AGATGGCTGC GTTCGCG 827

40

2) INFORMATION FOR SEQ ID NO: 154

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 841 bases
 45 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

50

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Pseudomonas fluorescens*
 (B) STRAIN: ATCC 13525

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 154

CGGCGCAATC CTGGTTTGCT CGGCCGCTGA TGGTCCGATG CCACAAACCC 50
 GTGAACACAT CCGCTGTGCC CGTCAGGTTG GCGTTCCGTA CATCGTGGTT 100
 TACCTGAACA AGGCTGACCT GGTAGACGAC CTGAGCTGC TGGAACTGGT 150
 60 TGAGATGGAA GTGCGCGATC TGCTGAGCAC TTACGACTTC CCAGGCGACG 200

	ACACTCCGAT	CATCATCGGT	TCTGCTCGTA	TGGCTCTGGA	AGGCAAAGAC	250
	GACAACGAAA	TGGGCACCAC	GTCCGTTTCGT	AAACTGGTTG	AAACTCTGGA	300
	CAGCTACATC	CCAGATCCAG	TTCGTGTTAT	CGACAAGCCG	TTCCTGATGC	350
	CAATCGAAGA	CGTGTTCTCG	ATCTCCGGTC	GCGGTACTGT	TGTGACTGGT	400
5	CGTATCGAGC	GCGGTATCGT	TAAGGTTCAA	GATCCACTGG	AAATCGTTGG	450
	TCTGCGTGAC	ACTACCGTCA	CCACCTGCAC	CGGTGTTGAA	ATGTTCCGTA	500
	AGCTGCTCGA	CGAAGGTCGT	GCTGGCGAGA	ACTGCGGCGT	TCTGCTGCGT	550
	GGTACCAAGC	GTGACGACGT	TGAGCGTGCG	CAGGTTCTGG	TTAAGCCAGG	600
	TTCGGTTAAG	CCGCACACCA	AGTTCGAAGC	TGAAGTCTAC	GTACTGAGCA	650
10	AAGAAGAAGG	CGGTCGTCAC	ACTCCGTTCT	TCAAAGGCTA	CCGTCCACAG	700
	TTCTACTTCC	GTACTACTGA	CGTGACTGGT	AACTGCGAGC	TGCCGGAAGG	750
	CGTTGAAATG	GTTATGCCAG	GCGACAACAT	CAAAATGGTT	GTTACCCTGA	800
	TCAAAACCAT	CGCAATGGAA	GACGGTCTGC	GTTTCGCTAT	T	841

15

2) INFORMATION FOR SEQ ID NO: 155

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 841 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

25

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Pseudomonas stutzeri*
 (B) STRAIN: ATCC 17588

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 155

	CGGCGCGATC	CTGGTCTGCT	CGGCTGCTGA	CGGCCCCATG	CCGCAGACTC	50
	GCGAGCACAT	CCTGCTGTCC	CGTCAGGTTG	GTGTTCCGTA	CATCGTCGTG	100
	TTCCTGAACA	AGGCCGACAT	GGTTGATGAC	GCCGAGCTGC	TCGAGCTGGT	150
35	CGAGATGGAA	GTTCGYGACC	TGCTGTCGAC	CTACGACTTC	CCGGGTGAYG	200
	ACACTCCGAT	CATCATCGGC	TCCGCGCTGA	TGGCGCTGAA	CGGCGAAGAC	250
	GACAACGAGC	TCCGCACCAC	TGCGGTGAAG	AAGCTGGTCG	AGACCCTGGA	300
	CAGCTACATT	CCCAGCCGG	TTCGTGCCAT	CGACAAGCCG	TTCCTGATGC	350
	CGATCGAAGA	CGTGTTCTCG	ATCTCCGGTC	GCGGCACSGT	GGTAACCGGT	400
40	CGCGTAGAGC	GCGGCATCGT	CAAGGTTTCA	GAAGAGATCG	AGATCGTCGG	450
	TCTGCGTCCG	ACCACCAAGA	CTACCTGCAC	CGGCGTTGAG	ATGTTCCGCA	500
	AGCTGCTCGA	YGARGGTCGT	GCTGGCGAGA	ACTGCGGYGT	GCTGCTGCGT	550
	GGCACCAGC	GTGACGAAGT	GGAGCGTGGT	CAGGTTCTGG	CCAAGCCGGG	600
	CACCATCAAG	CCGCACACCA	AGTTCGAAGC	CGAAGTGATC	GTGCTGTCCA	650
45	AGGAAGAAGG	TGGTCGTCAC	ACCCCGTTCT	TYAAGGGCTA	CCGTCCKCAG	700
	TTCTACTTCC	GTACCACTGA	YGTGACYGGW	TCGTGCGARC	TGCCGGAAGG	750
	CGTCGAGATG	GTAATGCCGG	GCGACAACGT	GAAGATGGTT	GTCACCCTGA	800
	TCAAGCCGAT	CGCCATGGAA	GACGGCCTGC	GCTTCGCGAT	T	841

50

2) INFORMATION FOR SEQ ID NO: 156

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 833 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

60

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Psychrobacter phenylpyruvicus*
 (B) STRAIN: ATCC 23333

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 156

	GCTATTCTAG	TAGTATCAGC	AACTGACGGT	CCAATGCCAC	AAACACGTGA	50
	GCACATTCTA	TTATCACGTC	AGGTTGGTGT	ACCATACATC	ATCGTATTCA	100
10	TGAACAAATG	TGACATGGTA	GATGACGAAG	AGTTACTAGA	GCTAGTAGAA	150
	ATGGAAGTGC	GTGAATTACT	TTCAGACTAC	GACTTCCCAG	GTGATGACAC	200
	TCCAATCATC	AAAGGTTTCAG	CTTTAGAAGC	GTAAATGGT	AACGACGGTA	250
	AGTACGGTGA	GCCAGCAGTT	ATCGAACTAC	TAAACACTCT	AGACACTTAC	300
	ATTCCAGAGC	CAGAGCGTGA	CATCGATAAG	CCATTCTCTAA	TGCCAATCGA	350
15	AGACGTATTC	TCAATCTCAG	GTCGTGGTAC	AGTAGTAACA	GGCCGTGTTG	400
	AATCTGGTAT	CATCAAAGTT	GGTGACGAAA	TCGAAATCGT	TGGTATCAAA	450
	GACACAGTTA	AAACAACCTG	TACTGGTATC	GAGATGTTCC	GTAAGTTACT	500
	AGACGAAGGT	CGTGCTGGTG	AGAAGTGTGG	TGTACTATTA	CGTGGTACTA	550
	AGCGTGAAGA	CGTACAACGT	GGTCAAGTAC	TTGCTAAGCC	AGGTTCAATC	600
20	ACTCCACACA	CCAACCTTCGA	CGCAGAAGTA	TACGTACTAT	CAAAAAGAAGA	650
	AGGTGCTCGT	CACACTCCAT	TCTTAAATGG	TTACCGTCCA	CAGTTCTACT	700
	TCCGTACTAC	TGACGTAACA	GGTGCAATCA	CGTTACAAGA	AGGTACTGAA	750
	ATGGTAATGC	CAGGCGATAA	CGTTGAGATG	AGCGTAGAGC	TAATCCACCC	800
25	AATCGCTAGG	ACAAAGGTTT	ACGTTTCGCA	ATC		833

2) INFORMATION FOR SEQ ID NO: 157

30 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 825 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Rahnella aquatilis*
 (B) STRAIN: ATCC 33071

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 157

	GGCGCTATCC	TGGTTGTTGC	TGCAACTGAC	GGCCCTATGC	CTCAGACTCG	50
45	TGAGCACATC	CTGCTGGGTC	GCCAGGTTGG	CGTTCCATAC	ATGATCGTGT	100
	TCATGAACAA	ATGCGACATG	GTAGATGACG	AAGAGCTGCT	GGAAGTGGTA	150
	GAAATGGAAG	TTCGCGAACT	TCTGTCTGCT	TACGAATTCC	CAGGCGACGA	200
	CATCCCGGTC	ATCAAAGGTT	CAGCGCTGAA	AGCACTGGAA	GGCGATGCTA	250
	CTTGGAAGC	GAAAATCATC	GAAGTGGCAG	AAGCACTGGA	CAGCTACATT	300
50	CCATTGCCAG	AGCGTGCTAT	CGATAAGCCA	TTCTTGCTGC	CAATCGAAGA	350
	CGTATTCTCC	ATCTCCGGTC	GTGGTACAGT	GGTTACCGGT	CGTGTAGAGC	400
	GCGGTATCGT	TAAAGTGGGC	GAAGAAGTTG	AAATCGTCCG	TATCAAGGAC	450
	ACTGTTAAGT	CTACTTGTA	TGGCGTTGAA	ATGTTCCGCA	AACTGCTGGA	500
	CGAAGGCCGT	GCGGGCGAGA	ACGTGGGTGT	TCTGCTGCGT	GGTATCAAGC	550
55	GTGAAGACAT	CGAAGCTGGT	CAGGTTCTGG	CTAAACCAGG	TTCAATCAAA	600
	CCACACACCA	AGTTTGATT	CGAAGTGTAC	ATCCTGAGCA	AAGATGAAGG	650
	TGGTCGTCAC	ACTCCATTCT	TCAAAGGCTA	CCGTCCACAG	TTCTACTTCC	700
	GTACAACCTG	CGTGACCGGT	ACTATCGAAT	TGCCAGAAGG	CGTTGAGATG	750
	GTTATGCCTG	GTGACAACGT	GAACATGGTT	GTTACCCTGA	TCCACCCAAT	800
60	CGCGATGGAT	GACGGTCTGC	GTTTC			825

2) INFORMATION FOR SEQ ID NO: 158

5

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 830 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

10

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Salmonella choleraesuis* subsp. *arizonae*
 (B) STRAIN: ATCC 13314

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 158

```

20  CGGCGCGATC CTGGTTGTTG CTGCGACTGA CGGCCCGATG CCGCAGACCC      50
    GTGAGCACAT CCTGCTGGGC CGTCAGGTAG GCGTTCCGTA CATCATCGTG      100
    TTCCTGAACA AATGCGACAT GGTGATGAC GAAGAGCTGC TGGAAGTGGT      150
    TGAAATGGAA GTTCGTGAAC TTCTGTCTCA GTACGACTTC CCGGGCGACG      200
    ATACGCCGAT CGTTCGTGGT TCTGCTCTGA AAGCGCTGGA AGGCGACGCA      250
25  GAGTGGGAAG CGAAAATCAT CGAACTGGCT GGCTTCCTGG ACTCTTACAT      300
    CCCGGAACCA GAGCGTGCGA TTGACAAGCC GTTCCTGCTG CCGATCGAAG      350
    ACGTATTCTC CATCTCCGGT CGTGGTACCG TTGTTACCGG TCGTGTAGAA      400
    CGCGGTATCA TCAAAGTGGG CGAAGAAGTT GAAATCGTTG GTATCAAAGA      450
    GACTCAGAAG TCTACCTGTA CTGGCGTTGA AATGTTCCGC AAAGTCTGCTG      500
30  ACGAAGGCCG TGCCGGTGAG AACGTAGGTG TTCTGCTGCG TGGTATCAAA      550
    CGTGAAGAAA TCGAACGTGG TCAGGTACTG GCTAAGCCGG GCACCATCAA      600
    GCCGCACACC AAGTTCGAAT CTGAAGTGTA CATTCTGTCC AAAGATGAAG      650
    GCGGCCGTCA TACTCCGTTT TTCAAAGGCT ACCGTCCGCA GTTCTACTTC      700
    CGTACTACTG ACGTGACTGG CACCATCGAA CTGCCGGAAG GCGTGGAGAT      750
35  GGTAATGCCG GCGGACAACA TCAAATGGT TGTTACCCTG ATCCACCCGA      800
    TCGCGATGGA CGACGGTCTG CGTTTCGCAA      830
  
```

40 2) INFORMATION FOR SEQ ID NO: 159

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 832 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

45

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Salmonella choleraesuis* subsp. *choleraesuis*
 serotype *Choleraesuis*
 (B) STRAIN: ATCC 7001

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 159

55

```

    CGGCGCGATC CTGGTTGTTG CTGCGACTGA CGGYCCGATG CCGCAGACCC      50
    GTGAGCACAT CCTGCTGGGT CGTCAGGTAG GCGTTCCGTA CATCATCGTG      100
    TTCCTGAACA AATGCGACAT GGTGATGAC GAAGAGCTGC TGGAAGTGGT      150
60  TGAAATGGAA GTTCGTGAAC TTCTGTCTCA GTACGACTTC CCGGGCGACG      200
  
```

	ACACGCCGAT	CGTTCGTGGT	TCTGCTCTGA	AAGCGCTGGA	AGGTGACGCA	250
	GAGTGGGAAG	CGAAAATCAT	CGAACTGGCT	GGCTTCCTGG	ATTCTTACAT	300
	TCCGGAACCA	GAGCGTGCGA	TTGACAAGCC	GTTCCCTGCTG	CCGATCGAAG	350
	ACGTATTCTC	CATCTCCGGT	CGTGGTACCG	TTGTTACCGG	TCGTGTAGAG	400
5	CGCGGTATCA	TCAAAGTGGG	YGAAGAAGTT	GAAATCGTTG	GTATCAAAGA	450
	GACTCAGAAAG	TCTACCTGTA	CTGGCGTTGA	AATGTTCCGC	AAACTGTTGG	500
	ACGAAGGCCG	TGCCGGTGAG	AACGTAGGTG	TTCTGCTGCG	TGGTATCAAA	550
	CGTGAAGAAA	TCGAACGTGG	TCAGGTACTG	GCTAAGCCGG	GCACCATCAA	600
	GCCGCACACC	AAGTTCGAAT	CTGAAGTGT	CATTCTGTCC	AAAGATGAAG	650
10	GCGGCEGTEA	TACTCCGTTT	TTCAAAGGCT	ACCGTCCGCA	GTTCTACTTC	700
	CGTACTACTG	ACGTGACTGG	CACCATCGAA	CTGCCGGAAG	GCGTAGAGAT	750
	GGTAATGCCG	GGCGACAACA	TCAAAATGGT	TGTTACCCTG	ATCCACCCGA	800
	TCGCAATGGA	CGACGGTCTG	CGTTTCGCAA	TC		832

15

2) INFORMATION FOR SEQ ID NO: 160

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 807 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

25 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Salmonella choleraesuis* subsp. *diarizonae*
 (B) STRAIN: ATCC 43973

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 160

	CCTGGTTGTT	GCTGCGACTG	ACGGCCCGAT	GCCGCAGACC	CGTGAGCACA	50
	TCCTGCTGGG	TCGTCAGGTA	GGCGTTCGGT	ACATTATCGT	GTTCTGAAC	100
35	AAATGCCACA	TGGTTGATGA	CGAAGAGCTG	CTGGAAGTGG	TAGAAATGGA	150
	AGTTCGTGAA	CTTCTGTCTC	AGTACGACTT	CCCGGGCGAC	GACACGCCAA	200
	TCGTTCTGGG	TTCTGCTCTG	AAAGCGCTGG	AAGGCGACGC	AGAGTGGGAA	250
	GCGAAAATCA	TCGAACTGGC	TGGCTTCCTG	GATTCTTACA	TCCCGGAACC	300
	AGAGCGTGCG	ATTGACAAGC	CGTTCCTGCT	GCCGATCGAA	GACGTATTCT	350
40	CCATCTCCGG	TCGTGGTACC	GTTGTTACCG	GTCGTGTAGA	GCGCGGTATC	400
	ATCAAAGTGG	GCGAAGAAGT	TGAAATCGTT	GGTATCAAAG	AGACTCAGAA	450
	GTCTACCTGT	ACTGGCGTTG	AAATGTTCCG	CAARCTGCTG	GACGAAGGCC	500
	GTGCWGCTGA	GAACGTAGGT	GTTCTGCTGC	GTGGTATCAA	ACGTGAAGAA	550
	ATCGAACGTG	GTCAGGTACT	GGCTAAGCCG	GGCACCATCA	AGCCGCACAC	600
45	CAAGTTCGAA	TCTGAAGTGT	ATATTCTGTC	CAAAGATGAA	GGCGGCCGTC	650
	ATACTCCGTT	CTTCAAAGGC	TACCGTCCGC	AGTTCTACTT	CCGTACCACT	700
	GACGTGACTG	GCACCATCGA	ACTGCCGGAA	GGCGTGGAGA	TGGTAATGCC	750
	GGGCGACAAC	ATCAAAATGG	TTGTTACCCT	GATCCACCCG	ATCGCGATGG	800
	ACGACGG					807

50

2) INFORMATION FOR SEQ ID NO: 161

(i) SEQUENCE CHARACTERISTICS:

- 55 (A) LENGTH: 832 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

60

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Salmonella choleraesuis* subsp. *choleraesuis*
 serotype Heidelberg
 (B) STRAIN: ATCC 8326

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 161

```

10  CGGCGCGATC CTGGTTGTTG CTGCGACTGA CGGCCCGATG CCGCAGACCC      50
    GTGAGCACAT CCTGCTGGGT CGTCAGGTAG GCGTTCCGTA CATCATCGTG      100
    TTCCTGAACA AATGCGACAT GGTGTATGAC GAAGAGCTGC TGGAACTGGT      150
    TGAAATGGAA GTTCGTGAAC TTCTGTCTCA GTACGACTTC CCGGGCGACG      200
    ACACTCCGAT CGTTCGTGGT TCTGCTCTGA AAGCGCTGGA AGGCGACGCA      250
15  GAGTGGGAAG CGAAAATCAT CGAACTGGCT GGCTTCCTGG ATTCTTACAT      300
    CCCGGAACCA GAGCGTGCGA TTGACAAGCC GTTCCTGCTG CCGATCGAAG      350
    ACGTATTCTC CATCTCCGGT CGTGGTACCG TTGTTACCGG TCGTGTAGAA      400
    CGCGGTATCA TCAAAGTGGG CGAAGAAGTT GAAATCGTTG GTATCAAAGA      450
    GACTCAGAAG TCTACCTGTA CTGGCGTTGA AATGTTCCGC AAATGCTGCG      500
20  ACGAAGGCCG TGCCGGTGAG AACGTAGGTG TTCTGCTGCG TGGTATCAAA      550
    CGTGAAGAAA TCGAACGTGG TCAGGTACTG GCTAAGCCGG GCACCATCAA      600
    GCCGCACACC AAGTTCGAAT CTGAAGTGTA CATTCTGTCC AAAGATGAAG      650
    GCGGCCGTCA YACTCCGTTT TTCAAAGGCT ACCGTCCGCA GTTCTACTTC      700
    CGTACTACTG ACGTGACTGG CACCATCGAA TTGCCGGAAG GCGTAGAGAT      750
25  GGTAATGCCG GGCAGACAACA TCAAATGGT TGTTACCCTG ATCCACCCGA      800
    TCGCGATGGA CGACGGTCTG CGTTTCGCAA TC                      832
  
```

30 2) INFORMATION FOR SEQ ID NO: 162

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 807 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Salmonella choleraesuis* subsp. *houtenae*
 (B) STRAIN: ATCC 43974

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 162

```

45  CCTGGTTGTT GCTGCGACTG ACGGCCCGAT GCCGCAGACC CGTGAGCACA      50
    TCCTGCTGGG TCGTCAGGTA GCGGTTCCGT ACATCATCGT GTTCCTGAAC      100
    AAATGCGACA TGGTTGATGA CGAAGAGCTG CTGGAAGTGG TAGAAATGGA      150
    AGTTTCGTGAA CTTCTGTCTC AGTACGATTT CCCGGGCGAC GACACGCCGA      200
50  TCGTGCGTGG TTCTGCTCTG AAAGCGCTGG AAGGCGACGC AGAATGGGAA      250
    GCGAAAATCA TCGAACTGGC TGGCTACCTG GATTCTTACA TCCCGGAACC      300
    AGAGCGTGCG ATTGACAAAC CGTTCCTGCT GCCGATCGAA GACGTATTCT      350
    CTATCTCCGG TCGTGGTACC GTTGTTACCG GTCGTGTAGA GCGCGGTATC      400
    ATCAAAGTGG GCGAAGAAGT TGAAATCGTT GGTATCAAAG AGACTCAGAA      450
55  GTCGACCTGT ACTGGCGTTG AAATGTTCCG CAAACTGCTG GACGAAGGCC      500
    GTGCTGGCGA GAACGTAGGT GTTCTGCTGC GTGGTATCAA ACGTGAAGAA      550
    ATCGAACGTG GTCAGGTACT GGCTAAGCCG GGCACCATCA AGCCGCACAC      600
    CAAGTTCGAA TCTGAAGTGT ACATTCTGTC CAAAGATGAA GGCGGCCGTC      650
    AATTCCGTTT CTTCAAAGGC TACCGTCCGC AATTCTACTT CCGTACGACT      700
60  GACGTGACTG GCACCATCGA ACTGCCGGAA GCGGTGGAGA TGGTAATGCC      750
  
```

GGGCGACAAC ATCAAAATGG TTGTTACCCT GATCCACCCG ATCGCGATGG 800
ACGACGG 807

5

2) INFORMATION FOR SEQ ID NO: 163

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 827 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

15

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Salmonella choleraesuis* subsp. *indica*
(B) STRAIN: ATCC 43976

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 163

CGCGATCCTG GTTGTGCTG CGACTGACGG CCGATGCCG CAGACCCGTG 50
AGCACATCCT GCTGGGTCGT CAGGTAGGCG TTCCGTACAT CATCGTGTTT 100
CTGAACAAAT GCGACATGGT TGATGACGAA GAGCTGCTGG AACTGGTTGA 150
25 AATGGAAGTT CGTGAAC TTC TCTCAGTA CGACTTCCCG GGTGACGACA 200
CGCCGATCGT GCGTGGTTCT GCTCTGAAAG CGCTGGAAGG CGACGCAGAG 250
TGGGAAGCGA AAATCATCGA ACTGGCTGGC TTCCTGGATT CTTACATTCC 300
GGAACCAGAG CGTGCGATTG ACAAGCCGTT CCTGCTGCCG ATCGAAGACG 350
TATTCTCCAT CTCCGGTCGT GGTACYGTTG TTACCGGTG TG TAGAGCGC 400
30 GGTATCATCA AAGTGGGCGA AGAAGTTGAA ATCGTTGGTA TCAAAGAGAC 450
TCAGAAGTCT ACCTGTACTG GCGTTGAAAT GTTCCGCAA CTGCTGGACG 500
AAGGCCGTGC CCGTGAGAAC GTAGGTGTTT TGCTGCGTGG TATCAAACGT 550
GAAGAAATCG AACGTGGTCA GGTACTGGCT AAGCCGGGCA CCATCAAGCC 600
GCACACCAAG TTCGAATCTG AAGTGATCAT TCTGTCCAAA GATGAAGGCG 650
35 GCCGTCATAC TCCGTTCTTC AAAGGCTACC GTCCGCAGTT CTACTTCCGT 700
ACTACTGACG TGACTGGCAC CATCGAACTG CCGGAAGGCG TAGAGATGGT 750
AATGCCGGGC GACAACATCA AAATGGTTGT TACCCTGATC CATCCGATCG 800
CRATGGACGA CCGTCTGCGT TTCGCAA 827

40

2) INFORMATION FOR SEQ ID NO: 164

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 807 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Salmonella choleraesuis* subsp. *salamae*
(B) STRAIN: ATCC 43972

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 164

CCTGGTTGTT GCTGCGACTG ACGGCCCGAT GCCGCAGACC CGTGAGCACA 50
TCCTGCTGGG TCGTCAGGTA GGCGTTCCGT ACATCATCGT GTTCCTGAAC 100
60 AAATGCGACA TGGTTGATGA CGAAGAGCTG CTGGAAGTGG TAGAAATGGA 150

	AGTTCGTGAA	CTTCTGTCTC	AGTACGACTT	CCCGGGCGAC	GACACGCCGA	200
	TCGTGCGTGG	TTCCGCTCTG	AAAGCGCTGG	AAGGCGAMGC	TGAGTGGGAA	250
	GMGAAAATCA	TCGAACTGGC	TGGCTWCCTG	GATTCTTACA	TTCCGGAACC	300
	AGAGCGTGCG	ATTGACAAGC	CGTTCCTGCT	GCCGATCGAA	GACGTATTCT	350
5	CCATCTCCGG	TCGTGGTACC	GTTGTTACCG	GTCGTGTAGA	GCGCGGTATC	400
	ATCAAAGTGG	GCGAAGAAGT	TGAAATCGTT	GGTATCAAAG	AGACTCAGAA	450
	GTCTACCTGT	ACTGGCGTTG	AAATGTTCCG	CAAACGTCTG	GACGAAGGCC	500
	GTGCCGGTGA	GAACGTAGGT	GTTCTGCTGC	GTGGTATCAA	ACGTGAAGAA	550
	ATCGAACGTG	GTCAGGTACT	GGCTAAGCCG	GGCACCATCA	AGCCGCACAC	600
10	CAAGTTCGAA	TCTGAAGTGT	ACATTCTGTC	CAAAGATGAA	GGCGGCCGTC	650
	ATACTCCGTT	CTTCAAAGGC	TACCGTCCGC	AGTTCTACTT	CCGTACCCT	700
	GACGTGACTG	GCACCATCGA	ACTGCCGGAA	GGCGTGGAGA	TGGTAATGCC	750
	GGGCGACAAC	ATCAAATGG	TTGTTACCCT	GATCCACCCG	ATCGCGATGG	800
	ACGACGG					807

15

2) INFORMATION FOR SEQ ID NO: 165

20 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 832 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

25

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Salmonella choleraesuis* subsp. *choleraesuis*
 serotype Typhi
 (B) STRAIN: ATCC 10749

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 165

35	CGGCGCGATC	CTGGTTGTTG	CTGCGACTGA	CGGCCCGATG	CCGCAGACCC	50
	GTGAGCACAT	CCTGCTGGGT	CGTCAGGTAG	GCGTTCCGTA	CATCATCGTG	100
	TTCCTGAACA	AATGCGACAT	GGTTGATGAC	GAAGAGCTGC	TGGAAGTGGT	150
	TGAAATGGAA	GTTCTGTAAC	TTCTGTCTCA	GTACGACTTC	CCGGGCGACG	200
	ACACGCCGAT	CGTTCGTGGT	TCTGCTCTGA	AAGCGCTGGA	AGGCGACGCA	250
40	GAGTGGGAAG	CGAAAATCAT	CGAACTGGCT	GGCTTCCTGG	ATTCTTACAT	300
	CCCGGAACCA	GAGCGTGCGA	TTGACAAGCC	GTTCTGCTG	CCGATCGAAG	350
	ACGTATTCTC	CATCTCCGGT	CGTGGTACCG	TTGTTACCGG	TCGTGTAGAA	400
	CGCGGTATCA	TCAAAGTGGG	CGAAGAAGTT	GAAATCGTTG	GTATCAAAGA	450
	GAFTCAGAAG	TCTACCTGTA	CTGGCGTTGA	AATGTTCCGC	AAACTGCTGG	500
45	ACGAAGGCCG	TGCNNGTGAG	AACGTAGGTG	TTCTGCTGCG	TGGTATCAAA	550
	CGTGAAGAAA	TCGAACGTGG	TCAGGTACTG	GCTAAGCCGG	GCACCATCAA	600
	GCCGCACACY	AAGTTCGAAT	CTGAAGTGTA	CATTCTGTCC	AAAGATGAAG	650
	GCGGCCGTCA	TACTCCGTTT	TTCAAAGGCT	ACCGTCCGCA	GTTCTACTTC	700
	CGTACTACTG	ACGTGACTGG	CACCATCGAA	CTGCCGGAAG	GCGTAGAGAT	750
50	GGTAATGCCG	GGCGACAACA	TCAAATGGT	TGTTACCCTG	ATCCACCCGA	800
	TCGCAATGGA	CGACGGTCTG	CGTTTCGCAA	TC		832

55 2) INFORMATION FOR SEQ ID NO: 166

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 817 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double

50

100

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

5 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Serratia fonticola*

(B) STRAIN: DSM 4576

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 166

10

	CGGCGCTATC	CTGGTTGTAG	CTGCGACTGA	CGGCCCTATG	CCTCAGACTC	50
	GTGAGCACAT	CCTGCTGGGT	CGTCAGGTTG	GCGTTCCTTA	CATCATCGTA	100
	TTCATGAACA	AATGCGACAT	GGTTGATGAT	GAAGAGCTGC	TGGAAGTGGT	150
	AGAAATGGAA	GTTTCGTGAAC	TTCTGTCTGC	TTATGACTTC	CCTGGTGATG	200
15	ACCTGCCGGT	TGTTTCGTGGT	TCAGCGCTGA	AAGCACTGGA	AGGCGAAGCT	250
	GAGTGGGAAG	CTAAAATCAT	CGAGCTGGCC	GGTCACCTGG	ATTCCTACAT	300
	CCCAGAACCA	GAGCGTGCTA	TCGATCAGCC	GTTTCCTGCTG	CCAATCGAAG	350
	ACGTATTCTC	CATCTCCGGT	CGTGGTACCG	TAGTTACCGG	TCGTGTTGAG	400
	CGCGGTATCG	TTAAAGTTGG	CGAAGAAGTT	GAAATCGTTG	GTATCAAAGA	450
20	CACCGTTAAG	TCTACCTGTA	CTGGCGTTGA	AATGTTCCGC	AAACTGCTGG	500
	ACGAAGGCCG	TGCTGGTGAG	AACGTTGGTG	TTCTGCTGCG	TGGTATCAAG	550
	CGTGAAGACA	TCGAACGTGG	TCAGGTACTG	GCTAAACCAG	GTTCCATCAA	600
	GCCGCACACT	CAGTTCGATT	CAGAAGTGTA	TATCCTGAGC	AAAGAAGAAG	650
	GTGGTCGTCA	TACTCCATTC	TTCAAAGGCT	ACCGTCCACA	GTTCTACTTC	700
25	CGTACAAC TG	ACGTGACCGG	TACCATCGAA	CTGCCAGAAG	GCGTAGAGAT	750
	GGTAATGCCA	GGCGATAACG	TGAACATGGT	TGTTACCCTG	ATCCACCCAA	800
	TCGCTATGGA	CCAAGGC				817

30

2) INFORMATION FOR SEQ ID NO: 167

(i) SEQUENCE CHARACTERISTICS:

35 (A) LENGTH: 787 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

40

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Serratia liquefaciens*

(B) STRAIN: ATCC 27592

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 167

	GCTGCGACTG	ACGGCCCAAT	GCCTCAGACC	CGTGAGCACA	TCCTGCTGGG	50
	TCGTCAGGTT	GGCGTTCCTT	TCATCATCGT	ATTCATGAAC	AAATGCGACA	100
	TGGTTGATGA	TGAAGAGCTG	CTGGAAGTGG	TAGAAATGGA	AGTTCGTGAA	150
50	CTTCTGTCTG	CTTACGACTT	CCCTGGTGAT	GACCTGCCGG	TTGTTTCGTGG	200
	TTCAGCGCTG	AAAGCACTGG	AAGGCGAAGC	TGAGTGGGAA	GCTAAAATCA	250
	TCGAGCTGGC	CGGTTACCTG	GATTCTTACA	TCCCAGAACC	AGAGCGTGCT	300
	ATCGACAAGC	CGTTCCTGCT	GCCAATCGAA	GACGTCTTCT	CCATCTCCGG	350
	TCGTGGTACC	GTTGTTACCG	GTCGTGTTGA	GCGCGGTATC	GTTAAAGTTG	400
55	GCGAAGAAGT	TGAAATCGTT	GGTATCAAAG	ACACCGTTAA	GTCTACCTGT	450
	ACTGGCGTTG	AAATGTTCCG	CAAAGTCTG	GACGAAGGCC	GTGCTGGTGA	500
	GAACGTTGGT	GTTCTGCTGC	GTGGTATCAA	GCGTGAAGAC	ATCGAACGTG	550
	GTCAGGTACT	GGCTAAACCA	GGTTCAATCA	AGCCACACAC	CAAGTTCGAC	600
	TCAGAAGTGT	ACATCCTGAG	CAAAGAAGAA	GGTGGTCGTC	ATACTCCATT	650
60	CTTCAAAGGC	TACCGTCCAC	AGTTCTACTT	CCGTACAAC	GACGTGACCG	700

GTACCATCGA ACTGCCAGAA GGC GTT GAAA TGGTAATGCC AGGTGACAAC 750
 GTGAACATGG TTGTTACCCT GATCCACCCA ATCGCGA 787

5

2) INFORMATION FOR SEQ ID NO: 168

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 745 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

15

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Serratia marcescens*
 (B) STRAIN: ATCC 13880

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 168

GCCTCAGACT CGTGAGCACA TCCTGCTGGG TCGTCAGGTT GGC GTT CCTT 50
 TCATCATCGT ATTCATGAAC AAATGCGACA TGGTTGATGA TGAAGAGCTG 100
 YTGGAAC TGG TAGAAATGGA AGTTCGCGAA CTGCTGTCCG CTTACGACTT 150
 25 CCCTGGCGAC GACCTGCCGG TAATCCGCGG TTCCGCGCTG AAAGCGCTGG 200
 AAGGCGAAGC TGAGTGGGAA GCGAAAATCA TCGAACTGGC CGAAGCCCTG 250
 GACAGCTACA TCCCAGAGCC AGAGCGTGCT ATCGACAAGC CGTTCCTGCT 300
 GCCAATCGAA GACGTATTCT CCATCTCCGG TCGTGGTACC GTTGTTACCG 350
 GTCGTGTTGA GCGCGGCATC ATCAAAGTTG GCGAAGAAGT TGAAATCGTT 400
 30 GGTATCAAAG ACACCGTTAA GTCTACCTGT ACTGGCGTTG AAATGTTCCG 450
 CAAACTGCTG GACGAAGGCC GTGCTGGTGA GAACGTAGGT GTTCTGCTGC 500
 GTGGTATCAA ACGTGAAGAA ATCGAACGTG GTCAGGTACT GGCTAAGCCA 550
 GGCTCCATCA AGCCGCACAC CCAGTTCGAA TCTGAAGTGT ACATCCTGAG 600
 CAAAGATGAA GGTGGTCGTC ACACKCCATT CTTCAAAGGC TACCGTCCAC 650
 35 AGTTCTACTT CCGTACCACT GACGTGACCG GTACCATCGA ACTGCCAGAA 700
 GCGCTAGAGA TGGTAATGCC AGGCGACAAC GTGAACATGG TTGTA 745

40 2) INFORMATION FOR SEQ ID NO: 169

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 829 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

50

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Serratia odorifera*
 (B) STRAIN: ATCC 33077

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 169

55

GGCGCAATCC TGGTTGTTGC TGCGACTGAC GGCCCTATGC CTCAGACCCG 50
 TGAGCACATC CTGCTGGGTC GCCAGGTTGG CGTTCCTTTC ATCATCGTGT 100
 TCATGAACAA ATGTGACATG GTTGATGACG AAGAGCTGCT GGAAGCTGTA 150
 GAAATGGAAG TTCGCGAGCT GCTGTCTGCT TACGATTTC CTGGCGACGA 200
 60 CCTGCCAGTA ATCCGCGGTT CTGCGCTGAA AGCGCTGGAA GGCGAAGCAG 250

	AGTGGGAAGC	TAAGATTGTA	GAAGCTGGCTG	AAGCGCTGGA	TTCTTACATC	300
	CCAGAACCAG	AGCGTGCTAT	CGACAAGCCG	TTCCTGCTGC	CAATCGAAGA	350
	CGTATTCTCC	ATCTCCGGTC	GTGGTACCGT	TGTTACCGGT	CGTGTGAGC	400
	GCGGTATCAT	CAAAGTTGGC	GAAGAAGTTG	AAATCGTTGG	TATCAAAGAC	450
5	ACCGTTAAGT	CTACCTGTAC	CGGTGTAGAA	ATGTTCCGCA	AACTGCTGGA	500
	CGAAGGCCGT	GCTGGTGAGA	ACGTTGGTGT	TCTGCTGCGT	GGTATCAAGC	550
	GTGAAGACAT	CGAACGTGGT	CAGGTTCTGG	CTAAACCAGG	TTCTATCAAG	600
	CCGCACACCA	AATTCGACTC	AGAAGTGTAC	ATCCTGAGCA	AAGAAGAAGG	650
	TGGTCGTCAC	ACGCCATTCT	TCAAAGGCTA	CCGTCCACAG	TTCTACTTCC	700
10	GTACTACTGA	CGTGACCGGT	ACCATCGAAC	TGCCAGAAGG	CGTAGAGATG	750
	GTAATGCCAG	GCGATAACGT	GAACATGGTT	GTTACCCCTGA	TTCACCCAAT	800
	CGCAATGGAC	GACGGTCTGC	GTTTCGCAA			829

15

2) INFORMATION FOR SEQ ID NO: 170

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 830 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

25

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Serratia plymuthica*
 (B) STRAIN: DSM 4540

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 170

	CGGCGCAATC	CTGGTTGTTG	CTGCGACTGA	CGGCCCAATG	CCTCAGACCC	50
	GTGAGCACAT	CCTGCTGGGT	CGTCAGGTTG	GCGTTCCTTT	CATCATCGTA	100
	TTCATGAACA	AATGCGACAT	GGTTGATGAT	GAAGAGCTGC	TGGAAGTGGT	150
35	AGAAATGGAA	GTTCTGTGAAC	TTCTGTCTGC	TTACGACTTC	CCTGGTGATG	200
	ACCTGCCGGT	TGTTCTGTGGT	TCAGCGCTGA	AAGCACTGGA	AGGCGAACCA	250
	GAGTGGGAAG	CTAAAATCAT	CGAGCTGGCT	GGTTTCCTGG	ATTCTTACAT	300
	CCCAGAACCA	GAGCGTGCTA	TCGACAAGCC	GTTCTCTGCTG	CCAATCGAAG	350
	ACGTATTCTC	CATCTCCGGT	CGTGGTACCG	TTGTTACCGG	TCGTGTTGAG	400
40	CGCGGTATCG	TTAAAGTTGG	CGAAGAAGTT	GAAATCGTGG	GTATCAAAGA	450
	CACCGTTAAG	TCTACCTGTA	CCGCGTGTGA	AATGTTCCGC	AAACTGCTGG	500
	ACGAAGGCCG	TGCTGGTGAG	AACGTGGGTG	TTCTGCTGCG	TGGTATCAAG	550
	CGCGAAGATA	TCGAACGTGG	TCAGGTCCTG	GCTAAACCAG	GTTCAATCAA	600
	GCCACACACC	AAGTTTGACT	CAGAAGTGTA	CATCCTGAGC	AAAGAAGAAG	650
45	GTGGTCGTCA	TACTCCATTG	TTCAAAGGCT	ACCGTCCACA	GTTCTACTTC	700
	CGTACAACCTG	ACGTGACCGG	TACCATCGAA	CTGCCAGAAG	GCGTAGAGAT	750
	GGTAATGCCA	GGTGACAACG	TGAACATGGT	TGTAACCCTG	ATCCACCCAA	800
	TCGCGATGGA	CGACGGCCTG	CGTTTCGCAA			830

50

2) INFORMATION FOR SEQ ID NO: 171

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 829 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Serratia rubidaea*
 (B) STRAIN: ATCC 27593

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 171

	GGCGCAATCC	TGGTAGTAGC	AGCGACTGAC	GGCCCAATGC	CTCAGACCCG	50
	TGAGCACATC	CTGCTGGGCC	GCCAGGTAGG	CGTACCTTAC	ATCATCGTAT	100
10	TCATGAACAA	ATGCGACATG	GTAGATGATG	AAGAGCTGCT	GGAAGCTGGTA	150
	GAGATGGAAG	TTCGCGAACT	GCTGTCTGCT	TACGACTTCC	CAGGCGACGA	200
	CCTGCCGGTA	ATCCGTGGTT	CCGCGCTGAA	AGCGCTGGAA	GGCGAAGCCG	250
	AGTGGGAAGC	GAAAATCGTT	GAGCTGGCAG	AAGCGCTGGA	CAGCTACATC	300
	CCAGAGCCAG	AGCGTGCTGT	AGACAAGCCG	TTCCTGCTGC	CAATCGAAGA	350
15	CGTATTCTCC	ATCTCCGGTC	GTGGTACCGT	TGTTACCGGT	CGTGTAGAGC	400
	GCGGTATCAT	CAAAGTTGGT	GAAGAAGTAG	AAATCGTAGG	TATCAAAGAC	450
	ACCGTTAAGT	CTACCTGTAC	TGGCGTAGAA	ATGTTCCGCA	AACTGCTGGA	500
	CGAAGGCCGT	GCTGGTGAGA	ACGTAGGTGT	TCTGCTGCGT	GGTATCAAGC	550
	GTGAAGAAAT	CGAACGTGGT	CAGGTACTGG	CGAAGCCAGG	TTCAATCAAG	600
20	CCGCACACCC	AGTTCGAATC	TGAAGTGATC	ATTCTGTCCA	AAGACGAAGG	650
	CGGCCGTCAT	ACTCCGTTCT	TCAAAGGCTA	CCGTCCACAG	TTCTACTTCC	700
	GTACAACTGA	CGTGACCGGT	ACCATCGAAC	TGCCAGAAGG	CGTAGAGATG	750
	GTAATGCCAG	GCGACAACGT	GAACATGAAA	GTTACTCTGA	TTCACCCAAT	800
	CGCAATGGAC	GACGGTCTGC	GTTTCGCAA			829

25

2) INFORMATION FOR SEQ ID NO: 172

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 826 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Shigella boydii*
 (B) STRAIN: ATCC 9207

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 172

	CGGCGCGATC	YTGGTAGTTG	CTGCGACTGA	CGGCCCGATG	CCGCAGACTC	50
45	GTGAGCACAT	CCTGCTGGGT	CGTCAGGTAG	GCGTTCCGTA	CATCATCGTG	100
	TTCCTGAACA	AATGCGACAT	GGTTGATGAC	GAAGAGCTGC	TGGAAGTGGT	150
	TGAAATGGAA	GTTCGTGAAC	TTCTGTCTCA	GTACGACTTC	CCGGGCGACG	200
	ACACTCCGAT	CGTTCGTGGT	TCTGCTCTGA	AAGCGCTGGA	AGGCGACGCA	250
	GAGTGGGAAG	CGAAAATCCT	GGAAGTGGCT	GGCTTCCTGG	ATTCTTACAT	300
50	TCCGGAACCA	GAGCGTGCGA	TTGACAAGCC	GTTCTGCTG	CCGATCGAAG	350
	ACGTATTCTC	CATCTCCGGT	CGTGGTACCG	TTGTTACCGG	TCGTGTAGAA	400
	CGCGGTATCA	TCAAAGTTGG	TGAAGAAGTT	GAAATCGTTG	GTATCAAAGA	450
	GAICTCAGAAG	TCTACCTGTA	CTGGCGTTGA	AATGTTCCGC	AAACTGCTGG	500
	ACGAAGGCCG	TGCTGGTGAG	AACGTAGGTG	TTCTGCTGCG	TGGTATCAAA	550
55	CGTGAAGAAA	TCGAACGTGG	TCAGGTACTG	GCTAAGCCGG	GCACCATCAA	600
	GCCGCACACC	AAGTTCGAAT	CTGAAGTGTA	CATTCTGTCC	AAAGATGAAG	650
	GCGGCCGTC	TACTCCGTT	TTCAAAGGCT	ACCGTCCGCA	GTTCTACTTC	700
	CGTACTACTG	ACGTGACTGG	TACCATCGAA	CTGCCGGAAG	GCGTAGAGAT	750
	GGTAATGCCG	GGCGACAACA	TCAAATGGT	TGTTACCCTG	ATCCACCCGA	800
50	TCGCGATGGA	CGACGGTCTG	CGTTTC			826

2) INFORMATION FOR SEQ ID NO: 173

5

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 818 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

10

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Shigella dysenteriae*
 (B) STRAIN: ATCC 11835

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 173

20	TGGTAGTTGC	TGCGACTGAC	GGCCCGATGC	CGCAGACTCG	TGAGCACATC	50
	CTGCTGGGTC	GTCAGGTAGG	CGTTCCGTAC	ATCATCGTGT	TCCTGAACAA	100
	ATGCGACATG	GTTGATGACG	AAGAGCTGCT	GGAAC TGGTT	GAAATGGAAG	150
	TTCGTGAACT	TCTGTCTCAG	TACGACTTCC	CGGGCGACGA	CACTCCGATC	200
	GTTCTGGT	CTGCTCTGAA	AGCGCTGGAA	GGCGACGCAG	AGTGGGAAGC	250
25	GAAAATCCTG	GAAC TGGCTG	GCTTCCTGGA	TTCYTAYATT	CCGGAACCAG	300
	AGCGTGCGAT	TGACAAGCCG	TTCCTGCTGC	CGATCGAAGA	CGTATTCTCC	350
	ATCTCCGGTC	GTGGTACCGT	TGTTACCGGT	CGTGTAGAAC	GCGGTATCAT	400
	CAAAGTTGGT	GAAGAAGTTG	AAATCGTTGG	TATCAAAGAG	ACYCAGAAGT	450
	CTACCTGTAC	TGGCGTTGAA	ATGTTCCGCA	AACTGCTGGA	CGAAGGCCGT	500
30	GCTGGTGAGA	ACGTAGGTGT	TCTGCTGCGT	GGTATCAAAC	GTGAAGAAAT	550
	CGAACGTGGT	CAGGTACTGG	CGAAGCCRG	CACCATCAAG	CCGCACACCA	600
	AGTTCGAATC	TGAAGTGTAC	ATTCTGTCCA	AAGATGAAGG	CGGCCGTCAT	650
	ACTCCGTTCT	TCAAAGGCTA	CCGTCCGCAG	TTCTACTTCC	GTACTACTGA	700
	CGTGACTGGT	ACCATCGAAC	TGCCGGAAGG	CGTAGAGATG	GTAATGCCGG	750
35	GCGACAACAT	CAAAATGGTT	GTTACCCTGA	TCCACCCGAT	CGCGATGGAC	800
	GACGGTCTGC	GTTTCGCA				818

40 2) INFORMATION FOR SEQ ID NO: 174

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 806 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

45

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Shigella flexneri*
 (B) STRAIN: ATCC 12022

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 174

55	CCTGGTAGTT	GCTGCGACTG	ACGGCCCGAT	GCCGCAGACT	CGTGAGCACA	50
	TCCTGCTGGG	TCGT CAGGTA	GGCGTTCGGT	ACATCATCGT	GTTCTGAAC	100
	AAATGCGACA	TGGTTGATGA	CGAAGAGCTG	CTGGAAC TGG	TTGAAATGGA	150
	AGTTCGTGAA	CTTCTGTCTC	AGTACGACTT	CCCGGGCGAC	GACACTCCGA	200
60	TCGTTCTGGT	TTCTGCTCTG	AAAGCGCTGG	AAGGCGACGC	AGAGTGGGAA	250

	CGGAAAATCC	TGGAAC TGGC	TGGCTTCCTG	GATTCTTACA	TTCCGGAACC	300
	AGAGCGTGCG	ATTGACAAGC	CGTTCCTGCT	GCCGATCGAA	GACGTATTCT	350
	CCATCTCCGG	TCGTGGTACC	GTTGTTACCG	GTCGTGTAGA	ACGCGGTATC	400
	ATCAAAGTTG	GTGAAGAAGT	TGAAATCGTT	GGTATCAAAG	AGACTCAGAA	450
5	GTCTACCTGT	ACTGGCGTTG	AAATGTTCCG	CAAAC T GCTG	GACGAAGGCC	500
	GTGCTGGTGA	GAACGTAGGT	GTTCTGCTGC	GTGGTATCAA	ACGTGAAGAA	550
	ATCGAACGTG	GTCAGGTACT	GGCTAAGCCG	GGCACCATCA	AGCCGCACAC	600
	CAAGTTCGAA	TCTGAAGTGT	ACATTCTGTC	CAAAGATGAA	GGCGGMCCTC	650
	ATACTCCGTT	CTTCAAAGGC	TACCGTCCGC	AGTTCTACTT	CCGTACTACT	700
10	GACGTGACTG	GTACCATCGA	ACTGCCGGAA	GGCGTAGAGA	TGGTAATGCC	750
	GGGCGACAAC	ATCAAAATGG	TTGTTACCCT	GATCCACCCG	ATCGCGATGG	800
	ACGACG					806

15

2) INFORMATION FOR SEQ ID NO: 175

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 832 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

25

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Shigella sonnei*
 (B) STRAIN: ATCC 29930

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 175

	CGGCGCGATC	CTGGTAGTTG	CTGCGACTGA	CGGCCCGATG	CCGCAGACTC	50
	GTGAGCACAT	CCTGCTGGGT	CGTCAGGTAG	GCGTTCCGTA	CATCATCGTG	100
	TTCTGAACA	AATGCGACAT	GGTTGATGAC	GAAGAGCTGC	TGGAAC TGGT	150
35	TGAAATGGAA	GTTCTGTGAAC	TTCTGTCTCA	GTACGACTTC	CCGGGCGACG	200
	ACACTCCGAT	CGTTCGTGGT	TCTGCTCTGA	AAGCGCTGGA	AGGCGACGCA	250
	GAGTGGGAAG	CGAAAATCCT	GGAAC TGGCT	GGCTTCCTGG	ATTCTTACAT	300
	TCCGGAACCA	GAGCGTGCGA	TTGACAAGCC	GTTCTGCTG	CCGATCGAAG	350
	ACGTATTCTC	CATCTCCGGT	CGTGGTACCG	TTGTTACCGG	TCGTGTAGAA	400
40	CGCGGTATCA	TCAAAGTTGG	TGAAGAAGTT	GAAATCGTTG	GTATCAAAGA	450
	GACTCAGAAG	TCTACCTGTA	CTGGCGTTGA	AATGTTCCGC	AAACTGCTGG	500
	ACGAAGGCCG	TGCTGGTGAG	AACGTAGGTG	TTCTGCTGCG	TGGTATCAAA	550
	CGTGAAGAAA	TCAACGTGG	TCAGGTACTG	GCTAAGCCGG	GCACCATCAA	600
	GCCGCACACC	AAGTTCGAAT	CTGAAGTGTA	CATTCTGTCC	AAAGATGAAG	650
45	GCGGYCGTCA	TACTCCGTTT	TTCAAAGGCT	ACCGTCCGCA	GTTCTACTTC	700
	CGTACTACTG	ACGTGACTGG	TACCATCGAA	CTGCCGGAAG	GCGTAGAGAT	750
	GGTAATGCCG	GGCGACAACA	TCAAAATGGT	TGTTACCCTG	ATCCACCCGA	800
	TCGCGATGGA	CGACGGTCTG	CGTTTCGCAA	TC		832

50

2) INFORMATION FOR SEQ ID NO: 176

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 716 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

60

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus aureus*
 (B) STRAIN: ATCC 13301

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 176

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TCTGCTGCTG ACGGTCCAAT GCCACAACT CGTGAACACA TTCTTTTATC      50
ACGTAACGTT GGTGTACCAG CATTAGTAGT ATTCTTAAAC AAAGTTGACA      100
10 TGGTTGACGA TGAAGAATTA TTAGAATTAG TAGAAATGGA AGTTCGTGAC      150
TTATTAAGCG AATATGACTT CCCAGGTGAC GATGTACCTG TAATCGCTGG      200
TTCAGCATTA AAAGCTTTAG AAGGCGATGC TCAATACGAA GAAAAAATCT      250
TAGAATTAAT GGAAGCTGTA GATACTTACA TTCCAACCTCC AGAACGTGAT      300
TCTGACAAAC CATTTCATGAT GCCAGTTGAG GACGTATTCT CAATCACTGG      350
15 TCGTGGTACT GTTGCTACAG GCCGTGTTGA ACGTGGTCAA ATCAAAGTTG      400
GTGAAGAAGT TGAAATCATC GGTTTACATG ACACATCTAA AACAACTGTT      450
ACAGGTGTTG AAATGTTCCG TAAATTATTA GACTACGCTG AAGCTGGTGA      500
CAACATTGGT GCATTATTAC GTGGTGTTCG TCGTGAAGAC GTACAACGTG      550
GTCAAGTATT AGCTGCTCCT GGTTC AATTA CACCACATAC TGAATTCAAA      600
20 GCAGAAGTAT ACGTATTATC AAAAGACGAA GGTGGACGTC ACACTCCATT      650
CTTCTCAAAC TATCGTCCAC AATTCTATTT CCGTACTACT GACGTAACCTG      700
GTGTTGTTCA CTTACC                                     716

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25

2) INFORMATION FOR SEQ ID NO: 177

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 719 bases
 30 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

35

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus aureus*
 (B) STRAIN: ATCC 29247

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 177

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TTCTTTTATC ACGTAACGTT GGTGTACCAG CATTAGTAGT ATTCTTAAAC      50
AAAGTTGACA TGGTTGACGA TGAAGAATTA TTAGAATTAG TAGAAATGGA      100
AGTTCGTGAC TTATTAAGCG AATATGACTT CCCAGGTGAC GATGTACCTG      150
45 TAATCGCTGG TTCAGCATTA AAAGCTTTAG AAGGCGATGC TCAATACGAA      200
GAAAAAATCT TAGAATTAAT GGAAGCTGTA GATACTTACA TTCCAACCTCC      250
AGAACGTGAT TCTGACAAAC CATTTCATGAT GCCAGTTGAG GACGTATTCT      300
CAATCACTGG TCGTGGTACT GTTGCTACAG GCCGTGTTGA ACGTGGTCAA      350
ATCAAAGTTG GTGAAGAAGT TGAAATCATC GGTTTACATG ACACATCTAA      400
50 AACAACTGTT ACAGGTGTTG AAATGTTCCG TAAATTATTA GACTACGCTG      450
AAGCTGGTGA CAACATTGGT GCATTATTAC GTGGTGTTCG TCGTGAAGAC      500
GTACAACGTG GTCAAGTATT AGCTGCTCCT GGTTC AATTA CACCACATAC      550
TGAATTCAAA GCAGAAGTAT ACGTATTATC AAAAGACGAA GGTGGACGTC      600
ACACTCCATT CTTCTCAAAC TATCGTCCAC AATTCTATTT CCGTACTACT      650
55 GACGTAACCTG GTGTTGTTCA CTTACCAGAA GGTMCTGAAA TGGTAATGCC      700
TGGTGATAAC GTTGAAATG                                     719

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60 2) INFORMATION FOR SEQ ID NO: 178

107

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 625 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus aureus*
 (B) STRAIN: ATCC 33591

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 178

```

15  GTGAACACAT TCTTTTATCA CGTAACGTTG GTGTACCAGC ATTAGTAGTA      50
    TTCTTAAACA AAGTTGACAT GGTTGACGAT GAAGAATTAT TAGAATTAGT      100
    AGAAATGGAA GTTCGTGACT TATTAAGCGA ATATGACTTC CCAGGTGACG      150
    ATGTACCTGT AATCGCTGGT TCAGCATTAA AAGCTTTAGA AGGCGATGCT      200
20  CAATACGAAG AAAAAATCTT AGAATTAATG GAAGCTGTAG ATACTTACAT      250
    TCCAACCTCA GAACGTGATT CTGACAAACC ATTCATGATG CCAGTTGAGG      300
    ACGTATTCTC AATCACTGGT CGTGGTACTG TTGCTACAGG CCGTGTTGAA      350
    CGTGGTCAAA TCAAAGTTGG TGAAGAAGTT GAAATCATCG GTTTACATGA      400
    CACATCTAAA ACAACTGTTA CAGGTGTTGA AATGTTCCGT AAATTATTAG      450
25  ACTACGCTGA AGCTGGTGAC AACATTGGTG CATTATTACG TGGTGTGCT      500
    CGTGAAGACG TACAACGTGG TCAAGTATTA GCTGCTCCTG GTTCAATTAC      550
    ACCACATACT GAATTCAAAG CAGAAGTATA CGTATTATCA AAAGACGAAG      600
    GTGGACGTCA CACTCCATTC TTCTC                                625
  
```

30

2) INFORMATION FOR SEQ ID NO: 179

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 704 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus aureus*
 (B) STRAIN: ATCC 43300

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 179

```

    GTTGGTGTA CAGCATTAGT AGTATTCTTA AACAAAGTTG ACATGGTTGA      50
    CGATGAAGAA TTATTAGAAT TAGTAGAAAT GGAAGTTCGT GACTTATTAA      100
50  GCGAATATGA CTTCCCAGGT GACGATGTAC CTGTAATCGC TGGTTCAGCA      150
    TTAAAGCTT TAGAAGCGA TGCTCAATAC GAAGAAAAAA TCTTAGAATT      200
    AATGGAAGCT GTAGATACTT ACATTCCAAC TCCAGAACGT GATTCTGACA      250
    AACCATTCA TATGCCAGTT GAGGACGTAT TCTCAATCAC TGCTCGTGGT      300
    ACTGTTGCTA CAGGCCGTGT TGAACGTGGT CAAATCAAAG TTGGTGAAGA      350
55  AGTTGAAATC ATCGGTTTAC ATGACACATC TAAACAACT GTTACAGGTG      400
    TTGAAATGTT CCGTAAATTA TTAGACTACG CTGAAGCTGG TGACAACATT      450
    GGTGCATTAT TACGTGGTGT TGCTCGTGAA GACGTACAAC GTGGTCAAGT      500
    ATTAGCTGCT CCTGGTTCAT TTACACCACA TACTGAATTC AAAGCAGAAG      550
    TATACGTATT ATCAAAAGAC GAAGGTGGAC GTCACACTCC ATTCTTCTCA      600
60  AACTATCGTC CACAATTCTA TTTCCGTACT ACTGACGTAA CTGGTGTTGT      650
  
```

TCACCTTACCA GAAGGTACTG AAATGGTAAT GCCTGGTGAT AACGTTGAAA 700
TGAC 704

5

2) INFORMATION FOR SEQ ID NO: 180

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 730 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

15

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus aureus* subsp. *aureus*
(B) STRAIN: ATCC 6538

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 180

GTGAACACAT TCTTTTATCA CGTAACGTTG GTGTACCAGC ATTAGTAGTA 50
TTCTTAAACA AAGTTGACAT GGTGACGAT GAAGAATTAT TAGAATTAGT 100
AGAAATGGAA GTTCGTGACT TATTAAGCGA ATATGACTTC CCAGGTGACG 150
25 ATGTACCTGT AATCGCTGGT TCAGCATTAA AAGCTTTAGA AGGCGATGCT 200
CAATACGAAG AAAAAATCTT AGAATTAATG GAAGCTGTAG ATACTTACAT 250
TCCAACCTCA GAACGTGATT CTGACAAACC ATTCATGATG CCAGTTGAGG 300
ACGTATTCTC AATCACTGGT CGTGGTACTG TTGCTACAGG CCGTGTTGAA 350
CGTGGTCAAA TCAAAGTTGG TGAAGAAGTT GAAATCATCG GTTTACATGA 400
30 CACATCTAAA ACAACTGTTA CAGGTGTTGA AATGTTCCGT AAATTATTAG 450
ACTACGCTGA AGCTGGTGAC AACATTGGTG CATTATTACG TGGTGTGCT 500
CGTGAAGACG TACAACGTGG TCAAGTATTA GCTGCTCCTG GTTCAATTAC 550
ACCACATACT GAATTCAAAG CAGAAGTATA CGTATTATCA AAAGACGAAG 600
GTGGACGTCA CACTCCATTG TTCTCAAAC ATCGTCCACA ATTCTATTTC 650
35 CGTACTACTG ACGTAACTGG TGTGTTCAC TTACCAGAAG GTACTGAAAT 700
GGTAATGCCT GGTGATAACG TTGAAATGAC 730

40 2) INFORMATION FOR SEQ ID NO: 181

(i) SEQUENCE CHARACTERISTICS:

- 45 (A) LENGTH: 834 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

50

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus auricularis*
(B) STRAIN: ATCC 33753

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 181

55

CGGTGCGATC TTAGTTGTAT CTGCAGCTGA TGGTCCAATG CCACAACTC 50
GTGAACACAT CTTATTATCA CGTAACGTTG GTGTACCAGC ATTAGTTGTA 100
TTCTTAAACA AAGTTGACCA AGTTGACGAC GAAGAATTAT TAGAATTAGT 150
AGAAATGGAA GTTCGTGACT TATTAAGCGA ATACGACTAC CCAGGTGACG 200
60 ATGTACCTGT AATCTCTGGT TCTGCGTTGA AAGCATTAGA AGGCGACAAA 250

	GAATACGAAC	AAAAAATCTT	AGACTTAATG	CAACAAGTTG	ACGATTACAT	300
	TCCAACCTCCA	GAACGTGACT	CTGATAAACC	ATTCATGATG	CCAGTTGAAG	350
	ACGTATTCTC	AATCACTGGT	CGTGGTACTG	TTGCAACAGG	CCGTGTTGAA	400
	CGTGGTCAAA	TCAAAGTCGG	TGAAGAAGTT	GAAATCATCG	GTATGAAAGA	450
5	CGGTTCACAA	AAAACAACAG	TTACTGGTGT	AGAAATGTTC	CGTAAATTAT	500
	TAGACTACGC	TGAAGCTGGT	GACAACATCG	GTGCTTTATT	ACGTGGTATT	550
	TCACGTGAAG	AAGTACAACG	TGGTCAAGTT	TTAGCTGCTC	CTGGTTCAAT	600
	TACACCACAC	ACTAAATTCA	CTGCAGAAGT	TTACGTATTA	TCTAAAGATG	650
	AAGGTGGACG	TCACACTCCA	TTCTTCTCTA	ACTACCGTCC	ACAATTCTAT	700
10	TTCCGCTACTA	CTGACGTAAC	AGGTGTTGTT	ACTTTACCAG	AAGGTACAGA	750
	AATGGTAATG	CCTGGCGATA	ACGTTAAAAT	GGAAGTTGAA	TTAATTTCTC	800
	CAATCGCTAT	CGAAGACGGT	ACTCGTTTCT	CAAT		834

15

2) INFORMATION FOR SEQ ID NO: 182

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 835 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

25

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus capitis* subsp. *capitis*
 (B) STRAIN: ATCC 27840

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 182

	CGGCGGTATC	TTAGTAGTAT	CTGCTGCTGA	CGGTCCAATG	CCACAAACTC	50
	GTGAACACAT	CTTATTATCA	CGTAACGTTG	GTGTACCAGC	ATTAGTTGTA	100
	TTCTTAAACA	AAGTTGACAT	GGTAGACGAC	GAAGAATTAT	TAGAATTAGT	150
35	TGAAATGGAA	GTTCTGACT	TATTAAGCGA	ATATGACTTC	CCAGGTGATG	200
	ATGTACCTGT	AATCGCTGGT	TCAGCATTAA	AAGCTTTAGA	AGGCGATGCT	250
	CAATACGAAG	AAAAAATCTT	AGAATTAATG	CAAGCAGTTG	ATGATTACAT	300
	TCCAACCTCCA	GAACGTGATT	CTGACAAACC	ATTCATGATG	CCAGTTGAGG	350
	ACGTATTCTC	AATCACTGGT	CGTGGTACTG	TTGCTACAGG	CCGTGTTGAA	400
40	CGTGGTCAAA	TCAAAGTTGG	TGAAGAAGTT	GAAATCATCG	GTATCCACGA	450
	AACTTCTAAA	ACAACTGTTA	CTGGTGTTAGA	AATGTTCCGT	AAATTATTAG	500
	ACTACGCTGA	AGCTGGTGAC	AACATCGGTG	CTTTATTACG	TGGTGTGCT	550
	CGTGAAGACG	TACAACGTGG	TCAAGTATTA	GCTGCTCCTG	GTTCAATCAC	600
	ACCACACACT	AAATTCAAAG	CGGAAGTTTA	CGTTTTATCT	AAAGACGAAG	650
45	GTGGACGTCA	CACTCCATTC	TTCAGTAACT	ACCGCCCACA	ATTCTATTTT	700
	CGTACTACTG	ACGTAACCTG	TGTTGTTAAC	TTACCAGAAG	GTAAGTAAAT	750
	GGTTATGCCT	GGCGACAACG	TTGAAATGAC	AGTTGAATTA	ATCGCTCCTA	800
	TCGCTATTGA	AGACGGTACT	CGTTTCTCAA	TCGGA		835

50

2) INFORMATION FOR SEQ ID NO: 183

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 804 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

110

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Macrococcus caseolyticus*
 (B) STRAIN: ATCC 13548

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 183

```

GTATCTTAGT AGTATCTGCT GCTGACGGTC CAATGCCACA AACTCGTGAA      50
CACATCCTTT TATCACGTAA CGTTGGTGTA CCAGCATTAG TAGTATTCTT      100
10 GAACAAAGTT GACATGGTTG ACGATGAAGA ATTATTAGAA TTAGTTGAAA      150
TGGAAGTTCG TGACTTATTA TCTGAATATG ACTTCCCTGG TGACGATGTA      200
CCTGTAATCG CTGGATCTGC TTTAAAAGCA TTAGAAGGCG TTGAAGAATA      250
CGAAGACAAA ATCATGGAAT TAATGGACGC AGTTGATGAG TACATCCCAA      300
CTCCAGAACG TGATTCTGAC AAACCATTCA TGATGCCAGT TGAGGACGTA      350
15 TTCTCAATCA CTGGTCGTGG TACAGTTGCA ACTGGACGTG TTGAGCGTGG      400
ACAAGTTAAA GTTGGTGAAG AAGTTGAAAT CATTGGTTTA ACTGAAGAAC      450
CAGCAAAAAC TACAGTTACA GGTGTAGAAA TGTTCCGTAA ATTATTAGAT      500
TACGCTGAAG CTGGAGATAA CATCGGTGCT TTATTACGTG GTGTTTCTCG      550
TGAAGACGTA CAACGTGGAC AAGTATTAGC TAAACCAGGT TCAATTACTC      600
20 CACATACTAA ATTCAAAGCT GAAGTTTACG TATTATCTAA AGAAGAAGGT      650
GGACGTCATA CTCCATTCTT CACTAACTAC CGCCCTCAGT TCTACTTCCG      700
TACAACTGAC GTAAGTGGTG TAGTTAACTT ACCAGAAGGT ACTGAAATGG      750
TAATGCCTGG AGATAACATC GAAATGAACG TTGAATTAAT TTCTCCAATC      800
GCGA                                                                804

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25

2) INFORMATION FOR SEQ ID NO: 184

30

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 832 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus cohnii*
 40 (B) STRAIN: DSM 20260

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 184

```

CGGAGCTATC TTAGTAGTAT CTGCTGCTGA TGGCCCAATG CCACAAACTC      50
45 GTGAACATAT CCTTTTATCA CGTAACGTTG GTGTTCCAGC ATTAGTTGTA      100
TTCTTAAACA AAGTTGACAT GGTTGACGAT GAAGAATTAT TAGAATTAGT      150
AGAAATGGAA GTTCGTGACT TATTAAGCGA ATATGACTTC CCAGGTGACG      200
ATGTACCTGT AATCTCTGGT TCAGCATTA AAGCTCTTGA AGGCGACGCT      250
GACTATGAGC AAAAAATCTT AGACTTAATG CAAGCTGTTG ATGACTTCAT      300
50 TCCAACACCA GAACGTGATT CTGACAAACC ATTATGATG CCAGTTGAGG      350
ACGTATTCTC AATCACTGGT CGTGGTACTG TTGCTACAGG GCGTGTTGAA      400
CGTGGTCAAA TCAAAGTCGG TGAAGAAGTT GAAATCATCG GTATGCAAGA      450
AGATTCAAGC AAAACAACCTG TTAAGTGGTGT AGAAATGTTT CGTAAATTAT      500
TAGACTACGC TGAAGCTGGT GACAACATTG GTGCGTTATT ACGTGGTGGT      550
GCACGTGAAG ACATCCAACG TGGTCAAGTT TTAGCTGCTC CTGGTTCAAT      600
TACACCACAC ACAAACCTTTA AAGCGGAAGT TTACGTTTTA TCAAAAGATG      650
AAGGTGGCCG TCATACGCCA TTCTTCAGTA ACTATCGCCC ACAATTCTAT      700
TTCCGTACTA CTGACGTAAC AGGTGTTGTT ACTTTACCAG AAGGTACTGA      750
AATGGTTATG CCTGGCGACA ACGTAGAAAT GGAAGTTGAA CTAATTTCTC      800
50 CAATCGCTAT CGAAGACGGT ACACGTTTCT CT                                                                832

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2) INFORMATION FOR SEQ ID NO: 185

5

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 699 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 10 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 15 (A) ORGANISM: *Staphylococcus epidermidis*
 (B) STRAIN: CSG 269

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 185

20 ATCTGCTGCT GACGGTCCAA TGCCACAAAC TCGTGAACAC ATCTTATTAT 50
 CACGTAACGT TGGTGTACCA GCATTAGTTG TATTCTTAAA CAAAGTTGAC 100
 ATGGTAGACG ACGAAGAATT ATTAGAATTA GTTGAAATGG AAGTTCGTGA 150
 CTTATTAAGC GAATATGACT TCCCAGGTGA CGATGTACCT GTAATCGCTG 200
 GTTCTGCATT AAAAGCATTGA GAAGGCGATG CTGAATACGA ACAAAAAATC 250
 25 TTAGACTTAA TGCAAGCAGT TGATGATTAC ATTCCAATC CAGAACGTGA 300
 TTCTGACAAA CCATTCATGA TGCCAGTTGA GGACGTATTC TCAATCACTG 350
 GTCGTGGTAC TGTGCTACA GGCCGTGTTG AACGTGGTCA AATCAAAGTT 400
 GGTGAAGAAG TTGAAATCAT CGGTATGCAC GAAACTTCTA AAACAATGT 450
 TACTGGTGTA GAAATGTTCC GTAAATTATT AGACTACGCT GAAGCTGGTG 500
 30 ACAACATCGG TGCTTTATTA CGTGGTGTG CACGTGAAGA CGTACAACGT 550
 GGTCAAGTAT TAGCTGCTCC TGGTTCTATT ACACCACACA CAAAATTCAA 600
 AGCTGAAGTA TACGTATTAT CTAAAGATGA AGGTGGACGT CACACTCCAT 650
 TCTTCACTAA CTATCGCCCA CAATTCTATT TCCGTACTAC TGACGTAAC 699

35

2) INFORMATION FOR SEQ ID NO: 186

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 829 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 45 (A) ORGANISM: *Staphylococcus haemolyticus*
 (B) STRAIN: ATCC 29970

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 186

CGGCGGTATC TTAGTAGTAT CTGCTGCTGA CGGTCCAATG CCACAACTC 50
 GTGAACACAT TCTTTTATCA CGTAACGTTG GTGTACCAGC ATTAGTAGTA 100
 55 TTCTTAAATA AAGTTGACAT GGTGACGAT GAAGAATTAT TAGAATTAGT 150
 TGAAATGGAA GTACGTGACT TATTATCTGA ATACGACTTC CCAGGTGACG 200
 ATGTACCTGT AATCGCTGGT TCAGCATTAA AAGCTTTAGA AGGCGATGCT 250
 CAATACGAAG AAAAAATCTT AGAATTAATG CAAGCAGTTG ATGACTACAT 300
 TCCAACCTCA GAACGTGATT CTGACAAACC ATTCATGATG CCAGTTGAGG 350
 60 ACGTATTCTC AATCACTGGT CGTGGTACTG TTGCTACAGG CCGTGTTGAA 400

	CGTGGGCAAA	TCAAAGTTGG	TGAAGAAGTT	GAAATCATTG	GTATCCATGA	450
	CACTTCTAAA	ACAACGTGTA	CTGGTGTAGA	AATGTTCCGT	AAATTATTAG	500
	ACTACGCTGA	AGCTGGTGAC	AACATCGGTG	CATTATTACG	TGGTGTGCT	550
	CGTGAAGACG	TACAACGTGG	TCAAGTATTA	GCTGCTCCAG	GTTCAATCAC	600
5	ACCTCACACA	AAATTTAAAG	CAGACGTATA	CGTTTTATCT	AAAGACGAAG	650
	GTGGACGTCA	CACTCCATTG	TTCACAAACT	ATCGTCCACA	ATTCTATTTC	700
	CGTACTACTG	ACGTAACGTG	TGTTGTTAAC	TTACCAGAAG	GTACTGAAAT	750
	GGTTATGCCT	GGCGACAACG	TTGAAATGAC	AGTAGAATTA	ATCGCTCCTA	800
	TCGCGATTGA	AGACGGTACT	CGTTTCTCA			829

2) INFORMATION FOR SEQ ID NO: 187

- 15 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 705 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Double
 - (D) TOPOLOGY: Linear
- 20 (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Staphylococcus warneri*
 - 25 (B) STRAIN: CSG 123

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 187

	CACAACTCG	TGAACACATT	CTTTTATCAC	GTAACGTTGG	TGTACCAGCT	50
30	TTAGTTGTAT	TCTTAAACAA	AGTTGATATG	GTAGACGACG	AAGAATTATT	100
	AGAATTAGTA	GAAATGGAAG	TTCGTGACTT	ATTATCTGAA	TATGACTTCC	150
	CAGGTGACGA	CGTACCTGTA	ATCGCTGGTT	CAGCATTAAG	AGCTTTAGAA	200
	GGCGACGAAA	AATACGAAGA	AAAAATCTTA	GAATTAATGC	AAGCAGTTGA	250
	TGACTACATT	CCAACTCCAG	AACGTGATTG	TGACAAACCA	TTCATGATGC	300
35	CAGTTGAGGA	CGTATTCTCA	ATCACTGGTC	GTGGTACTGT	TGCTACAGGC	350
	CGTGTGGAAC	GTGGTCAAAT	CAAAGTTGGT	GAAGAAAGTTG	AAATCATCGG	400
	TTTACATGAC	ACTTCTAAAA	CAACTGTTAC	TGGTGTAGAA	ATGTTCCGTA	450
	AGTTATTAGA	CTACGCTGAA	GCTGGTGACA	ACATCGGTGC	TTTATTACGT	500
	GGTGTGCTC	GTGAAGACGT	ACAACGTGGT	CAAGTATTAG	CTGCTCCTGG	550
40	TTCAATTACA	CCACATACAA	AATTCAAAGC	GGAAGTTTAC	GTTTTATCTA	600
	AAGACGAAGG	TGGACGTCAC	ACTCCATTCT	TCAGTAACTA	CCGCCACAA	650
	TTCTATTTC	GTACTACTGA	CGTAACTGGC	GTTGTTCAAT	TACCAGAAGG	700
	TACTG					705

2) INFORMATION FOR SEQ ID NO: 188

- 50 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 678 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Double
 - (D) TOPOLOGY: Linear
- 55 (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Staphylococcus haemolyticus*
 - 60 (B) STRAIN: CSG 23

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 188:

	TTTTATCACG	TAACGTTGGT	GTACCAGCAT	TAGTAGTATT	CTTAAACAAA	50
	GTTGACATGG	TTGACGATGA	AGAATTATTA	GAATTAGTTG	AAATGGAAGT	100
5	ACGTGACTTA	TTATCTGAAT	ACGACTTCCC	AGGTGACGAC	GTACCTGTAA	150
	TCGCTGGTTC	AGCTTTAAAA	GCTTTAGAAG	GCGATGCTCA	ATACGAAGAA	200
	AAAATCTTAG	AATTAATGCA	AGCAGTTGAT	GATTACATTC	CAACTCCAGA	250
	ACGTGACTCT	GATAAACCAT	TCATGATGCC	AGTTGAGGAC	GTATTCTCAA	300
	TCACTGGTCG	TGGTACTGTT	GCTACAGGTC	GTGTTGAACG	TGGTCAAATC	350
10	AAAGTTGGTG	AAGAAGTTGA	AATTATTGGT	ATCAAAGAAA	CTTCTAAAAC	400
	AACGTGTACT	GGTGTAGAAA	TGTTCCGTAA	ATTATTAGAC	TACGCTGAAG	450
	CTGGTGACAA	CATCGGTGCT	TTATTACGTG	GTGTTGCTCG	TGAAGATGTA	500
	CAACGTGGTC	AAGTATTAGC	TGCTCCAGGT	TCAATTACAC	CTCACACAAA	550
	ATTCAAAGCA	GACGTATACG	TTTTATCAAA	AGATGAAGGT	GGACGTCATA	600
15	CTCCATTCTT	CACTAACTAT	CGTCCACAAT	TCTATTTCCG	TACTACTGAC	650
	GTAAGTGGTG	TTGTTAACCT	ACCAGAAG			678

20 2) INFORMATION FOR SEQ ID NO: 189

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 668 bases
 (B) TYPE: Nucleic acid
 25 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

30 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus haemolyticus*
 (B) STRAIN: CSG 33

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 189

35	ACCAGCATTA	GTAGTATTCT	TAAATAAAGT	TGACATGGTT	GACGATGAAG	50
	AATTATTAGA	ATTAGTTGAA	ATGGAAGTAC	GTGACTTATT	ATCTGAATAC	100
	GACTTCCCAG	GTGACGATGT	ACCTGTAATC	GCTGGTTCAG	CATTAAAAGC	150
	TTTAGAAGGC	GATGCTCAAT	ACGAAGAAAA	AATCTTAGAA	TTAATGCAAG	200
40	CAGTTGATGA	CTACATTCCA	ACTCCAGAAC	GTGATTCTGA	CAAACCATTC	250
	ATGATGCCAG	TTGAGGACGT	ATTCTCAATC	ACTGGTCGTG	GTACTGTTGC	300
	TACAGGCCGT	GTTGAACGTG	GTCAAATCAA	AGTTGGTGAA	GAAGTTGAAA	350
	TCATTGGTAT	CCATGACACT	TCTAAAACAA	CTGTTACTGG	TGTAGAAATG	400
	TTCCGTAAAT	TATTAGACTA	CGCTGAAGCT	GGTGACAACA	TCGGTGCAAT	450
45	ATTACGTGGT	GTTGCTCGTG	AAGACGTACA	ACGTGGTCAA	GTATTAGCTG	500
	CTCCAGGTTT	AATCACACCT	CACACAAAAT	TTAAAGCAGA	CGTATACGTT	550
	TTATCTAAAG	ACGAAGGTGG	ACGTCACTAC	CCATTCTTCA	CAAACATATC	600
	TCCACAATTC	TATTTCCGTA	CTACTGACGT	AACTGGTGTT	GTTAACCTAC	650
50	CAGAAGGTAC	TGAAATGG				668

2) INFORMATION FOR SEQ ID NO: 190

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 593 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 50 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus haemolyticus*
 5 (B) STRAIN: CSG 8

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 190

```

10 AAAGTTGACA TGGTTGACGA TGAAGAATTA TTAGAATTAG TTGAAATGGA      50
   AGTACGTGAC TTATTATCTG AATACGACTT CCCAGGTGAC GATGTACCTG      100
   TAATCGCTGG TTCAGCATTAA AAAGCTTTAG AAGGCGATGC TCAATACGAA      150
   -----GAAAAAATCT TAGAATTAAT GCAAGCAGTT GATGATTACA TTCCAAC TCC----- 200
   AGAACGTGAT TCTGACAAAC CATTTCATGAT GCCAGTTGAG GACGTATTCT      250
   CAATCACTGG TCGTGGTACT GTTGCTACAG GCCGTGTTGA ACGTGGTCAA      300
15 ATCAAAGTTG GTGAAGAAGT TGAAATCATT GGTATCCATG ACACTTCTAA      350
   AACAACGTGT ACTGGTGTAG AAATGTTCCG TAAATTATTA GACTACGCTG      400
   AAGCTGGTGA CAACATTGGT GCATTATTAC GTGGTGTTGC TCGTGAAGAC      450
   GTACAACGTG GTCAAGTATT AGCTGCTCCA GGTTCATCA CACCTCACAC      500
   AAAATTTAAA GCAGACGTAT ACGTTTTATC TAAAGACGAA GGTGGACGTC      550
20 ACACTCCATT CTTCAAAAC TATCGTCCAC AATTCTATTT CCG              593

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2) INFORMATION FOR SEQ ID NO: 191

25

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 828 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 30 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 35 (A) ORGANISM: *Staphylococcus hominis* subsp. *hominis*
 (B) STRAIN: ATCC 27844

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 191

```

40 CGGCGCTATC TTAGTAGTAT CTGCTGCTGA TGGTCCAATG CCACAAACTC      50
   GTGAACACAT TCTTTTATCA CGTAACGTTG GTGTACCAGC ATTAGTAGTA      100
   TTCTTAAACA AAGTTGACAT GGTTGACGAT GAAGAATTAT TAGAATTAGT      150
   TGAAATGGAA GTACGTGACT TATTATCTGA ATACGACTTC CCAGGTGACG      200
   ACGTACCTGT AATCGCTGGT TCAGCTTTAA AAGCTTTAGA AGGCGATGCT      250
45 CAATACGAAG AAAAAATCTT AGAATTAATG CAAGCAGTTG ATGATTATAT      300
   TCCAAC TCCA GAACGTGACT CTGATAAACC ATTCATGATG CCAGTTGAGG      350
   ACGTATTCTC AATCACTGGT CGTGGTACTG TTGCTACAGG CCGTGTTGAA      400
   CGTGGTCAAA TCAAAGTTGG TGAAGAAGTT GAAATTATTG GTATCAAAGA      450
   AACTTCTAAA ACAACTGTTA CTGGTGTAGA AATGTTCCGT AAATTATTAG      500
50 ACTACGCTGA AGCTGGTGAC AACATCGGTG CTTTATTACG TGGTGTGCT      550
   CGTGAAGATG TACAACGTGG TCAAGTATTA GCTGCTCCAG GTTCAATTAC      600
   ACCTCACACA AAATTCAAAG CAGACGTATA CGTTTTATCA AAAGATGAAG      650
   GTGGACGTCA TACTCCATTC TTCTCTAACT ATCGTCCACA ATTCTATTTT      700
   CGTACTACTG ACGTAACTGG TGTTGTTAAC TTACCAGAAG GACTGAAAT      750
55 GGTAATGCCT GGTGACAAAC TTGAAATGAC AGTAGAATTA ATCGCTCCTA      800
   TCGCGATTGA AGACGGTACT CGTTTCTC              828

```

60 2) INFORMATION FOR SEQ ID NO: 192

115

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 620 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus warneri*
 (B) STRAIN: ATCC 35982

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 192

```

15  ATGGTCCAAT GCCACAAACT CGTGAACACA TTCTTTTATC ACGTAACGTT      50
    GGTGTACCAG CTTTAGTTGT ATTCTTAAAC AAAGTTGATA TGGTAGACGA      100
    CGAAGAATTA TTAGAATTAG TAGAAATGGA AGTTCGTGAC TTATTATCTG      150
    AATATGACTT CCCAGGTGAC GACGTACCTG TAATCGCTGG TTCAGCATTG      200
20  AAAGCTTTAG AAGGCGACGA AAAATACGAA GAAAAAATCT TAGAATTAAT      250
    GCAAGCAGTT GATGACTACA TTCCAACCTC AGAACGTGAT TCTGACAAAC      300
    CATTGATGAT GCCAGTTGAG GACGTATTCT CAATCACTGG TCGTGGTACT      350
    GTTGCTACAG GCCGTGTTGA ACGTGGTCAA ATCAAAGTTG GTGAAGAAGT      400
    TGAAATCATC GGTTTACATG ACACCTTCTAA AACAACTGTT ACTGGTGTAG      450
25  AAATGTTCCG TAAGTTATTA GACTACGCTG AAGCTGGTGA CAACATCGGT      500
    GCTTTATTAC GTGGTGTTCG TCGTGAAGAC GTACAACGTG GTCAAGTATT      550
    AGCTGCTCCT GGTTCAATTA CACCACATAC AAAATTCAAA GCGGAAGTTT      600
    ACGTTTTATC TAAAGACGAA                                     620
  
```

30

2) INFORMATION FOR SEQ ID NO: 193

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 692 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus hominis*
 (B) STRAIN: CSG 170

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 193

```

    CCAGCATTAG TAGTATTCTT AAACAAAGTT GACATGGTTG ACGATGAAGA      50
    ATTATTAGAA TTAGTTGAAA TGGAAGTACG TGACTTATTA TCTGAATACG      100
50  ACTTCCCAGG TGACGACGTA CCTGTAATCG CTGGTTCAGC TTTAAAAGCT      150
    TTAGAAGGCG ATGCTCAATA CGAAGAAAAA ATCTTAGAAT TAATGCAAGC      200
    AGTTGATGAT TATATTCCAA CTCCAGAACG TGACTCTGAT AAACCATTCA      250
    TGATGCCAGT TGAGGACGTA TTCTCAATCA CTGGTCGTGG TACTGTTGCT      300
    ACAGGCCCGT TGAACGTGG TCAAATCAAA GTTGGTGAAG AAGTTGAAAT      350
55  TATTGGTATC AAAGAAACTT CTAAAACAAC TGTTACTGGT GTAGAAATGT      400
    TCCGTAAATT ATTAGACTAC GCTGAAGCTG GTGACAACAT CCGTGCTTTA      450
    TTACGTGGTG TTGCTCGTGA AGATGTACAA CGTGGTCAAG TATTAGCTGC      500
    TCCAGGTTCA ATTACACCTC ACACAAAATT CAAAGCAGAC GTATACGTTT      550
    TATCAAAAGA TGAAGGTGGA CGTCATACTC CATTCTTCTC TAACTATCGT      600
60  CCACAATTCT ATTTCCGTAC TACTGACGTA ACTGGTGTTG TTAACCTACC      650
  
```

AGAAGGTACT GAAATGGTAA TGCCTGGTGA CAACGTTGAA AT :

5 2) INFORMATION FOR SEQ ID NO: 194

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 684 bases
 (B) TYPE: Nucleic acid
 10 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

15 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus hominis*
 (B) STRAIN: CSG 36

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 194

20 CATTCTTTTA TCACGTAACG TTGGTGTACC AGCATTAGTA GTATTCTTAA 50
 ACAAAGTTGA CATGGTTGAC GATGAAGAAT TATTAGAATT AGTTGAAATG 100
 GAAGTACGTG ACTTATTATC TGAATACGAC TTCCCAGGTG ACGACGTACC 150
 TGTAATCGCT GGTTCAGCTT TAAAAGCTTT AGAAGGCGAT GCTCAATACG 200
 25 AAGAAAAAAT CTTAGAATTA ATGCAAGCAG TTGATGATTA TATTCCAAC 250
 CCAGAACGTG ACTCTGATAA ACCATTTCATG ATGCCAGTTG AGGACGTATT 300
 CTCAATCACT GTCGTGGTGA CTGTTGCTAC AGGCCGTGTT GAACGTGGTC 350
 AAATCAAAGT TGGTGAAGAA GTTGAAATTA TTGGTATCAA AGAACTTCT 400
 AAAACAAC 450
 30 TGAAGCTGGT GACAACATCG GTGCTTTATT ACGTGGTGTG GCTCGTGAAG 500
 ATGTACAACG TGGTCAAGTA TTAGCTGCTC CAGGTTCAAT TACACCTCAC 550
 ACAAATTCA AAGCAGACGT ATACGTTTTA TCAAAAGATG AAGGTGGACG 600
 TCATACTCCA TTCTTCTCTA ACTATCGTCC ACAATTCTAT TTCCGTACTA 650
 CTGACGTAAC TGGTGTGTGTT AACTTACCAG AAGG 684
 35

2) INFORMATION FOR SEQ ID NO: 195

40 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 685 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 45 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus hominis*
 50 (B) STRAIN: CSG 6

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 195

ACCAGCATTG TAGTATTCT TAAACAAAGT TGACATGGTT GACGATGAAG 50
 55 AATTATTAGA ATTAGTTGAA ATGGAAGTAC GTGACTTATT ATCTGAATAC 100
 GACTTCCCAG GTGACGACGT ACCTGTAATC GCTGGTTCAG CTTTAAAAGC 150
 TTTAGAAGGC GATGCTCAAT ACGAAGAAAA AATCTTAGAA TTAATGCAAG 200
 CAGTTGATGA TTACATTCCA ACTCCAGAAC GTGACTCTGA TAAACCATTC 250
 ATGATGCCAG TTGAGGACGT ATTCTCAATC ACTGGTCGTG GTACTGTTGC 300
 60 TACAGGCCGT GTTGAACGTG GTCAAATCAA AGTTGGTGAA GAAGTTGAAA 350

TTATTGGTAT CAAAGAACT TCTAAAACAA CTGTTACTGG TGTAGAAATG 400
 TTCCGTAAAT TATTAGACTA CGCTGAAGCT GGTGACAACA TCGGTGCTTT 450
 ATTACGTGGT GTTGCTCGTG AAGATGTACA ACGTGGTCAA GTATTAGCTG 500
 CTCCAGGTTT AATTACACCT CACACAAAAT TCAAAGCAGA CGTATACGTT 550
 5 TTATCAAAAG ATGAAGGTGG ACGTCATACT CCATTCTTCA CTAACCTATCG 600
 TCCACAATTC TATTTCGGTA CTACTGACGT AACTGGTGTG GTTAACTTAC 650
 CAGAAGGTAC TGAAATGGTA ATGCCTGGCG ACAAC 685

10

2) INFORMATION FOR SEQ ID NO: 196

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 611 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

20

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus hominis*
 (B) STRAIN: CSG 62

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 196

GACTTATTAT CTGAATACGA CTTCCCAGGT GACGACGTAC CTGTAATCGC 50
 TGGTTCAGCT TTAAAAGCTT TAGAAGGCCA TGCTCAATAC GAAGAAAAAA 100
 TCTTAGAATT AATGCAAGCA GTTGATGATT ACATTCCAAC TCCAGAACGT 150
 30 GACTCTGATA AACCATTTCAT GATGCCAGTT GAGGACGTAT TCTCAATCAC 200
 TGGTCGTGGT ACTGTTGCTA CAGGCCGTGT TGAACGTGGT CAAATCAAAG 250
 TTGGTGAAGA AGTTGAAATT ATTGGTATCA AAGATACTTC TAAAACAAC 300
 GTTACTGGTG TAGAAATGTT CCGTAAATTA TTAGACTACG CTGAAGCTGG 350
 TGACAACATC GGTGCTTTAT TACGTGGTGT TGCTCGTGAA GATGTACAAC 400
 35 GTGGTCAAGT ATTAGCTGCT CCAGGTTCAA TCACACCTCA CACAAAATTC 450
 AAAGCAGACG TATATGTTTT ATCAAAGAT GAAGGTGGAC GTCATACTCC 500
 ATTCTTCACT AACTATCGTC CACAATTCTA TTTCCGTACT ACTGACGTAA 550
 CTGGTGTGTT TAACCTACCA GAAGGTACTG AAATGGTAAT GCCTGGCGAC 600
 AACGTTGAAA T 611

40

2) INFORMATION FOR SEQ ID NO: 197

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 828 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 55 (A) ORGANISM: *Staphylococcus lugdunensis*
 (B) STRAIN: ATCC 43809

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 197

CGGCGGTATC TTAGTAGTTT CTGCTGCAGA TGGTCCAATG CCACAAACTC 50
 50 GTGAACACAT TCTTTTATCA CGTAACGTTG GTGTGCCAGC ATTAGTAGTA 100

	TTCTTAAACA	AAGTTGACAT	GGTTGACGAT	GAAGAATTAT	TAGAATTAGT	150
	AGAAATGGAA	GTTCGTGATT	TATTAAGTGA	ATATGACTTC	CCAGGTGACG	200
	ATGTGCCTGT	AATCGCTGGT	TCAGCATTAA	AAGCTTTAGA	AGGCGACGAA	250
	AAATACGAAG	CTAAAATCTT	AGAATTAATG	GATGCAGTTG	ATAACTACAT	300
5	TCCAACCTCA	GAACGTGACT	CTGACAAACC	ATTGATGATG	CCAGTTGAGG	350
	ACGTATTCTC	AATCACTGGT	CGTGGTACTG	TTGCTACAGG	CCGTGTTGAA	400
	CGTGGTCAAA	TCAAAGTCGG	TGAAGAAGTT	GAAATTATTG	GTATCCACGA	450
	TACTACTAAA	ACAACGTGTA	CTGGTGTAGA	AATGTTCCGT	AAATTATTAG	500
	ACTACGCTGA	AGCTGGTGGT	AACATCGGTG	CGTTATTACG	TGGTGTGCT	550
10	CGTGAAGATG	TACAACGTGG	ACAAGTATTA	GCTGCTCCAG	GTTCAATTAC	600
	ACCTCACACT	AAATTTAAAG	CTGACGTATA	TGTTTTATCT	AAAGATGAAG	650
	GTGGACGTCA	TACACCATTG	TTCTCAAAC	ACCGCCCA	ATTCTATTTC	700
	CGTACTACAG	ACGTAACGGT	TGTTGTAAAC	TTACCAGAAG	GTACAGAAAT	750
	GGTTATGCCT	GGCGACAACG	TTGAAATGAC	AGTTGAATTA	ATCGCTCCAA	800
15	TCGCTATCGA	AGACGGAAC	CGTTTCTC			828

2) INFORMATION FOR SEQ ID NO: 198

20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 690 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

25

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

30

- (A) ORGANISM: *Staphylococcus saprophyticus*
 (B) STRAIN: ATCC 35552

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 198

35	AGTAGTATCT	GCTGCTGATG	GCCCAATGCC	ACAAACTCGT	GAACACATTC	50
	TTTTATCACG	TAACGTTGGT	GTTCCAGCAT	TAGTTGTATT	CTTAAACAAA	100
	GTTGACATGG	TTGACGATGA	AGAATTATTA	GAATTAGTAG	AAATGGAAGT	150
	TCGTGACTTA	TTAAGCGAAT	ATGACTTCCC	AGGTGACGAT	GTACCTGTAA	200
	TCTCTGGTTC	TGCATTAAAA	GCTTTAGAAG	GCGACGCTGA	CTATGAGCAA	250
40	AAAATCTTAG	ACTTAATGCA	AGCTGTTGAT	GACTTCATTC	CAACACCAGA	300
	ACGTGATTCT	GACAAACCAT	TCATGATGCC	AGTTGAGGAC	GTATTCTCAA	350
	TCACTGGTCG	TGGTACTGTT	GCTACAGGCC	GTGTTGAACG	TGGTCAAATC	400
	AAAGTCGGTG	AAGAAATCGA	AATCATCGGT	ATGCAAGAAG	AATCAAGCAA	450
	AACAACGTGT	ACTGGTGTAG	AAATGTTCCG	TAAATTATTA	GACTACGCTG	500
45	AAGCTGGTGA	CAACATTGGT	GCATTATTAC	GTGGTGTTC	ACGTGATGAC	550
	GTACAACGTG	GTCAAGTTTT	AGCTGCTCCT	GGTACTATTA	CACCACATAC	600
	AAAATTCAAA	GCGGATGTTT	ACGTTTTATC	TAAAGATGAA	GGTGGTCGTC	650
	ATACACCATT	CTTCACTAAC	TACCGCCAC	AATTCTATTT		690

50

2) INFORMATION FOR SEQ ID NO: 199

(i) SEQUENCE CHARACTERISTICS:

55

- (A) LENGTH: 723 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

60

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus saprophyticus*
 (B) STRAIN: CSG 83

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 199

```

GCATTAGTTG TATTCTTAAA CAAAGTTGAC ATGGTTGACG ATGAAGAATT      50
ATTAGAATTA GTAGAAATGG AAGTTCGTGA TTTATTAAGC GAATATGACT      100
10 TCCAGGTGA CGATGTACCT GTAATCTCTG GTTCTGCATT AAAAGCTTTA      150
GAAGGCGACG CTGACTATGA GCAAAAAATC TTAGACTTAA TGCAAGCTGT      200
TGATGACTTC ATTCCAACAC CAGAACGTGA TTCTGACAAA CCATTCATGA      250
TGCCAGTTGA GGACGTATTG TCAATCACTG GTCGTGGTAC TGTGCTACA      300
GGCCGTGTTG AACGTGGTCA AATCAAAGTC GGTGAAGAAA TCGAAATCAT      350
15 CGGTATGCAA GAAGAATCAA GCAAAACAAC TGTTACTGGT GTAGAAATGT      400
TCCGTAAATT ATTAGACTAC GCTGAAGCTG GTGACAACAT TGGTGCATTA      450
TTACGTGGTG TTTCACGTGA TGACGTACAA CGTGGTCAAG TTTTAGCTGC      500
TCCTGGTACT ATTACACCAC ATACAAATT CAAAGCGGAT GTTTACGTTT      550
TATCTAAAGA TGAAGGTGGT CGTCATACAC CATTCTTCAC TAACTACCGC      600
20 CCACAATTCT ATTTCCGTAC TACTGACGTA ACTGGTGTG TTAATTACC      650
AGAAGGTACT GAAATGGTTA TGCCTGGCGA TAACGTTGAA ATGGATGTTG      700
AATTAATTTT TCCAATCGCT ATT                                723
  
```

25

2) INFORMATION FOR SEQ ID NO: 200

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 697 bases
 30 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

35

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus saprophyticus*
 (B) STRAIN: CSsa 18

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 200

```

CGTTGGTGTT CCAGCATTAG TTGTATTCTT AAACAAAGTT GACATGGTTG      50
ACGATGAAGA ATTATTAGAA TTAGTAGAAA TGGAAAGTTCG TGACTTATTA      100
AGCGAATATG ACTTCCCAGG TGACGATGTA CCTGTAATCT CTGGTTCTGC      150
45 ATTAAAAGCT TTAGAAGGCG ACGCTGACTA TGAGCAAAAA ATCTTAGACT      200
TAATGCAAGC TGTGATGAC TTCATTCCAA CACCAGAACG TGATTCTGAC      250
AAACCATTCA TGATGCCAGT TGAGGACGTA TTCTCAATCA CTGGTCGTGG      300
TACTGTTGCT ACAGGCCGTG TTGAACGTGG TCAAATCAAA GTCGGTGAAG      350
AAATCGAAAT CATCGGTATG CAAGAAGAAT CAAGCAAAAC AACTGTTACT      400
50 GGTGTAGAAA TGTTCCGTAA ATTATTAGAC TACGCTGAAG CTGGTGACAA      450
CATTGGTGCA TTATTACGTG GTGTTTCACG TGATGACGTA CAACGTGGTC      500
AAGTTTTAGC TGCTCCTGGT ACTATTACAC CACATACAAA ATTCAAAGCG      550
GATGTTTACG TTTTATCTAA AGATGAAGGT GGTGTCATA CACCATCTT      600
CACTAACTAC CGCCACAAT TCTATTTCCG TACTACTGAC GTAAGTGGTG      650
55 TTGTTAACTT ACCAGAAGGT ACTGAAATGG TTATGCCTGG CGATAAC      697
  
```

60

2) INFORMATION FOR SEQ ID NO: 201

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 835 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus sciuri* subsp. *sciuri*
 (B) STRAIN: ATCC 29060

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 201

```

15  CGGCGGTATC TTAGTAGTAT CTGCTGCTGA CGGTCCAATG CCTCAAACCTC      50
    GTGAGCACAT TCTTTTATCA CGTAACGTAG GTGTTCTCTGC ATTAGTAGTA      100
    TTCTTAAACA AAGTTGACAT GGTGACGAT GAAGAATTAT TAGAATTAGT      150
    TGAAATGGAA GTTCGTGACT TATTATCTGA ATATGACTTC CCAGGCGACG      200
    ACGTTCCTGT AATTGCTGGT TCAGCATTAA AAGCATTAGA AGGCGACGAA      250
20  GCTTACGAAG ACAAATCAT GGAATTAATG GATGCTGTTG ATACATTTCAT      300
    CCCAACTCCA GAACGTGACT CTGACAAACC ATTCATGATG CCAGTTGAGG      350
    ACGTATTCTC AATCACTGGT CGTGGTACTG TTGCTACAGG CCGTGTTGAA      400
    CGTGGTCAAA TCACTGTTGG TGAAGAAGTT GAAATCATCG GTTTAACTGA      450
    AGAATCTTCT AAAACAACTG TAACTGGTGT TGAAATGTTC CGTAAATTAT      500
25  TAGACTTCGC TGAAGCTGGA GATAACATCG GTGCATTATT ACGTGGTGTG      550
    GCTCGTGAAG ACGTTAACCG TGGTCAAGTA TTAGCTAAAC CAGGTTCAAT      600
    CACACCTCAC ACTAAATTCA AAGCTGAAGT TTATGTATTA TCTAAAGACG      650
    AAGGTGGACG TCATACTCCA TTCTTCACAA ACTACCGCCC ACAATTCTAT      700
    TTCCGTACTA CTGACGTAAC TGGTGTAGTT AACTTACCAG AAGGTACTGA      750
30  AATGGTTATG CCTGGCGACA ACGTTGAAAT GGACGTTGAA TTAATTTTAC      800
    CAATCGCTAT TGAAGACGGT ATCGTTTCTC AATCA                      835
  
```

35 2) INFORMATION FOR SEQ ID NO: 202

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 831 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus warneri*
 (B) STRAIN: ATCC 27836

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 202

```

50  CGGCGGTATC TTAGTTGTAT CTGCAGCTGA TGGTCCAATG CCACAAACTC      50
    GTGAACACAT TCTTTTATCA CGTAACGTTG GTGTACCAGC TTTAGTTGTA      100
    TTCTTAAACA AAGTTGATAT GGTAGACGAC GAAGAATTAT TAGAATTAGT      150
    AGAAATGGAA GTTCGTGACT TATTATCTGA ATATGACTTC CCAGGTGACG      200
55  ACGTACCTGT AATCGCTGGT TCAGCATTAA AAGCTTTAGA AGGCGACGAA      250
    AAATACGAAG AAAAAATCTT AGAATTAATG CAAGCAGTTG ATGACTACAT      300
    TCCAACTCCA GAACGTGATT CTGACAAACC ATTCATGATG CCAGTTGAGG      350
    ACGTATTCTC AATCACTGGT CGTGGTACTG TTGCTACAGG CCGTGTTGAA      400
    CGTGGTCAAA TCAAAGTTGG TGAAGAAGTT GAAATCATCG GTTTACATGA      450
60  CACTTCTAAA ACAACTGTTA CTGGTGTAGA AATGTTCCGT AAGTTATTAG      500
  
```

	ACTACGCTGA	AGCTGGTGAC	AACATCGGTG	CTTTATTACG	TGGTGTGCT	550
	CGTGAAGACG	TACAACGTGG	TCAAGTATTA	GCTGCTCCTG	GTTCAATTAC	600
	ACCACATACA	AAATTCAAAG	CGGAAGTTTA	CGTTTTATCT	AAAGACGAAG	650
	GTGGACGTCA	CACTCCATTC	TTCAGTAACT	ACCGCCCACA	ATTCTATTTT	700
5	CGTACTACTG	ACGTAACCTG	CGTTGTTCAA	TTACCAGAAG	GTAAGTAAAT	750
	GGTTATGCCT	GGTGATAACG	TTGAAATGAC	AGTAGAATTA	ATCGCTCCTA	800
	TCGCGATTGA	AGACGGTACT	CGTTTCTCAA	C		831

10

2) INFORMATION FOR SEQ ID NO: 203

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 829 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Double
 - (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Staphylococcus warneri*
 - (B) STRAIN: CSG 50
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 203

	CGGCGGTATC	TTAGTTGTAT	CTGCAGCTGA	TGGTCCAATG	CCACAAACTC	50
	GTGAACACAT	TCTTTTATCA	CGTAACGTTG	GTGTACCAGC	TTTAGTTGTA	100
	TTCTTAAACA	AAGTTGATAT	GGTAGACGAC	GAAGAATTAT	TAGAATTAGT	150
30	AGAAATGGAA	GTTTCGTGACT	TATTATCTGA	ATATGACTTC	CCAGGTGACG	200
	ACGTACCTGT	AATCGCTGGT	TCAGCATTAA	AAGCTTTAGA	AGGCGACGAA	250
	AAATACGAAG	AAAAATCTT	AGAATTAATG	CAAGCAGTTG	ATGACTACAT	300
	TCCAACCTCA	GAACGTGATT	CTGACAAACC	ATTCATGATG	CCAGTTGAGG	350
	ACGTATTCTC	AATCACTGGT	CGTGGTACTG	TTGCTACAGG	CCGTGTTGAA	400
35	CGTGGTCAAA	TCAAAGTTGG	TGAAGAAGTT	GAAATCATCG	GTTTACATGA	450
	CACTTCTAAA	ACAACTGTTA	CTGGTGTAGA	AATGTTCCGT	AAGTTATTAG	500
	ACTACGCTGA	AGCTGGTGAC	AACATCGGTG	CTTTATTACG	TGGTGTGCT	550
	CGTGAAGACG	TACAACGTGG	TCAAGTATTA	GCTGCTCCTG	GTTCAATTAC	600
	ACCACATACA	AAATTCAAAG	CGGAAGTTTA	CGTTTTATCT	AAAGACGAAG	650
40	GTGGACGTCA	CACTCCATTC	TTCAGTAACT	ACCGCCCACA	ATTCTATTTT	700
	CGTACTACTG	ACGTAACCTG	CGTTGTTCAA	TTACCAGAAG	GTAAGTAAAT	750
	GGTTATGCCT	GGTGATAACG	TTGAAATGAC	AGTAGAATTA	ATCGCTCCTA	800
	TCGCGATTGA	AGACGGTACT	CGTTTCTCAA			829

45

2) INFORMATION FOR SEQ ID NO: 204

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 839 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Double
 - (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Bifidobacterium longum*
 - (B) STRAIN: ATCC 15707

60

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 204

	TGGCGCTATC	CTCGTTGTGG	CCGCCACCGA	CGGCCCCGATG	GCCCAGACTC	50
	GCGAGCACGT	GCTGCTCGCC	CGTCAGGTTG	GCGTTCCGAA	GATCCTCGTC	100
5	GCCCTGAACA	AGTGCGACAT	GGTCGACGAT	GAAGAGCTCA	TCGAGCTCGT	150
	CGAAGAAGAG	GTCCGCGACC	TCCTCGACGA	GAACGGCTTC	GACCGTGACT	200
	GCCCGGTTCAT	CCACACCTCC	GCTTACGGTG	CTCTGCACGA	CGACGCTCCG	250
	GACCACGAGA	AGTGGGTCCA	GTCCGGTTAAG	GACCTCATGG	ACGCTGTCGA	300
	CGACTACATC	CCGACCCCGG	TTCACGACCT	GGACAAGCCG	TTCCTGATGC	350
10	CGATCGAGGA	CGTCTTCACC	ATCTCCGGCC	GTGGTACCGT	TGTCACCGGT	400
	CGTGTTCGAGC	GTGGCCAGCT	GGCCGTCAAC	ACCCCGGTTCG	AGATCGTTGG	450
	TATCCGTCCG	ACCCAGCAGA	CCACCGTCAC	CTCCATCGAG	ACCTTCCACA	500
	AGACCATGGA	CGCCTGCGAG	GCTGGCGACA	ACACCGGTCT	GCTTCTGCGT	550
	GGTCTCGGCC	GTGACGATGT	CGAGCGTGGC	CAGGTTGTGG	CCAAGCCGGG	600
15	CTCCGTCACC	CCGCACACCA	AGTTCGAGGG	CGAAGTCTAC	GTGCTGACCA	650
	AGGACGAAGG	CGGCCGTCAC	TCGCCGTTCT	TCTCCAATA	CCGTCCGCAG	700
	TTCTACTTCC	GCACCACCGA	CGTCACCGGC	GTCATCGAGC	TGCCGGAAGG	750
	CGTCGAGATG	GTTTCAGCCG	GCGACCACGC	TACCTTCACC	GTTGAGCTGA	800
	TTCAGCCCAT	CGCTATGGAG	GAAGGCCTGA	CCTTCGCTG		839

2) INFORMATION FOR SEQ ID NO: 205

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 754 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Stenotrophomonas maltophilia*

(B) STRAIN: CDC F3338

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 205

	CGGCGCGATC	CTGGTGTGCT	CGGCCGCTGA	CGGCCCCGATG	CCGCAGACCC	50
10	GTGAGCACAT	CCTGCTGTCG	CGCCAGGTCG	GCGTGCCGTA	CATCGTCGTG	100
	TTCCTGAACA	AGGCCGACAT	GGTCGACGAC	GCCGAGCTGC	TCGAGCTGGT	150
	CGAGATGGAA	GTGCGCGAAC	TGCTGAGCAA	GTACGAGTTC	CCGGGCGACG	200
	ACACCCCGAT	CATCGCCGGT	TCGGCCCGCC	TGGCGCTGGA	AGGCGACCAG	250
	AGCGACATCG	GCGTGCCGGC	CATCCTGAAG	CTGGTCGACG	CGCTGGACAG	300
15	CTGGATTCCG	GAGCCGGAGC	GTGCGATCGA	CAAGCCGTTC	CTGATGCCGG	350
	TGGAAGACGT	GTTCTCGATC	TCGGGCCGCG	GCACCGTGGT	GACCGGTCGT	400
	ATCGAGCGCG	GCGTGATCAA	GGTTGGCGAC	GAAATCGAAA	TCGTCGGCAT	450
	CCGTCCGGTG	CAGAAGACCA	CCGTGACCGG	CGTTGAAATG	TTCCGCAAGC	500
	TGCTGGACCA	GGGTCAGGCA	GGCGACAACG	CTGGCCTGCT	GCTGCGCGGC	550
50	ACCAAGCGTG	ATGACGTCGA	GCGTGGCCAG	GTGCTGGCCA	AGCCGGGCAC	600
	GATCAAGCCG	CACACCAAGT	TCGAAGGCGA	AGTGTACGTC	CTGTCAAGG	650
	ACGAGGGCGG	CCGCCACACC	CCGTTCTTCA	ACGGCTACCG	TCCGCAGTTC	700
	TACTTCCGCA	CCACCGACAT	CACCGGCGCC	GCTGCACTGC	CGGAAGGCGT	750
	CGAA					754

2) INFORMATION FOR SEQ ID NO: 206

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 835 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

5

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus acidominimus*
 (B) STRAIN: ATCC 51726

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 206

	TGGTGCTATC	CTTG TAGTAG	CTTCAACTGA	CGGACCAATG	CCACAAACTC	50
15	GTGAGCACAT	CCTTCTTTCA	CGTCAAGTTG	GTGTTAAAAA	CCTTATCGTT	100
	TTCATGAACA	AAGTTGACCT	TGTTGATGAT	GAAGAATTGC	TTGAATTGGT	150
	TGAAATGGAA	ATCCGTGACC	TTCTTTCAGA	ATACGATTTC	CCAGGTGATG	200
	ATCTTCCAGT	TGTTCAAGGT	TCAGCTCTTA	AAGCGCTTGA	AGGTGATTCA	250
	GCACAAGAAG	ATGTTATCAT	GGAATTGATG	TCAATCGTTG	ACACATACAT	300
20	TCCAGAACCA	GAACGTGATA	CTGACAAACC	ATTGCTTCTT	CCAGTCGAGG	350
	ATGTATTCTC	AATCACTGGA	CGTGGTACTG	TTGCTTCAGG	ACGTATCGAC	400
	CGTGGTACTG	TTAAAGTTAA	TGACGAAGTT	GAAATCGTTG	GTATCAAAGA	450
	CGAAATCTCT	AAAGCAGTTG	TTACTGGTGT	TGAAATGTTT	CGTAAACAAC	500
	TTGACGAAGG	TCTTGCTGGA	GATAACGTTG	GTGTTCTTCT	TCGTGGTGTA	550
25	CAACGTGATG	AAATCGAACG	TGGTCAAGTT	CTTGCTAAAC	CAGGTTCAAT	600
	CAACCCACAC	ACTAAATTCA	AAGGTGAAGT	TTACGTTCTT	TCTAAAGAAG	650
	AAGGTGGACG	TCACACTCCA	TTCTTCGATA	ACTACCGTCC	TCAGTTCTAC	700
	TTCCGTACAA	CTGACGTAAAC	TGGTTCAATC	AAATTGCCAG	AAGGTACTGA	750
	AATGCTAATG	CCTGGTGATA	ACGTAACAT	CGAAGTTGAG	TTGATCCACC	800
30	CAATCGCCGT	TGAACAAGGT	ACTACTTTCT	CTATC		835

2) INFORMATION FOR SEQ ID NO: 207

35

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 819 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

40

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus agalactiae*
 (B) STRAIN: ATCC 12403

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 207

50	CTATCCTTGT	AGTTGCTTCA	ACTGATGGAC	CAATGCCACA	AACTCGTGAG	50
	CACATCCTTC	TTTCACGTCA	AGTTGGTGTT	AAACACCTTA	TCGTATTTCAT	100
	GAACAAAGTT	GACCTTGTTG	ATGATGAAGA	ATTGCTTGAA	TTGGTTGAAA	150
	TGGAAATTCT	TGACCTTCTT	TCAGAATACG	ACTTCCCAGG	TGATGACCTT	200
	CCAGTTATCC	AAGGTTTCAGC	TCTTAAAGCA	CTTGAAGGCG	ACGAAAAATA	250
55	CGAAGACATC	ATCATGGAAT	TGATGAGCAC	TGTTGATGAG	TACATTCCAG	300
	AACCAGAACG	TGATACTGAC	AAACCTTTAC	TTCTTCCAGT	TGAAGATGTA	350
	TTCTCAATCA	CTGGACGTGG	TACAGTTGCT	TCAGGACGTA	TCGACCGTGG	400
	TACTGTTTCG	GTCAACGACG	AAGTTGAAAT	CGTTGGTATT	AAAGAAGATA	450
	TCCAAAAGC	AGTTGTTACT	GGTGTGAAA	TGTTCCGTAA	ACAACTTGAC	500
50	GAAGGTCTTG	CAGGGGACAA	CGTTGGTGTT	CTTCTTCGTG	GTGTTCAACG	550

	TGATGAAATC	GAACGTGGTC	AAGTTCTTGC	TAAACCAGGT	TCAATCAACC	200
	CACACACTAA	ATTTAAAGGT	GAAGTTTACA	TCCTTTCTAA	AGAAGAAGGT	650
	GGACGTCATA	CTCCATTCTT	CAACAACACTAC	CGTCCACAAT	TCTACTTCCG	700
	TACAACTGAC	GTAACAGGTT	CAATCGAACT	TCCAGCAGGA	ACAGAAATGG	750
5	TTATGCCTGG	TGATAACGTT	ACTATCGAAG	TTGAATTGAT	TCACCCAATC	800
	GCCGTAGAAC	AAGGTACTA				819

10 2) INFORMATION FOR SEQ ID NO: 208

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 819 bases
 (B) TYPE: Nucleic acid
 15 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

20 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus agalactiae*
 (B) STRAIN: ATCC 12973

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 208

25	CTATCCTTGT	AGTTGCTTCA	ACTGATGGAC	CAATGCCACA	AACTCGTGAG	50
	CACATCCTTC	TTTCACGTCA	AGTTGGTGTT	AAACACCTTA	TCGTATTCAT	100
	GAACAAAGTT	GACCTTGTTG	ATGATGAAGA	ATTGCTTGAA	TTGGTTGAAA	150
	TGGAAATTCG	TGACCTTCTT	TCAGAATACG	ACTTCCCAGG	TGATGACCTT	200
30	CCAGTTATCC	AAGGTTTCAGC	TCTTAAAGCA	CTTGAAGGCG	ATGAAAAATA	250
	CGAAGACATC	ATCATGGAAT	TGATGAGCAC	TGTTGATGAG	TACATTCCAG	300
	AACCAGAACG	TGATACTGAC	AAACCTTTAC	TTCTTCCAGT	CGAAGATGTA	350
	TTCTCAATCA	CTGGACGTGG	TACAGTTGCT	TCAGGACGTA	TCGACCGTGG	400
	TACTGTTTCG	GTCAACGACG	AAGTTGAAAT	CGTTGGTATT	AAAGAAGATA	450
35	TCCAAAAAGC	AGTTGTTACT	GGTGTGAAA	TGTTCCGTAA	ACAACTTGAC	500
	GAAGGTCTTG	CAGGGGACAA	CGTTGGTGTT	CTTCTTCGTG	GTGTTCAACG	550
	TGATGAAATC	GAACGTGGTC	AAGTTCTTGC	TAAACCAGGT	TCAATCAACC	600
	CACACACTAA	ATTTAAAGGT	GAAGTTTACA	TCCTTTCTAA	AGAAGAAGGT	650
	GGACGTCATA	CTCCATTCTT	CAACAACACTAC	CGTCCACAAT	TCTACTTCCG	700
40	TACAACTGAC	GTAACAGGTT	CAATCGAACT	TCCAGCAGGA	ACAGAAATGG	750
	TTATGCCTGG	TGATAACGTT	ACTATCGAAG	TTGAATTGAT	TCACCCAATC	800
	GCCGTAGAAC	AAGGTACTA				819

45

2) INFORMATION FOR SEQ ID NO: 209

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 822 bases
 50 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

55

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus agalactiae*
 (B) STRAIN: ATCC 13813

60 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 209

	AGCTATCCTT	GTAGTTGCTT	CAACTGATGG	ACCAATGCCA	CAAACCTCGTG	50
	AGCACATCCT	TCTTTCACGT	CAAGTTGGTG	TTAAACACCT	TATCGTATTC	100
	ATGAACAAAG	TTGACCTTGT	TGATGATGAA	GAATTGCTTG	AATTGGTTGA	150
5	AATGGAAATT	CGTGACCTTC	TTTCAGAATA	CGACTTCCCA	GGTGATGACC	200
	TTCCAGTTAT	CCAAGGTTCA	GCTCTTAAAG	CACTTGAAGG	CGATGAAAAA	250
	TACGAAGACA	TCATCATGGA	ATTGATGAGC	ACTGTTGATG	AGTACATTCC	300
	AGAACCAGAA	CGTGATACTG	ACAAACCTTT	ACTTCTTCCA	GTCGAAGATG	350
	TATTCTCAAT	CACTGGACGT	GGTACAGTTG	CTTCAGGACG	TATCGACCGT	400
10	GGTACTGTTT	GTGTCAACGA	CGAAGTTGAA	ATCGTTGGTA	TTAAAGAAGA	450
	TATCCAAAAA	GCAGTTGTTA	CTGGTGTGTA	AATGTTCCGT	AAACAACCTG	500
	ACGAAGGTCT	TGCAGGGGAC	AACGTTGGTG	TTCTTCTTCG	TGGTGTTCAA	550
	CGTGATGAAA	TCGAACGTGG	TCAAGTTCTT	GCTAAACCAG	GTTCAATCAA	600
	CCCACACACT	AAATTTAAAG	GTGAAGTTTA	CATCCTTTCT	AAAGAAGAAG	650
15	GTGGACGTCA	TACTCCATTC	TTCAACAAC	ACCGTCCACA	ATTCTACTTC	700
	CGTACAAC	ACGTAACAGG	TTCAATCGAA	CTTCCAGCAG	GAACAGAAAT	750
	GGTTATGCCT	GGTGATAACG	TTACTATCGA	AGTTGAATTG	ATTCACCCAA	800
	TCGCCGTAGA	ACAAGGTACT	AC			822

20

2) INFORMATION FOR SEQ ID NO: 210

- (i) SEQUENCE CHARACTERISTICS:
- 25 (A) LENGTH: 825 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

- 30 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus agalactiae*
- 35 (B) STRAIN: CDCss-1073

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 210

	CGGAGCTATC	CTTGTAGTTG	CTTCAACTGA	TGGACCAATG	CCACAAACTC	50
	GTGAGCACAT	CCTTCTTTCA	CGTCAAGTTG	GTGTTAAACA	CCTTATCGTA	100
10	TTCATGAACA	AAGTTGACCT	TGTTGATGAT	GAAGAATTGC	TTGAATTGGT	150
	TGAAATGGAA	ATTCGTGACC	TTCTTTCAGA	ATACGACTTC	CCAGGTGATG	200
	ACCTTCCAGT	TATCCAAGGT	TCAGCTCTTA	AAGCACTTGA	AGGCGACGAA	250
	AAATACGAAG	ACATCATCAT	GGAATTGATG	AGCACTGTTG	ATGAGTACAT	300
	TCCAGAACCA	GAACGTGATA	CTGACAAACC	TTTACTTCTT	CCAGTTGAAG	350
15	ATGTATTCTC	AATCACTGGA	CGTGGTACAG	TTGCTTCAGG	ACGTATCGAC	400
	CGTGGTACTG	TTCGTGTCAA	CGACGAAGTT	GAAATCGTTG	GTATTAAAGA	450
	AGATATCCAA	AAAGCAGTTG	TTACTGGTGT	TGAAATGTTT	CGTAAACAAC	500
	TTGACGAAGG	TCTTGCAGGG	GACAACGTTG	GTGTTCTTCT	TCGTGGTGT	550
	CAACGTGATG	AAATCGAACG	TGGTCAAGTT	CTTGCTAAAC	CAGGTTCAAT	600
50	CAACCCACAC	ACTAAATTTA	AAGGTGAAGT	TTACATCCTT	TCTAAAGAAG	650
	AAGGTGGACG	TCATACTCCA	TTCTTCAACA	ACTACCGTCC	ACAATTCTAC	700
	TTCCGTACAA	CTGACGTAAC	AGGTTCAATC	GAACTTCCAG	CAGGAACAGA	750
	AATGGTTATG	CCTGGTGATA	ACGTTACTAT	CGAAGTTGAA	TTGATTCACC	800
55	CAATCGCCGT	AGAACAAGGT	ACTAC			825

2) INFORMATION FOR SEQ ID NO: 211

- 60 (i) SEQUENCE CHARACTERISTICS:

126

- (A) LENGTH: 826 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

5

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus anginosus*
 (B) STRAIN: ATCC 33397

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 211

	GGAGCTATCC	TTGTAGTAGC	TTCAACTGAC	GGACCAATGC	CTCAAACCTCG	50
15	TGAACACATC	CTTCTTTCAC	GCCAAGTAGG	TGTTAAATAC	CTTATCGTCT	100
	TCATGAATAA	AGTTGACTTG	GTTGACGATG	AAGAATTGCT	TGAATTGGTT	150
	GAAATGGAAA	TCCGTGACCT	TCTTTCAGAA	TACGATTTC	CAGGTGATGA	200
	AATCCCAGTT	ATCCAAGGTT	CAGCTCTTAA	AGCTCTTGAA	GGTGATGAAA	250
	AATATGAAGA	CATCATCATG	GAATTGATGG	ATACTGTTGA	TGAATACATT	300
20	CCAGAACCAG	AACGTGACAC	TGACAAACCA	TTGCTTCTTC	CAGTTGAAGA	350
	TGTATTCTCA	ATTACTGGAC	GTGGTACTGT	TGCTTCAGGA	CGTATCGACC	400
	GTGGTACTGT	TAAAGTCAAC	GACGAAGTTG	AAATCGTTGG	TATCCGTGAT	450
	GAAATCCAAA	AAGCAGTTGT	TACTGGTGT	GAAATGTTCC	GTAAACAATT	500
	GGACGAAGGT	CTTGCTGGAG	ATAACGTAGG	GGTTCTTCTT	CGTGGTATCC	550
25	AACGTGACGA	AATCGAACGT	GGACAAGTTC	TTGCTAAACC	AGGTTCAATT	600
	CATCCACACA	CTAAATTCAA	AGGTGAAGTT	TACATCCTTA	CTAAAGAAGA	650
	AGGTGGACGT	CATACTCCAT	TCTTCAACAA	CTACCGTCCT	CAATTCTACT	700
	TCCGTACTAC	AGACGTTACA	GGTTCAATCG	AACTTCCTGC	AGGTACTGAA	750
	ATGGTAATGC	CTGGTGATAA	CGTAACAATC	GACGTTGAAT	TGATCCACCC	800
30	AATTGCCGTA	GAACAAGGAA	CTACAT			826

2) INFORMATION FOR SEQ ID NO: 212

35

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 827 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

40

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus bovis*
 (B) STRAIN: ATCC 33317

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 212

50	TGGTGCTATC	CTTGTAGTAG	CTTCTACAGA	TGGTCCAATG	CCACAAACAC	50
	GTGAACACAT	CCTTCTTTCA	CGTCAAGTTG	GTGTTAAACA	CCTTATCGTC	100
	TTCATGAACA	AAGTTGACCT	TGTTGATGAC	GAAGAATTGC	TTGAATTGGT	150
	TGAAATGGAA	ATCCGTGACC	TTCTTTCAGA	ATATGATTTC	CCAGGTGATG	200
	AAATCCCTGT	AATCCAAGGT	TCAGCTCTTA	AAGCCCTTGA	AGGTGACACT	250
55	CACTACGAAG	ACATCATCAT	GGAATTGATG	AACACTGTAG	ATGAATACAT	300
	TCCAGAACCA	AAACGTGATA	CTGACAAACC	ATTGCTTCTT	CCAGTCGAAG	350
	ACGTATTCTC	AATCACTGGT	CGTGGTACTG	TAGCATCAGG	ACGTATCGAC	400
	CGTGGTACTG	TTAAAGTCAA	CGACGAAGTT	GAAATCGTTG	GTATCCGTGA	450
	CGACATCCAA	AAAGCTGTTG	TTACTGGTGT	TGAAATGTTT	CGTAAACAAC	500
60	TTGATGAAGG	TATCGCAGGG	GATAACGTTG	GTGTTCTTCT	TCGTGGTATC	550

CAACGTGATG AAATCGAACG TGGTCAAGTT CTTGCTAAAC CAGGTTCAAT 600
 CCACCCACAC ACTAAATTCA AAGGTGAAGT TTACATCCTT ACTAAAGAAG 650
 AAGGTGGACG TCACACTCCA TTCTTCAACA ACTACCGTCC TCAATTCTAC 700
 TTCCGTACAA CTGACGTTAC AGGTTCAATC GAACTTCCAG CAGGTTACTGA 750
 5 AATGGTAATG CCTGGTGATA ACGTTACTAT CGACGTTGAA TTGATTCCAC 800
 CAATCGCCGT TGAACAAGGT ACTACAT 827

10 2) INFORMATION FOR SEQ ID NO: 213

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 821 bases
 (B) TYPE: Nucleic acid
 15 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

20 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus anginosus* (deposited as
Streptococcus constellatus)
 (B) STRAIN: ATCC 27823

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 213

GCTATCCTCG TAGTAGCTTC AACTGATGGA CCAATGCCTC AAACTCGTGA 50
 ACATATCCTT CTTTCACGTC AAGTAGGTGT TAAATACCTT ATCGTCTTCA 100
 TGAACAAAGT TGACTTGGTT GACGATGAAG AATTGCTTGA ATTGGTTGAA 150
 30 ATGGAAATCC GTGACCTTCT TTCAGAATAC GATTTCCTCAG GTGATGAAAT 200
 CCCAGTTATC CAAGGTTTCAG CTCTTAAAGC TCTTGAAGGT GATGAAAAAT 250
 ATGAAGACAT CATCATGGAA TTGATGGATA CTGTTGATGA ATACATTCCA 300
 GAACCAGAAC GTGACACTGA CAAACCATT CTTCCTCCAG TCGAAGATGT 350
 ATTCTCAATC ACTGGACGTG GTACTGTTGC TTCAGGACGT ATCGACCGTG 400
 35 GTACTGTAA AGTCAATGAT GAAAGTTGAAA TTGTTGGTAT TCGTGACGAA 450
 ATCCAAAAAG CAGTTGTTAC TGGTGTGAA ATGTTCCGTA AACAAATTGGA 500
 CGAAGGTCTT GCTGGAGATA ACGTAGGGGT TCTTCTTCGT GGTATCCAAC 550
 GTGACGAAAT CGAACGTGGA CAAGTTCTTG CTAAACCAGG TTCAATTCAT 600
 CCACACACTA AATTCAAAGG TGAAGTTTAC ATCCTTACTA AAGAAGAAGG 650
 40 TGGACGTCAT ACTCCATTCT TCAACAATA CCGTCCTCAA TTCTACTTCC 700
 GTACTACAGA CGTTACAGGT TCAATCGAAC TTCCTGCAGG TACTGAAATG 750
 GTAATGCCGT GTGATAACGT AACAAATTGAT GTTGAGTTGA TCCACCCAAT 800
 TGCCGTAGAA CAAGGAACTA C 821

45

2) INFORMATION FOR SEQ ID NO: 214

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 821 bases
 50 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus cricetus*
 (B) STRAIN: ATCC 19642

60

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 214

	GCTATCCTTG	TAGTAGCTTC	TACAGACGGA	CCAATGCCAC	AAACTCGTGA	50
	ACACATCTTG	CTTTCACGCC	AAGTTGGTGT	TAAGAGCCTT	ATCGTCTTCA	100
5	TGAACAAGGT	TGACTTGTT	GACGATGAAG	AATTGCTTGA	ATTGGTTGAA	150
	ATGGAAATCC	GTGATCTTCT	TTCAGAATAC	GATTTCCCAG	GTGATGATAT	200
	CCCTGTTGTT	CAAGGTTTCA	CTCTTAAAGC	CCTTGAAGGT	GATACAGCTG	250
	CCGAAGACAA	GATCATGGAA	TTGATGGACA	TCGTTGATGA	CTACATTCCA	300
	GAACCAAAAC	GTGATACTGA	TAAGCCATTG	CTTCTTCCAG	TCGAAGACGT	350
10	ATTCTCAATC	ACTGGACGTG	GTACTGTTGC	TTCAGGACGT	ATCGACCGTG	400
	GTACTGTTAA	GGTCAATGAC	GAAGTTGAAA	TCGTTGGTAT	CAAGGACGAA	450
	ATCCAAAAAG	CGGTTGTTAC	CGGAGTTGAA	ATGTTCCGTA	AACAATTGGA	500
	TGAAGGTCTT	GCAGGGGATA	ACGTTGGTGT	GCTTCTTCGT	GGTATCCAAC	550
	GTGATGAAAT	CGAACGTGGT	CAAGTATTGG	CTGCACCTGG	TTCAATCCAT	600
15	CCACACACTA	AATTCAAGGG	TGAAGTTTAC	ATCCTTTCTA	AAGATGAAGG	650
	TGGACGTCAC	ACTCCATTCT	TCAACAACATA	CCGTCCACAG	TTCTACTTCC	700
	GTACAACTGA	CGTAACTGGT	TCAATCGAAT	TGCCAGCAGG	TACTGAAATG	750
	GTTATGCCTG	GTGATAACGT	TACTATCGAC	GTTGAATTGA	TCCACCCAAT	800
	CGCTGTTGAA	AAAGGTACTA	C			821

2) INFORMATION FOR SEQ ID NO: 215

25 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 821 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

30

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus cristatus*
 (B) STRAIN: ATCC 51100

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 215

	TATCCTTGTA	GTAGCTTCAA	CTGACGGACC	AATGCCACAA	ACTCGTGAGC	50
40	ACATCCTTCT	TTCACGTCAG	GTTGGTGTTA	AACACCTTAT	CGTCTTCATG	100
	AACAAGATCG	ACTTGGGTGA	TGACGAAGAA	TTGCTTGAAT	TGGTTGAAAT	150
	GGAAATCCGT	GACCTCTTGT	CAGAATACGA	CTTCCCAGGT	GACGATCTTC	200
	CAGTTATCCA	AGGTTTCACT	CTTAAAGCTC	TTGAAGGTGA	TACTAAGTAC	250
	GAAGACATCA	TCATGGAATT	GATGAACACT	GTTGATGAGT	ACATCCCAGA	300
45	ACCAGAACGT	GATACTGACA	AACCTCTTCT	TCTTCCAGTC	GAAGACGTAT	350
	TCTCAATCAC	TGGTCGTGGT	ACAGTTGCTT	CAGGACGTAT	CGACCGTGGT	400
	ACTGTTTCGTG	TCAACGATGA	AATCGAAATC	GTTGGTATCA	AAGAAGAAAT	450
	CCAAAAGCA	GTTGTTACTG	GTGTTGAAAT	GTTCCGTAAA	CAGCTTGACG	500
	AAGGTCTTGC	AGGGGACAAC	GTAGGTGTAC	TTCTTCGTGG	TATCCAACGT	550
50	GATGAAATCG	AACGTGGTCA	AGTTATCGCT	AAACCAGGTT	CAATCAACCC	600
	ACACACTAAA	TTCAAGGGTG	AAGTTTACAT	CCTTACTAAA	GAAGAAGGTG	650
	GACGTCACAC	TCCATTCTTC	AACAACCTACC	GTCCACAGTT	CTACTTCCGT	700
	ACAACCTGACG	TTACAGGTTT	AATCGAACTT	CCAGCAGGTA	CTGAAATGGT	750
	AATGCCTGGT	GATAACGTAA	CTATCGACGT	TGAGTTGATC	CACCCAATCG	800
55	CCGTTGAACA	AGGTACTCCT	T			821

2) INFORMATION FOR SEQ ID NO: 216

60

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 792 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus downei*
 (B) STRAIN: ATCC 33748

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 216

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15  AGTAGCTTCT ACTGATGGAC CAATGCCACA AACTCGTGAA CACATCTTGC      50
    TTTCACGTCA GGTGTTGGTGT AAGAACCTTA TCGTCTTCAT GAACAAGGTT      100
    GACTTGGTTG ACGATGAAGA ATTGCTTGAA TTGGTTGAAA TGGAAATCCG      150
    TGACCTGCTT TCAGAATACG ATTTCCCAGG TGATGATATC CCTGTTGTTC      200
    AAGGTTTCAGC TCTTAAGGCT CTTGAAGGTG ATACAGCTGC CGAAGACAAG      250
20  ATCATGGAAT TGATGGACAT CGTTGATGAC TACATTCCAG AACCAAAACG      300
    TGATACTGAT AAGCCTTTGC TTCTTCCAGT CGAAGATGTA TTCTCAATCA      350
    CTGGACGTGG TACTGTAGCT TCAGGACGTA TCGACCGTGG TACTGTTAAG      400
    GTCAACGACG AAGTTGAAAT CGTTGGTATC AAGGACGAAA TCCAAAAAGC      450
    AGTTGTTACC GGAGTTGAAA TGTTCCGTAA ACAATTGGAC GAAGGTCTTG      500
25  CAGGGGATAA CGTTGGTGTG CTTCTTCGTG GTATCCAACG TGATGAAATC      550
    GAACGTGGTC AAGTGTGGC TGCGCCTGGT TCGATTCAAC CACACACTAA      600
    GTTTAAAGGT GAAGTTTACA TCCTTTCTAA AGAAGAAGGT GGACGTCATA      650
    CTCCATTCTT TAACAACTAC CGTCCACAGT TCTACTTCCG TACAAC TGAC      700
    GTAAC TGGT CAATCGAATT GCCAGCGGGT ACTGAAATGG TTATGCCTGG      750
30  TGATAACGTT ACTATCGACG TTGAATTGAT CCACCCAATT GC              792
  
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2) INFORMATION FOR SEQ ID NO: 217

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 795 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus dysgalactiae*
 (B) STRAIN: ATCC 43078

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 217

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50  GTAGTTGCTT CAACAGACGG ACCAATGCCA CAAACTCGTG AGCACATCCT      50
    CCTTTCACGT CAGGTTGGTG TTAAACACCT TATCGTGTC ATGAACAAAA      100
    TTGACCTTGT TGACGATGAA GAATTGCTTG AATTGGTTGA AATGGAAATC      150
    CGTGACCTTC TTTCAGAATA CGATTTCCCA GGTGATGACC TTCCAGTTAT      200
    CCAAGGTTCA GCTCTTAAAG CTCTTGAAGG CGACACTAAA TTTGAAGACA      250
55  TCATCATGGA ATTGATGGAT ACTGTTGATT CATAATTCC AGAACCAGAA      300
    CGTGACACTG ACAAACCATT GCTTCTTCCA GTCGAAGACG TATTCTCAAT      350
    CACAGGTCGT GGTACAGTTG CTTCAGGACG TATCGACCGT GGTACTGTTC      400
    GTGTCAACGA CGAAATCGAA ATCGTTGGTA TCAAAGAAGA AACTAAAAAA      450
    GCTGTTGTTA CTGGTGTGTA AATGTTCCGT AAACAAC TTG ACGAAGGTCT      500
50  TGCAGGAGAC AACGTAGGTA TCCTTCTTCG TGGTGTTCAG CGTGACGAAA      550
  
```

	TCGAACGTGG	TCAAGTTATT	GCTAAACCAG	GTTCAATCAA	CCCACACACT	600
	AAATTCAAAG	GTGAAGTATA	TATCCTTTCT	AAAGACGAAG	GTGGACGTCA	650
	CACTCCATTC	TTCAACAAC	ATCGTCCACA	ATTCTACTTC	CGTACAAC	700
	ACGTAACAGG	TTCAATCGAA	CTTCCAGCTG	GTACAGAAAT	GGTTATGCCT	750
5	GGTGATAACG	TGACAATCAA	CGTTGAGTTG	ATCCACCCAA	TCGCC	795

2) INFORMATION FOR SEQ ID NO: 218

10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 828 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 15 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 20 (A) ORGANISM: *Streptococcus equi* subsp. *equi*
 (B) STRAIN: ATCC 9528

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 218

25	CGGAGCTATC	CTTGTAGTTG	CTTCAACTGA	CGGACCAATG	CCACAAACTC	50
	GTGAGCACAT	CCTTCTTTCA	CGTCAGGTTG	GTGTTAAGCA	CCTTATCGTG	100
	TTCATGAACA	AGGTTGACCT	TGTTGACGAT	GAAGAATTGC	TTGAGCTTGT	150
	TGAAATGGAA	ATTCGTGACC	TTCTTTTCAGA	ATATGATTTC	CCAGGTGATG	200
	ACCTTCCAGT	TATCCAAGGT	TCAGCGCTTA	AGGCTCTTGA	AGGCGACAGC	250
30	AAATACGAAG	ATATCATCAT	GGAATTGATG	GATACTGTTG	ATTTCATACAT	300
	TCCAGAACCA	GAACGTGACA	CAGACAAGCC	ATTGCTTCTT	CCAGTCGAGG	350
	ACGTATTCTC	AATCACTGGA	CGTGGTACTG	TTGCTTCAGG	ACGTATCGAC	400
	CGCGGTACTG	TTCGTGTAA	CGACGAAATC	GAAATCGTTG	GTATCAGAGA	450
	CGAGATCAAA	AAAGCAGTTG	TTACTGGTGT	CGAAATGTTC	CGTAAACAGC	500
35	TTGACGAAGG	TCTTGCAGGG	GACAACGTTG	GTGTTCTTCT	TCGTGGTGTA	550
	CAACGTGATG	AAATCGAACG	TGGTCAAGTT	ATTGCTAAGC	CAGGTTCTAT	600
	CAACCCACAC	ACTAAATTTA	AAGGTGAAGT	ATATATCCTT	ACTAAAGAAG	650
	AAGGTGGACG	TCACACACCA	TTCTTCAACA	ACTATCGTCC	ACAATTCTAC	700
	TTCCGTACTA	CTGACGTAAC	AGGTTCAATC	GAGCTTCCAG	CAGGTACAGA	750
40	AATGGTTATG	CCTGGTGATA	ACGTGACTAT	TGACGTTGAG	TTGATCCACC	800
	CAATCGCCGT	AGAACAAGGT	ACTACATT			828

45 2) INFORMATION FOR SEQ ID NO: 219

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 825 bases
 (B) TYPE: Nucleic acid
 50 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 55 (A) ORGANISM: *Streptococcus ferus*
 (B) STRAIN: ATCC 33477

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 219

60

	CGGTGCAATC	CTTGTAGTAG	CTTCTACAGA	TGGACCAATG	CCACAACTC	50
	GTGAGCACAT	CCTTCTTTCA	CGTCAGGTAG	GTGTTAAACA	CCTTATCGTC	100
	TTCATGAACA	AAGTTGACTT	GGTTGACGAT	GAAGAATTGC	TTGAATTGGT	150
	TGAAATGGAA	ATCCGTGACC	TGCTTTCAGA	ATATGATTTC	CCAGGTGATG	200
5	ACCTTCCAGT	TATCCAAGGT	TCAGCTCTTA	AAGCGCTTGA	AGGTGATACT	250
	GCTCAAGAAG	ATGTTATCAT	GGAATTGATG	AAAACCGTTG	ATGAGTACAT	300
	CCCAGAACCA	GAACGTGATA	CTGACAAACC	ATTGCTTCTT	CCAGTCGAAG	350
	ATGTATTCTC	AATCACAGGT	CGTGGTACTG	TAGCTTCAGG	ACGTATCGAT	400
	CGTGGTACTG	TAAGAGTCAA	CGATGAAGTT	GAAATCGTTG	GTATCAAAGA	450
10	CGAAATCACT	AAAGCAGTTG	TTACCGGTGT	TGAAATGTTT	CGTAAACAAT	500
	TGGACGAAGG	TCTTGCTGGT	GATAACGTTG	GTGTGCTTCT	CCGTGGTGTG	550
	CAACGTGATG	AAATCGAACG	TGGTCAAGTA	TTGGCTAAAC	CAGGTTCAAT	600
	CAACCCACAC	ACTAAATTTA	AAGGTGAAGT	TTACATCCTT	ACTAAAGAAG	650
	AAGGTGGACG	TCATACACCA	TTCTTCAACA	ACTACCGTCC	ACAGTTCTAC	700
15	TTCCGTACAA	CTGACGTAAC	TGGTTCATC	GAATTGCCAG	CAGGTACTGA	750
	AATGGTTATG	CCTGGTGATA	ACGTGACTAT	CGACGTTGAA	TTGATCCACC	800
	CAATCGCCGT	TGAACAAGGT	ACTAC			825

20

2) INFORMATION FOR SEQ ID NO: 220

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 826 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

30

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus gordonii*
 (B) STRAIN: ATCC 10558

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 220

	CGGAGCTATC	CTTGTAGTAG	CTTCAACTGA	TGGTCCTATG	CCACAACTC	50
	GTGAGCACAT	CCTTCTCTCA	CGCCAAGTTG	GTGTTAAACA	CTTGATCGTG	100
	TTCATGAACA	AAGTTGACTT	GGTTGACGAT	GAAGAATTGC	TTGAGTTGGT	150
40	TGAAATGGAA	ATCCGTGACC	TCTTGTGAGA	ATACGACTTC	CCAGGTGACG	200
	ATCTTCCAGT	TATCCAAGGT	TCAGCTCTTA	AAGCTCTTGA	AGGTGACTCT	250
	AAATATGAAG	ATATCATCAT	GGAATTGATG	AACACTGTTG	ATGAGTACAT	300
	CCCAGAACCA	GAACGCGACA	CTGACAAACC	ATTGCTTCTT	CCAGTCGAAG	350
	ACGTATTCTC	AATCACTGGA	CGTGGTACAG	TTGCTTCAGG	ACGTATCGAC	400
45	CGTGGTATCG	TTAAAGTCAA	TGACGAAATC	GAAATCGTTG	GTATCAAAGA	450
	AGAAATCCAA	AAAGCAGTTG	TTACTGGTGT	TGAAATGTTT	CGTAAACAGC	500
	TTGACGAAGG	TCTTGCAAGG	GACAACGTTG	GTGTGCTTCT	TCGTGGTATC	550
	CAACGTGATG	AAATCGAACG	TGGACAAGTT	ATTGCTAAAC	CAGGTTCAAT	600
	CAACCCACAC	ACTAAATTCA	AAGGTGAAGT	TTATATCCTT	ACTAAAGAAG	650
50	AAGGTGGACG	TCACACTCCA	TTCTTCAACA	ACTACCGTCC	ACAGTTCTAC	700
	TTCCGTACAA	CTGACGTTAC	AGGTTCAATC	GAATTCCAG	CAGGTACTGA	750
	AATGGTAATG	CCTGGTGATA	ACGTAACAT	CGACGTTGAG	TTGATCCACC	800
	CAATCGCCGT	TGAACAAGGT	ACTACT			826

55

2) INFORMATION FOR SEQ ID NO: 221

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 799 bases

- (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

5 (ii)MOLECULE TYPE: Genomic DNA

(vi)ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus anginosus*
 (B) STRAIN: ATCC 27335

10

(xi)SEQUENCE DESCRIPTION: SEQ ID NO: 221

	TGTAGTAGCT	TCAACTGACG	GACCAATGCC	TCAAACCTCGT	GAACATATCC	50
	TTCTTTTACG	TCAAGTAGGT	GTTAAATACC	TTATTGTCTT	CATGAACAAA	100
15	GTTGACTTGG	TTGACGATGA	AGAATTGCTT	GAATTGGTTG	AAATGGAAAT	150
	CCGTGATCTT	CTTTCAGAAT	ACGATTTCCT	AGGTGATGAT	ATTCCAGTAA	200
	TCCAAGGTTC	AGCACTTAAA	GCTCTTGAAG	GTGATGAAAA	ATATGAAGAC	250
	ATCATCATGG	AATTGATGAA	TACTGTTGAT	GAATATATTC	CAGAACCAGA	300
	ACGTGATACT	GACAAACCAT	TGCTTCTTCC	AGTCGAAGAT	GTATTCTCAA	350
20	TCACTGGACG	TGGTACTGTT	GCTTCAGGAC	GTATCGACCG	TGGTACTGTT	400
	AAAGTCAACG	ATGAAGTTGA	AATCGTTGGT	ATCCGCGAGG	AAATCCAAAA	450
	AGCAGTTGTT	ACTGGTGTG	AAATGTTCCG	TAAACAATTG	GACGAAGGTC	500
	TTGCTGGAGA	TAACGTAGGG	GTTCTTCTTC	GTGGTATCCA	ACGTGACGAA	550
	ATTGAACGTG	GACAAGTTCT	TGCTAAACCA	GGTTCAATTC	ATCCACACAC	600
25	TAAATTCAAA	GGTGAAGTTT	ACATCCTTAC	TAAAGAAGAA	GGTGGACGTC	650
	ATACTCCATT	CTTCAACAAC	TACCGTCCTC	AATTCTACTT	CCGTACTACA	700
	GACGTTACAG	GTTCAATCGA	ACTTCCTGCA	GGTACTGAAA	TGGTAATGCC	750
	TGGTGATAAC	GTAACAATTG	ATGTTGAGTT	GATCCACCCA	ATTGCCGTA	799

30

2) INFORMATION FOR SEQ ID NO: 222

(i)SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 825 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

40 (ii)MOLECULE TYPE: Genomic DNA

(vi)ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus macacae*
 (B) STRAIN: ATCC 35911

45

(xi)SEQUENCE DESCRIPTION: SEQ ID NO: 222

	TGGTGCTATT	CTTGTAGTAG	CTTCAACTGA	CGGTCCAATG	CCTCAAACGC	50
	GTGAACATAT	CCTTCTTTCA	CGCCAAGTAG	GTGTTAAAAA	CCTTATTGTT	100
50	TTCATGAATA	AAGTTGACTT	AGTTGATGAT	GAAGAATTGC	TTGAATTGGT	150
	TGAAATGGAA	ATCCGTGATC	TTCTTACAGA	ATATGATTTC	CCAGGCGATG	200
	AACTTCCAGT	TATCCAAGGT	TCAGCACTTA	AAGCTCTTGA	AGGTGATACT	250
	AAGTACGAAG	ATATTATCAT	GGAATTGTTG	GATACTGTAG	ATGATTACAT	300
	CCCAGAACCA	CAACGTGATA	CTGACAAGCC	ATTGCTTCTT	CCAGTCGAAG	350
55	ATGTTTTTCTC	TATTACTGGA	CGTGGTACTG	TTGCTTCAGG	ACGTATTGAC	400
	CGTGGTACTG	TTAAGGTTAA	TGATGAAGTT	GAAATCGTTG	GTATTCGTGA	450
	CGATATTCAA	AAAGCAGTTG	TTACTGGTGT	TGAAATGTTC	CGTAAACAGC	500
	TTGACGAAGG	TCTTGCTGGT	GATAACGTCG	GTGTCCTTCT	TCGTGGTATC	550
	CAACGTGATG	AAATTGAACG	CGGTCAAGTT	CTTGCTAAAC	CAGGATCAAT	600
50	TCATCCACAT	ACTAAATTCA	AAGGTGAAGT	TTATATTCTT	ACTAAAGAAG	650

AAGGTGGACG	TCATACTCCA	TTCTTTAACA	ACTACCGTCC	ACAGTTCTAC	700
TTCCGTACAA	CTGATGTAAC	TGGTTCAATT	GATTTGCCAG	CAGGTACTGA	750
AATGGTTATG	CCTGGTGATA	ATGTTACGAT	TGATGTTGAA	CTGATCCACC	800
CAATCGCTGT	TGAACAAGGT	ACAAC			825

5

2) INFORMATION FOR SEQ ID NO: 223

10 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 822 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

15

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus gordonii* (deposited as
Streptococcus mitis)
 (B) STRAIN: ATCC 33399

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 223

25	CTATCCTTGT	AGTAGCTTCA	ACTGACGGAC	CAATGCCACA	AACTCGTGAG	50
	CACATCCTTC	TTTCACGTCA	GGTTGGTGTT	AAACACCTTA	TCGTCTTCAT	100
	GAACAAAGTT	GACTTGGTG	ACGACGAAGA	ATTGCTTGAA	TTGGTTGAAA	150
	TGGAAATCCG	TGACCTATTG	TCAGAATACG	ACTTCCCAGG	TGACGATCTT	200
	CCAGTTATCC	AAGGTTTCAGC	TCTTAAAGCC	CTTGAAGGTG	ACACTAAATA	250
30	CGAAGACATC	GTTATGGAAT	TGATGAACAC	AGTTGATGAG	TACATCCCAG	300
	AACCAGAACG	TGACACTGAC	AAACCATTCG	TTCTTCCAGT	CGAAGACGTA	350
	TTCTCAATCA	CTGGTCGTGG	TACAGTTGCT	TCAGGACGTA	TCGACCGTGG	400
	TATCGTTAAA	GTCAACGACG	AAATCGAAAT	CGTTGGTATC	AAAGAAGAAA	450
	CTCAAAAAGC	AGTTGTTACT	GGTGTGAAA	TGTTCCGTAA	ACAACTTGAC	500
35	GAAGGTCTTG	CCGGAGATAA	TGTAGGTGTC	CTTCTTCGTG	GTGTTCAACG	550
	TGATGAAATC	GAACGTGGAC	AAGTTATTGC	TAAACCAGGT	TCAATCAACC	600
	CACACACTAA	ATTCAAAGGT	GAAGTTTACA	TCCTTACTAA	AGAAGAAGGT	650
	GGACGTCACA	CTCCATTCTT	CAACAACACT	CGTCCACAAT	TCTACTTCCG	700
	TACTACTGAC	GTTACAGGTT	CAATCGAACT	TCCAGCAGGT	ACTGAAATGG	750
40	TAATGCCTGG	TGATAACGTG	ACAATCGACG	TTGAGTTGAT	CCACCCAATC	800
	GCCGTAGAAC	AAGGTACTAC	AT			822

45 2) INFORMATION FOR SEQ ID NO: 224

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 827 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus mutans*
 (B) STRAIN: ATCC 25175

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 224

50

	CCCTGGTGCT	ATCCTTGTAG	TAGCTTCAAC	TGATGGACCA	ATGCCACAAA	50
	CTCGTGAACA	CATTCTTCTT	TCACGTCAAG	TTGGTGTAA	ATACCTCATT	100
	GTCTTCATGA	ATAAAGTTGA	TTTGGTTGAC	GATGAAGAAT	TGCTTGAATT	150
	GGTTGAAATG	GAAATCCGTG	ATCTTCTTTC	AGAATATGAT	TTCCCAGGTG	200
5	ATGATATTCC	AGTTATTCAA	GGTTCAGCTC	TTAAAGCTCT	TGAAGGCGAT	250
	ACTGCTCAAG	AAGATATCAT	CATGGAATTA	ATGCATACTG	TTGATGACTA	300
	CATTCCAGAT	CCAGAACGTG	ATACTGACAA	GCCGCTCCTT	CTTCCAGTCG	350
	AAGATGTTTT	CTCAATCACT	GGTCGTGGTA	CTGTTGCTTC	AGGACGTATT	400
	GATCGTGGTA	CTGTTAAAGT	TAACGATGAA	GTTGAAATCG	TTGGTATCCG	450
10	TGATGACATT	CAAAAAGCTG	TTGTTACTGG	TGTTGAAATG	TTCCGTAAAC	500
	AATTGGATGA	AGGTATTGCA	GGGGATAATG	TTGGTGTTCT	CCTTCGTGGT	550
	ATCCAACGTG	ATGAAATCGA	ACGTGGTCAA	GTTCTTGCTA	AACCAGGTTC	600
	AATTCACCCA	CATACTAAAT	TCAAAGGTGA	AGTTTATATC	CTTACTAAAG	650
	AGGAAGGTGG	ACGTCATACA	CCATTCTTCA	ATAACTATCG	TCCACAATTC	700
15	TACTTCCGTA	CAACTGACGT	AACTGGTTCA	ATTGAGTTGC	CAGCAGGTAC	750
	TGAAATGGTT	ATGCCTGGTG	ATAACGTTAC	TATTGACGTT	GAATTGATCC	800
	ATCCAATCGC	TGTTGAACAA	GGTACTA			827

20

2) INFORMATION FOR SEQ ID NO: 225

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 824 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

30

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus parasanguinis*
 (B) STRAIN: ATCC 15912

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 225

	AGCTATCCTT	GTAGTAGCTT	CAACTGACGG	ACCAATGCCA	CAAACACGTG	50
	AACACATCCT	TCTTTCACGT	CAGGTTGGTG	TTAAACACTT	GATCGTCTTC	100
	ATGAACAAAG	TTGACTTGGT	TGATGATGAA	GAATTGCTTG	AATTGGTTGA	150
40	AATGGAAATC	CGTGACCTTC	TTTCAGAATA	CGATTTCCTA	GGTGATGACC	200
	TTCCAGTTAT	CCAAGGTTCA	GCTCTTAAAG	CTCTTGAAGG	TGACTCTAAA	250
	TATGAAGATA	TCATCATGGA	ATTGATGGAT	ACTGTTGATG	AGTACATCCC	300
	AGAACCAGAA	CGCGATACTG	ACAAACCATT	GCTTCTTCCA	GTCGAAGACG	350
	TATTCTCAAT	CACTGGACGT	GGTACAGTTG	CTTCAGGACG	TATCGACCGT	400
45	GGTGTTGTTC	GTGTCAATGA	TGAAATCGAA	ATCGTTGGTA	TCAAAGAAGA	450
	AATCCAAAAA	GCAGTTGTGA	CTGGTGTTGA	AATGTTCCGT	AAACAACCTG	500
	ACGAAGGTCT	TGCAGGGGAT	AACGTTGGTG	TGCTTCTTCG	TGGTATCCAA	550
	CGTGATGAAA	TCGAACGTGG	ACAAGTTATC	GCTAAACCAG	GTTCAATCAA	600
	CCCACACACT	AAATTCAAAG	GTGAAGTTTA	CATCCTTACT	AAAGAAGAAG	650
50	GTGGACGTCA	TACTCCATTC	TTCAACAAC	ACCGTCCACA	GTTCTACTTC	700
	CGTACAAC	ACGTAAC	ATCTATCGAA	CTTCCACCAG	GAAGTGAAT	750
	GGTAATGCCT	GGTGATAACG	TGACTATCGA	CGTTGAGTTG	ATCCACCCAA	800
	TCGCCGTTGA	ACAAGGTACT	ACAT			824

55

2) INFORMATION FOR SEQ ID NO: 226

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 824 bases

- (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

5 (ii)MOLECULE TYPE: Genomic DNA

(vi)ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus ratti*
 (B) STRAIN: ATCC 19645

10

(xi)SEQUENCE DESCRIPTION: SEQ ID NO: 226

	TGGTGCTATC	CTTGCTTTCA	CGTCAAGTTG	GTGTTAAATA	CCTTATCGTC	50
	GTGAACACAT	CTTGCTTTCA	CGTCAAGTTG	GTGTTAAATA	CCTTATCGTC	100
15	TTCATGAACA	AGGTTGACTT	GGTTGATGAT	GAAGAATTGC	TTGAATTGGT	150
	TGAAATGGAA	ATCCGTGATC	TTCTTTTCAGA	ATACGATTTT	CCAGGTGATG	200
	ACATTCCAGT	TATCCAAGGT	TCAGCCCTTA	AAGCTCTTGA	AGGTGACACT	250
	GAACAAGAAG	ATGTTATCAT	GGAATTGATG	AAAACAGTTG	ATGAGTACAT	300
	CCCAGATCCA	GAACGCGATA	CTGATAAGCC	ATTGCTTCTT	CCAGTCGAAG	350
20	ACGTGTTCTC	AATCACTGGA	CGTGGTACTG	TTGCATCAGG	ACGTATCGAC	400
	CGTGGTACTG	TTAAAGTCAA	TGACGAAGTT	GAAATCGTTG	GTATCCGTGA	450
	TGACATCCAA	AAAGCTGTTG	TTACTGGTGT	TGAAATGTTT	CGTAAACAGC	500
	TTGACGAAGG	TCTTGCTGGT	GATAACGTTG	GTGTACTTCT	TCGTGGTATC	550
	CAACGTGATG	AAATCGAACG	CGGTCAAGTT	CTTGCTAAAC	CAGGTTCAT	600
25	TCATCCGCAT	ACTAAATTTA	AAGGTGAAGT	TTACATCCTT	ACTAAAGAAG	650
	AAGGCGGACG	TCACACTCCA	TTCTTCAACA	ACTACCGTCC	ACAGTTCTAC	700
	TTCCGTACAA	CTGACGTAAC	TGGTTCAATC	GAATTGCCAG	CAGGTACTGA	750
	AATGGTTATG	CCTGGTGATA	ACGTGACTAT	CGACGTTGAA	TTGATCCACC	800
30	CAATCGCTGT	TGAACAAGGT	ACTA			824

2) INFORMATION FOR SEQ ID NO: 227

35 (i)SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 795 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

40

(ii)MOLECULE TYPE: Genomic DNA

(vi)ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus sanguinis*
 (B) STRAIN: ATCC 10556

45

(xi)SEQUENCE DESCRIPTION: SEQ ID NO: 227

	TGTAGTAGCT	TCAACTGACG	GACCAATGCC	ACAAACTCGT	GAGCACATCT	50
50	TGCTTTTCACG	TCAGGTTGGT	GTAAACACT	TGATCGTCTT	CATGAACAAA	100
	GTTGACTTGG	TTGACGATGA	AGAATTGCTT	GAATTGGTTG	AAATGGAAAT	150
	CCGTGACCTC	TTGTCAGAAT	ACGACTTCCC	AGGTGACGAT	CTTCCAGTTA	200
	TCCAAGGTTT	AGTCTTTAAA	GCTCTTGAAG	GTGACTCTAA	ATATGAAGAC	250
	ATCATCATGG	AATTGATGGA	CACTGTTGAT	GAGTACATCC	CAGAACCAGA	300
55	ACGCGATACT	GACAAGCCAT	TGCTTCTTCC	AGTCGAAGAC	GTATTCTCAA	350
	TCACTGGTCG	TGGTACAGTT	GCTTCAGGAC	GTATCGACCG	TGGTATCGTT	400
	AAAGTCAACG	ACGAAATCGA	AATCGTTGGT	ATCAAAGAAG	AAATCCAAAA	450
	AGCAGTTGTT	ACTGGTGTTG	AAATGTTCCG	TAAACAGCTT	GACGAAGGTC	500
	TTGCAGGGGA	CAACGTAGGT	GTGCTTCTCC	GTGGTATCCA	ACGTGATGAA	550
50	ATCGAACGTG	GACAAGTTAT	CGCTAAACCA	GGTTCAATCA	ACCCACACAC	600

TAAATTCAAG	GGTGAAGTTT	ATATCCTTAC	TAAAGAAGAA	GGCGGACGTC	650
ACACTCCATT	CTTCAACAAC	TACCGTCCAC	AGTTCTACTT	CCGTACAAC	700
GACGTACAG	GTTCAATCGA	ACTTCCAGCA	GGTACTGAAA	TGGTAATGCC	750
TGGTGATAAC	GTAACAATCG	ACGTTGAGTT	GATCCACCCA	ATCGC	795

5

2) INFORMATION FOR SEQ ID NO: 228

10 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 795 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

15

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus sobrinus*
 (B) STRAIN: ATCC 33478

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 228

TGTAGTAGCT	TCTACTGACG	GACCAATGCC	ACAAACTCGT	GAACACATCT	50
25 TGCTTTCACG	CCAAGTTGGT	GTAAAGAACC	TCATCGTCTT	CATGAACAAG	100
GTTGACTTGG	TTGATGATGA	AGAATTGCTT	GAATTGGTTG	AAATGGAAAT	150
CCGTGATCTT	CTTTCAGAAAT	ACGATTTCCC	AGGTGACGAC	ATTCCTGTTG	200
TTCAAGGTTT	AGCTCTTAAG	GCTCTTGAAG	GTGATACAGC	TGCCGAAGAC	250
AAGATTATGG	AATTGATGGA	CATCGTTGAT	GATTACATTC	CAGAACCAAA	300
30 ACGCGATACT	GATAAGCCAT	TGCTTCTCCC	AGTCGAAGAC	GTATTCTCAA	350
TCACTGGTCG	TGGTACTGTT	GCTTCAGGAC	GTATTGACCG	TGGTACTGTT	400
AAGGTTAACG	ACGAAGTTGA	AATCGTTGGT	ATCCGTGACG	ATATCCAAAA	450
AGCAGTTGTT	ACTGGAGTTG	AAATGTTCCG	TAAGCAATTG	GACGAAGGTC	500
TTGCTGGAGA	TAACGTTGGT	GTGCTTCTTC	GTGGTATCCA	ACGTGATGAA	550
35 ATTGAACGTG	GTCAAGTATT	GGCTGCACCT	GGTTCAATCC	ACCCACACAC	600
TAAAGTTCAAG	GGTGAAGTTT	ACATCCTTTC	TAAAGATGAA	GGTGGACGTC	650
ACACTCCATT	CTTCAACAAC	TACCGTCCAC	AGTTCTACTT	CCGTACAAC	700
GACGTAAC	GTTCAATCGA	ATTGCCAGCA	GGTACTGAAA	TGGTTATGCC	750
40 TGGTGATAAC	GTTACTATCG	ACGTTGAATT	GATCCACCCA	ATCGC	795

2) INFORMATION FOR SEQ ID NO: 229

45 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 797 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus suis*
 (B) STRAIN: ATCC 43765

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 229

TGTAGTAGCT	TCAACTGACG	GTCCAATGCC	ACAAACTCGT	GAGCACATCC	50
50 TTCTTTCACG	TCAGGTTGGT	GTAAACACC	TTATCGTCTT	CATGAACAA	100

	GTTGACTTGG	TTGACGATGA	AGAATTGCTT	GAGTTGGTTG	AAATGGAAAT	150
	CCGTGACCTT	CTTTCAGAAT	ACGATTTCCC	AGGTGATGAT	CTTCCAGTTA	200
	TCCAAGGTTT	AGCTCTTAAA	GCTCTTGAAG	GTGACTCTAA	GTACGAAGAC	250
	ATCGTTATGG	AATTGATGAA	CACTGTTGAT	GAGTACATTC	CAGAACCAGA	300
5	ACGCGACACT	GACAAACCAT	TGTTGCTTCC	AGTCGAGGAC	GTATTCTCAA	350
	TCACTGGTCG	TGGTACTGTA	GCTTCAGGAC	GTATCGACCG	TGGTACTGTT	400
	CGTGTCAACG	ACGAAATCGA	AATCGTTGGT	CTTCAAGAAG	AAAAATCTAA	450
	AGCAGTTGTT	ACTGGTGTG	AAATGTTCCG	TAAACAACCT	GACGAAGGTC	500
	TTGCCGGCGA	TAACGTTGGT	GTGCTTCTTC	GTGGTGTACA	ACGTGATGAA	550
10	ATCGAACGTG	GTCAAGTTAT	CTCTAAACCA	GGTTCTATCA	ACCCACACAC	600
	TAAATTCAAA	GGTGAAGTTT	ACATCCTTAC	TAAAGAAGAA	GGTGGACGTC	650
	ACACTCCATT	CTTCGACAAC	TACCGTCCAC	AGTTCTACTT	CCGTACAACCT	700
	GACGTAACCTG	GTTCAATCAA	ATTGCCAGAA	GGTACTGAAA	TGGTAATGCC	750
	TGGTGATAAC	GTTACTATCG	ACGTTGAATT	GATCCACCCA	ATCGCCG	797

2) INFORMATION FOR SEQ ID NO: 230

20 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 793 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

25 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus uberis*
 (B) STRAIN: ATCC 19436

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 230

	TTGTTGTTGC	ATCAACTGAT	GGACCAATGC	CACAAACTCG	TGAGCACATC	50
35	TTTCTTTCAC	GCCAAGTTGG	TGTTAAACAC	CTTATCGTTT	TCATGAACAA	100
	AATCGACCTT	GTTGACGATG	AAGAATTGCT	TGAATTAGTT	GAAATGGAAA	150
	TCCGTGACCT	TCTTTCAGAA	TACGATTTCC	CAGGTGATGA	CCTACCAGTT	200
	ATCCAAGGTT	CAGCTCTTAA	AGCTCTTGAA	GGTGATTCTA	AATACGAAGA	250
	CATCATCATG	GAATTGATGA	AAACTGTTGA	TGAGTATATT	CCAGAACCAG	300
40	AACGTGATAC	AGACAAACCA	TTACTTCTTC	CAGTCGAAGA	CGTATTCTCA	350
	ATCACAGGTC	GTGGTACTGT	AGCTTCAGGA	CGTATCGATC	GTGGTACTGT	400
	TCGTGTCAAC	GACGAAATTG	AAATCGTTGG	TATCAAAGAA	GAAACTAAAA	450
	AAGCAGTTGT	TACTGGTGTG	GAAATGTTCC	GTAAACAACCT	TGACGAAGGT	500
	CTTGCAGGAG	ATAACGTAGG	TATCCTTCTT	CGTGGTGTTC	AACGTGACGA	550
45	AATCGAACGT	GGACAAGTTA	TTGCTAAACC	AGGTTCAATC	AACCCACACA	600
	CTAAATTCAA	AGGTGAAGTT	TACATCCTTT	CTAAAGATGA	AGGTGGACGT	650
	CATACTCCAT	TCTTCAACAA	CTACCGTCTT	CAATTCTATT	TCCGTACAAC	700
	TGACGTAAAC	GGTTCAATCG	AACTTCCAGC	TGGTACTGAA	ATGGTAATGC	750
	CTGGTGATAA	CGTGACAATC	AGCGTTGAGT	TGATCCACCC	AAT	793

2) INFORMATION FOR SEQ ID NO: 231

55 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 798 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus vestibularis*
 5 (B) STRAIN: ATCC 49124

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 231

	TTGTAGTAGC	ATCTACTGAC	GGACCAATGC	CACAAACTCG	TGAGCACATC	50
10	CTTCTTTCAC	GTCAGGTTGG	TGTTAAACAC	CTTATCGTCT	TCATGAACAA	100
	AGTTGACTTG	GTTGACGATG	AAGAATTGCT	TGAATTGGTT	GAAATGGAAA	150
	TCCGTGACCT	TCTTTCAGAA	TACGATTTC	CAGGTGATGA	TATTCCAGTT	200
	ATCCAAGGTT	CAGCTCTTAA	AGCTCTTGAA	GGTGATTCTA	AATACGAAGA	250
	CATCATCATG	GACTTGATGA	ACACTGTTGA	CGAATACATT	CCAGAACCAG	300
15	AACGTGACAC	TGACAAACCA	TTGTTGCTTC	CAGTCGAAGA	CGTATTCTCA	350
	ATCACTGGTC	GTGGTACTGT	TGCTTCAGGA	CGTATCGACC	GTGGTGTTGT	400
	TCGTGTTAAT	GACGAAGTTG	AAATCGTTGG	TCTTAAAGAA	GAAATCCAAA	450
	AAGCAGTTGT	TACTGGTGTA	GAAATGTTCC	GTAAACAAC	TGACGAAGGT	500
	ATTGCCGGAG	ATAACGTCGG	TGTCCTTCTT	CGTGGTATCC	AACGTGATGA	550
20	AATTGAACGT	GGTCAAGTAT	TGGCTGCACC	TGGTTCAATC	AACCCACACA	600
	CTAAATTCAA	AGGTGAAGTT	TACATCCTTT	CTAAAGAAGA	AGGTGGACGT	650
	CACACTCCAT	TCTTCAACAA	CTACCGTCCA	CAGTTCTACT	TCCGTACAAC	700
	TGACGTAACA	GGTTCAATCG	AACCTCCTGC	AGGTACTGAA	ATGGTTATGC	750
25	CTGGTGATAA	CGTGACTATC	GACGTTGAGT	TGATCCACCC	AATCGCCG	798

2) INFORMATION FOR SEQ ID NO: 232

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 829 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

35 (ii) MOLECULE TYPE: Genomic DNA

- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Tatumella ptyseos*
 40 (B) STRAIN: ATCC 33301

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 232

	GGCGCTATCC	TGGTTGTTGC	TGCAACTGAC	GGCCCTATGC	CTCAGACCCG	50
45	TGAGCACATC	CTGCTGGGCC	GCCAGGTAGG	CGTTCCTTAC	ATCATCGTGT	100
	TCCTGAACAA	ATGTGACATG	GTTGATGATG	AAGAGCTGCT	GGAAGTGGTA	150
	GAAATGGAAG	TCCGTGACCT	GCTGTACAG	TACGACTTCC	CGGGTGACGA	200
	CACGCCAATC	GTTGCGGTT	CAGCGCTGAA	AGCACTGGAA	GGTGAAGGCG	250
	AGTGGGAAGA	GAAGATTCTG	GAGCTGGCTG	GCTTCCTGGA	TTCTTACATC	300
50	CCTGAGCCAG	AGCGTGCTAT	CGATCAGCCG	TTCCTGCTGC	CAATCGAAGA	350
	CGTATTCTCA	ATCTCCGGTC	GTGGTACAGT	TGTTACCGGT	CGTGTAGAGC	400
	GCGGGATCAT	CAAAGTCGGT	GAAGAAGTTG	AGATCGTTGG	TATCAAAGAT	450
	ACTGCGAAAT	CAACCTGTAC	CGGTGTTGAA	ATGTTCCGTA	AACTGCTGGA	500
	CCAGGGTCAG	GCGGGTGAGA	ACGTTGGTGT	TCTGCTGCGT	GGTATCAAGC	550
55	GTGAAGAGAT	CGAACGTGGT	CAGGTTCTGG	CTAAACCAGG	TTCAATCAAA	600
	CCACACACCC	AGTTCGAGTC	AGAAGTTTAT	ATTCTGTCTA	AAGACGAAGG	650
	CGGCCGTCAT	ACTCCGTTCT	TCAAAGGCTA	CCGTCCACAG	TTCTACTTCC	700
	GTACAACTGA	CGTGACCGGA	ACCATCGAAC	TGCCGGAAGG	CGTAGAGATG	750
	GTAATGCCTG	GTGACAACAT	CAAAATGGTT	GTTACCCTGA	TCCATCCAAT	800
50	CGCGATGGAC	GATGGTCTGC	GTTTCGCAA			829

2) INFORMATION FOR SEQ ID NO: 233

5

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 829 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 10 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 15 (A) ORGANISM: *Trabulsiella guamensis*
 (B) STRAIN: ATCC 49490

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 233

```

20  GCGCAATCC TGGTAGTAGC AGCGACTGAC GGCCCGATGC CGCAGACTCG      50
    TGAGCACATC CTGCTGGGTC GTCAGGTAGG CGTTCCGTAC ATCATCGTGT      100
    TCCTGAACAA ATGCGACATG GTTGATGACG AAGAGCTGCT GGAAGCTGGTA      150
    GAGATGGAAG TTCGTGAACT GCTGTCTCAG TACGATTTCC CGGGCGATGA      200
    CACGCCGATC GTACGTGGTT CTGCTCTGAA AGCGCTGGAA GGCGACGCAG      250
25  AGTGGGAAGC GAAAATCATC GAACTGGCAG GTTTCCTGGA TTCTTACATT      300
    CCGGAACCAG AGCGTGCGAT TGACAAGCCG TTCCTGCTGC CGATCGAAGA      350
    CGTATTCTCC ATCTCTGGTC GTGGTACCGT TGTTACCGGT CGTGTAAGAGC      400
    GCGGTATCAT CAAAGTGGGT GAAGAAGTAG AAATCGTTGG TATCAAAGAG      450
    ACTGCGAAGT CAACCTGTAC TGGCGTAGAA ATGTTCCGCA AACTGCTGGA      500
30  CGAAGGCCGT GCTGGTGAGA ACGTAGGTGT TCTGCTGCGT GGTATCAAAC      550
    GTGAAGAAAT CGAACGTGGT CAGGTACTGG CTAAGCCGGG CACCATCAAC      600
    CCGCACACCA AGTTCGAATC TGAAGTGTAC ATTCTGTCCA AAGACGAAGG      650
    CGGCCGTCAC ACTCCGTTCT TCAAAGGCTA CCGTCCGCAG TTCTACTTCC      700
    GTACAACTGA CGTGACTGGC ACCATCGAAC TGCCGGAAGG CGTAGAGATG      750
35  GTAATGCCGG GCGACAACAT CAAAATGGTT GTTACCCTGA TCCACCCGAT      800
    CGCGATGGAC GACGGTCTGC GTTTCGCAA      829
  
```

40 2) INFORMATION FOR SEQ ID NO: 234

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 825 bases
 (B) TYPE: Nucleic acid
 45 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 50 (A) ORGANISM: *Veillonella parvula*
 (B) STRAIN: ATCC 10790

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 234

```

55  CGGCGCTATC TTGGTTGTAT CCGCAGCTGA CGGCCCTATG CCTCAAACCT      50
    GCGAACACAT CTTGTTGGCT CGCCAAGTTG GTGTTCCCTGC AATCGTAGTA      100
    TTCTTGAACA AAGCTGACAT GGTGACGAT GAAGAATTGA TCGAATTGGT      150
    AGAAATGGAA GTTCGTGAAC TTCTTTCTTC CTACGAATTC CCTGGCGACG      200
60  AAGTACCTAT CGTTGTAGGT TCCGCGTTGA AAGCTTTGGA AGGCGATGCT      250
  
```

	CAATATGTAG	CTAAAATTGA	CGAATTGATG	GACGCTGTAG	A [~] TCCTACAT	300
	CCCAACACCA	GTTTCGTGACA	CTGATAAACC	ATTCTTGATG	CCTGTGGAAG	350
	ATGTTTTTAC	AATCACTGGT	CGTGGTACAG	TAGCAACTGG	CCGTGTTGAA	400
	CGTGGTCAAG	TAAACGTTGG	TGATACTGTT	GAAGTAGTAG	GCTTGAAAGA	450
5	AAAAGCTGAA	CAATACGTAG	TAACAGGTCT	TGAAATGTTT	CGTAAAGTGT	500
	TGGATTCTGC	AGTAGCAGGT	GACAACGTAG	GTGCATTGCT	TCGTGGTGTT	550
	GATCGTAAAG	ACATYGAACG	TGGTCAAGTA	TTGGCTAAAC	CAGGTTCCAT	600
	CAACCCACAY	ACAAAATTCA	AAGCAGAAGT	ATACGTATTG	ACTAAAGAAG	650
	AAAGGTGGTCG	TCATACTCCA	TTCTTCTCCA	ACTACCGTCC	ACAATTCTAC	700
10	TTCCGTACAA	CAGACGTAAC	AGGTGTTGTA	AACCTTCCTG	AAGGTGTAGA	750
	AATGTGTATG	CCTGGCGATA	ACGTAACAAT	GGAAATCGAA	TTGATTACTC	800
	CAATCGCTAT	CGAAGAAGGT	CTTCG			825

15

2) INFORMATION FOR SEQ ID NO: 235

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 825 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

25

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Yersinia enterocolitica*
 (B) STRAIN: ATCC 9610

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 235

	CGCTATCCTG	GTTGTTGCTG	CAACTGATGG	CCCAATGCCA	CAGACTCGTG	50
	AGCACATCCT	GTTGGGTCGT	CAGGTGCGTG	TTCCTTACAT	CATCGTATTC	100
	ATGAACAAAT	GTGACATGGT	TGACGATGAA	GAGCTGCTAG	AACTGGTAGA	150
35	AATGGAAGTG	CGCGATCTTC	TGTCTACCTA	CGATTTCCCA	GGCGATGATA	200
	CGCCAGTTGT	TCGTGGTTCC	GCGCTGAAAG	CATTGGAAGG	CGAACCTGAG	250
	TGGGAAGCAA	AAATTATCGA	ACTGGCTGGC	TACCTGGATT	CTTACATCCC	300
	AGAACCAGAG	CGTGCTATCG	ATAAGCCGTT	CCTGCTGCCA	ATCGAAGACG	350
	TATTCTCTAT	CTCTGGTCGT	GGTACTGTTG	TAACGGGTCG	TGTAGAGCGC	400
40	GGTATCGTTA	AAGTTGGTGA	AGAAGTCGAA	ATTGTTGGCC	TGAAAGATAC	450
	CGTTAAATCT	ACTTGTAAGT	GCGTTGAAAT	GTTCCGCAAA	CTGCTGGATG	500
	AAGGCCGTGC	AGGTGAGAAC	GTTGGTGTTT	TGCTGCGTGG	TATCAAGCGT	550
	GAAGATATCG	AACGTGGTCA	AGTTCTTGCT	AAACCAGGTT	CGATTAAACC	600
	ACACACCAAA	TTTGAATCAG	AAGTTTATAT	TCTGAGCAAA	GATGAAGGTG	650
45	GTCGCCATAC	TCCGTTCTTC	AAAGGCTACC	GTCCTCAGTT	CTACTTCCGT	700
	ACAACTGATG	TAACCGGTAC	TATTGAACTG	CCAGAAGGCG	TTGAGATGGT	750
	GATGCCAGGT	GATAACATTC	AAATGATTGT	TAACCTGATT	GCTCCTATCG	800
	CAATGGATGA	CGGCTTGCGC	TTTGC			825

50

2) INFORMATION FOR SEQ ID NO: 236

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 828 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

60

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Yersinia frederiksenii*
 (B) STRAIN: ATCC 33641

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 236

```

GGCGCGATCC TGGTTGTTGC TGCCACTGAT GGCCCGATGC CACAGACTCG      50
CGAGCACATT CTGTTAGGGC GTCAGGTGGG TGTTCCCTTAC ATCCTGGTCT      100
10 TCCTGAACAA ATGTGACATG GTTGACGACG AAGAGCTGCT GGAAGTGGTA      150
GAAATGGAAG TTCGTGAACT TCTGTCTCAG TACGATTTCCT CTGGCGACGA      200
CACTCCAGTT ATCCGTGGTT CTGCGCTGAA AGCGCTGGAA GGCGAAGCTG      250
AGTGGGAAGC AAAAATCATC GAATTGGCTG AGGCGCTGGA TAGCTATATT      300
CCACAGCCAG AGCGTGCGAT TGATAAACCA TTCCTGCTGC CAATCGAAGA      350
15 CGTATTCTCA ATCTCTGGCC GTGGTACTGT TGTCAACCGT CGTGTAAGAGC      400
GCGGTATCGT TAAAGTCGGC GAAGAAGTCG AAATCGTTGG TATCATTGAT      450
ACCATCAAGA CTACCTGTAC TGGTGTGTA AATGTTCCGCA AATTGCTGGA      500
CGAAGGCCGT GCGGGTGAGA ACGTTGGTGT TCTGCTACGT GGTACTAAAC      550
GTGATGACGT ACAACGTGGT CAGGTATTGG CAAAACCAGG TTCTATCAAG      600
20 CCACACACCA AATTTGAATC AGAAGTTTAT ATTCTGAGCA AAGATGAAGG      650
TGGTCGCCAT ACTCCGTTCT TCAAAGGTTA TCGTCCTCAG TTCTACTTCC      700
GTACAACTGA CGTGACCGGT ACTATCGAAC TGCCAGAAGG CGTTGAGATG      750
GTGATGCCAG GTGATAACAT TCAAATGATT GTTAACCTGA TTGCTCCTAT      800
CGCAATGGAT GACGGTCTGC GCTTTGCG                                828
25

```

2) INFORMATION FOR SEQ ID NO: 237

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 813 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Yersinia intermedia*
 (B) STRAIN: ATCC 29909

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 237

```

CTTGTTGTC GCTGCAACTG ATGGTCCTAT GCCACAGACT CGCGAGCACA      50
45 TCCTGCTAGG TCGTCAGGTG GGTGTTCTT ACATCCTGGT CTTCTGAAC      100
AAGTGTGACA TGGTTGACGA TGAGGAGTTG CTGGAATTGG TAGAAATGGA      150
AGTCCGCGAA CTTCTGTCTC AATATGATTT CCCTGGCGAT GATACTCCTG      200
TTATCCGTGG TTCAGCGCTG AAGGCGTTGG AAGGCGAGCC TGAATGGGAA      250
GCAAAAATTA TCGAATTAGC TGAGGCGCTG GATAGTTATA TTCCACAGCC      300
50 AGAGCGCGCG ATTGATAGAC CATTCTTGCT GCCAATCGAA GACGTATTCT      350
CTATCTCAGG TCGTGGTACA GTCGTCCTG GTCGTGTAGA GCGTGGGATC      400
GTAAAGTTG GCGAAGAAGT TGAAATCGTT GGTATTATCG ATTCCATTAG      450
AACAACATGT ACTGGCGTTG AAATGTTCCG CAAATTGCTG GACGAAGGCC      500
GCGCGGGTGA GAACGTTGGT GTTCTACTGC GTGGGACTAA ACGTGATGAC      550
55 GTACAGCGTG GTCAGGTATT AGCTAAGCCA GGTTCTATCA AGCCACATAC      600
TAAATTCGAA TCCGAAGTTT ATATTCTGAG CAAAGATGAA GGCGGGCGTC      650
ACACGCCGTT CTTCAAAGGC TACCGTCCTC AGTTCTACTT CCGTACAACG      700
GATGTAACCG GTACTATTGA ATTGCCAGAC GCGGTTGAGA TGGTGATGCC      750
AGGTGATAAC ATTCAAATGA TTGTTAACCT GATTGCACCT ATTGCGATGG      800
50 ATGATGGTCT GCG                                813

```

2) INFORMATION FOR SEQ ID NO: 238

5

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 829 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 10 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 15 (A) ORGANISM: *Yersinia pestis*
 (B) STRAIN: KIM D27

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 238

20	GGAGCGATCT TGGTTGTTGC TGCAACCGAT GGCCCTATGC CGCAGACTCG	50
	TGAGCATATC CTGCTGGGCC GCCAGGTTGG TGTCCCATAC ATTATTGTCT	100
	TCCTGAACAA ATGTGACATG GTTGACGATG AAGAGTTGCT AGAGTTGGTT	150
	GAAATGGAGG TTCGTGAGCT TCTGTCTCAA TACGATTTC CAGGCGACGA	200
	CACTCCAGTC ATCCGTGGTT CAGCGTTGAA AGCCCTGGAA GGTGACGCTG	250
25	AGTGGGAAGC TAAAATTATC GAGTTGGCAG AAGCTCTGGA TAGCTATATT	300
	CCGCAACCAG AACGCGCTAT TGATAGACCA TTCCTATTGC CAATTGAAGA	350
	CGTATTCTCT ATTTCTGGTC GTGGTACTGT AGTTACTGGT CGTGTAAGAC	400
	GTGGTATTGT TAAGGTCGGC GAAGAAGTTG AAATCGTTGG TATTATCGAT	450
	ACGATTAAAA CAACTTGTA TGGCGTTGAA ATGTTCCGCA AGCTGCTGGA	500
30	TGAAGGCCGT GCTGGTGAAG ATGTTGGTGT TCTGCTGCGT GGTACTAAGC	550
	GTGACGATGT TCAGCGTGGT CAAGTACTGG CGAAACCAGG TTCTATCAAG	600
	CCACACACGA AGTTTGAGTC AGAAGTTTAT ATTCTGAGCA AAGATGAAGG	650
	CGGCCGTCAT ACACCGTTCT TCAAGGGCTA CCGTCCTCAG TTCTACTTCC	700
	GTACAACTGA CGTGACCGGT ACCATTGAGC TGCCAGAAGG CGTTGAAATG	750
35	GTCATGCCTG GTGACAACGT AAACATGGTT GTTAACCTAA TTGCTCCTAT	800
	CGCAATGGAT GATGGTCTGC GCTTCGCAA	829

40 2) INFORMATION FOR SEQ ID NO: 239

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 817 bases
 (B) TYPE: Nucleic acid
 45 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 50 (A) ORGANISM: *Yersinia pseudotuberculosis*
 (B) STRAIN: ATCC 29833

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 239

55	TGGAGCGATC TTGGTTGTTG CTGCAACCGA TGGCCCTATG CCGCAGACTC	50
	GTGAGCATAT CCTGCTGGGC CGCCAGGTTG GTGTCCCATA CATTATTGTC	100
	TTCCTGAACA AATGTGACAT GGTGACGAT GAAGAGTTGC TAGAGTTGGT	150
	TGAAATGGAG GTTCGTGAGC TTCTGTCTCA ATACGATTTC CCAGGCGACG	200
50	ACACTCCAGT CATCCGTGGT TCAGCGTTGA AAGCCCTGGA AGGTGACGCT	250

	GAGTGGGAAG	CTAAAATTAT	CGAGTTGGCA	GAAGCTCTGG	ATAGCTATAT	300
	TCCGCAACCA	GAACGCGCTA	TTGATAGACC	ATTCCTATTG	CCAATTGAAG	350
	ACGTATTCTC	TATTTCTGGT	CGTGGTACTG	TAGTTACTGG	TCGTGTAGAA	400
	CGCGGTATTG	TTAAGGTCGG	CGAAGAAGTT	GAAATCGTTG	GTATTATCGA	450
5	TACGATTAAA	ACAACTTGTA	CTGGCGTTGA	AATGTTCCGC	AAGCTGCTGG	500
	ATGAAGGCCG	TGCTGGTGAA	AATGTTGGTG	TTCTGCTGCG	TGGTACTAAG	550
	CGTGACGATG	TTCAGCGTGG	TCAAGTACTG	GCGAAACCAG	GTTCTATCAA	600
	GCCACACACG	AAGTTTGAGT	CAGAAGTTTA	TATTCTGAGC	AAAGATGAAG	650
	GCGGCCGTCA	TACACCGTTC	TTCAAGGGCT	ACCGTCCTCA	GTTCTACTTC	700
10	CGTACAACCTG	ACGTGACCGG	TACCATTGAG	CTGCCAGAAG	GCGTTGAAAT	750
	GGTCATGCCT	GGTGACAACG	TAAACATGGT	TGTTAACCTA	ATTGCTCCTA	800
	TCGCAATGGA	TGATGGT				817

15

2) INFORMATION FOR SEQ ID NO: 240

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 829 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

25

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Yersinia rohdei*
 (B) STRAIN: ATCC 43380

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 240

	TGGCGCGATC	CTGGTTGTTG	CTGCAACTGA	TGGCCCAATG	CCACAGACTC	50
	GCGAGCACAT	CCTGTTGGGT	CGTCAAGTGG	GTGTTCCCTA	CATCTTAGTC	100
	TTCCTGAACA	AGTGTGACAT	GGTTGACGAC	GAAGAGTTGC	TGGAACGGT	150
35	TGAAATGGAA	GTTCGTGAGC	TTCTGTCTCA	ATACGATTTC	CCTGGCGATG	200
	AACTCCGGT	TATTCGTGGT	TCCGCGCTGA	AAGCGCTGGA	AGGCGAGGCC	250
	GAGTGGGAAG	CCAAAATTAT	TGAAGTTGCT	GAAGCACTGG	ATAGCTACAT	300
	TCCACAGCCA	GAGCGCGCGA	TTGATAAACC	ATTCTTGCTG	CCAATCGAAG	350
	ACGTATTCTC	TATCTCAGGC	CGTGGAACAG	TTGTTACCGG	GCGTGTGAG	400
40	CGCGGTATCG	TCAGAGTGGG	CGAAGAAGTT	GAAATCGTGG	GTATCATCGA	450
	CACCATTAAA	ACCACTTGTA	CCGGTGTTGA	AATGTTCCGC	AAACTGCTGG	500
	ACGAAGGCCG	TGCCGGTGAG	AACGTTGGTG	TTCTGCTGCG	CGGTACTAAA	550
	CGCGATGACG	TGCAACGTGG	TCAAGTGTG	GCTAAACCAG	GTTCTATTAA	600
	GCCGCATACC	AAATTTGAGT	CAGAAGTTTA	TATTCTGAGC	AAAGATGAAG	650
45	GTGGTCGTCA	TACTCCGTTC	TTCAAAGGTT	ACCGTCCACA	GTTCTACTTC	700
	CGTACAACCTG	ACGTGACCGG	TACCATCGAA	CTGCCAGACG	GTGTTGAGAT	750
	GGTGATGCCA	GGTGATAACA	TTCAAATGAT	TGTTAACCTG	ATTGCGCCTA	800
	TTGCAATGGA	TGACGGTCTA	CGATTTGCA			829

50

2) INFORMATION FOR SEQ ID NO: 241

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 804 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Yokenella regensburgei*
 (B) STRAIN: ATCC 35313

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 241

	TGGCGCGATC	CTGGTTGTTG	CTGCGACTGA	CGGCCCGATG	CCGCAGACTC	50
	GTGAGCACAT	CCTGCTGGGT	CGTCAGGTAG	GCGTTCCGTA	CATCATCGTG	100
10	TTCCTGAACA	AATGCGACAT	GGTTGATGAC	GAAGAGCTGC	TGGAAGCTGGT	150
	AGAAATGGAA	GTTCGTGAAC	TTCTGTCTCA	GTACGATTTC	CCGGGCGACG	200
	ACACTCCGAT	CATCCGTGGT	TCTGCTCTGA	AAGCGCTGGA	AGGCGAAGCA	250
	GAGTGGGAAG	CTAAAATCGT	TGAGCTGGCT	GGCTTCCTGG	ATTCTTACAT	300
	CCCAGAACCA	GTTCGTGCTA	TCGACCTGCC	GTTCTGCTG	CCGATCGAAG	350
15	ACGTATTCTC	CATCTCCGGT	CGTGGCACC	TTGTTACCGG	TCGTGTAGAG	400
	CGCGGTATCG	TTAAAGTTGG	CGAAGAAGTT	GAAATCGTTG	GTATCAAAGA	450
	GACTGCTAAG	TCTACCTGTA	CCGGCGTTGA	AATGTTCCGC	AAACTGCTGG	500
	ACGAAGGCCG	TGCTGGTGAG	AACGTTGGTG	TTCTGCTGCG	TGGTATCAAA	550
	CGTGAAGAAA	TCGAACGTGG	TCAGGTACTG	GCTAAGCCGG	GTTCCATCAA	600
20	GCCGCACACC	AAATTGGAAT	CTGAAGTTTA	TATCCTGTCC	AAAGACGAAG	650
	GCGGCCGTCA	TACTCCGTTC	TTCAAAGGCT	ACCGTCCGCA	GTTCTACTTC	700
	CGTACAACCTG	ACGTGACTGG	TACCATCGAA	CTGCCGGAAG	GCGTAGAGAT	750
	GGTAATGCCG	GGCGACAACA	TCAAATGGT	TGTTACCCTG	ATCCACCCGA	800
	TCGC					804

25

2) INFORMATION FOR SEQ ID NO: 242

30 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 849 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Achromobacter xylosoxidans* subsp.
denitrificans
 (B) STRAIN: ATCC 15173

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 242

45	TCAGTTCCCC	CGCGATCACA	TGCCCAAGAT	CTACGAAGCG	CTTACTCTGG	50
	CCGACGAGGG	TTCCTCGTTC	GCCGAAAAGG	GTCTGACGCT	GGAAGTGCAG	100
	CAACAGCTGG	GCGACGGCGT	GGTGCGTACC	ATCGCGCTGG	GCTCCAGCGA	150
	CGGCCTGCGC	CGCGGTATGA	AGGTCACCGG	TACGGGCGCG	CCGATCTCGG	200
	TGCCGGTCCG	CACCGGCACG	CTGGGCCGCA	TCATGGACGT	GCTGGGTCGT	250
50	CCCATCGACG	AAGCCGGCCC	GATCCAGCAC	GAAGAAAAGC	GTGGCATTCA	300
	CCAGCCGGCT	CCCCGTTTCG	ACGAAGTGTG	GCCGTCGGTG	GAAGTGTGCT	350
	AAACCGGCAT	CAAGGTTATT	GACCTGGTCT	GCCCGTTCGC	CAAGGGCGGC	400
	AAGGTCGGCC	TGTTTCGGCG	CGCCGGCGTG	GGCAAGACCG	TCAACATGAT	450
	GGAAGTATGC	AACAACATCG	CCAAGCAGCA	CAGCGGCTTG	TCGGTGTTCG	500
55	CCGGCGTGGG	CGAGCGTACC	CGCGAAGGCA	ACGACTTCTA	CCACGAAATG	550
	GAAGAGTCGA	ACGTTCTGGA	CAAGGTTGCG	ATGGTGTTCG	GTCAGATGAA	600
	CGAACCCCGG	GGCAACCGTC	TGCGCGTGCC	GCTGACCGGC	CTGACCATGG	650
	CCGAGAAGTT	CCGCGACGAA	GGCCGCGACA	TCCTGTTCTT	CGTGGAACAAC	700
	ATCTACCGCT	ACACCCTGGC	CGGTACGGAA	GTGTCCGCGC	TGCTGGGCCG	750
60	TATGCCGTCG	GCAGTGGGCT	ACCAGCCAC	GCTGGCCGAA	GAAATGGGCA	800

5 2) INFORMATION FOR SEQ ID NO: 243

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 787 bases
(B) TYPE: Nucleic acid
10 (C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

15 (vi) ORIGINAL SOURCE:
(A) ORGANISM: *Acinetobacter baumannii*
(B) STRAIN: ATCC 19606

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 243
20 TGAAACTACT TTAGAAGTTC AGCAACAAC TGGTGATGGT GTTGTTTCGTA 50
CCATCGCAAT GGGTTCTACA GAAGGTCTTA AACGTGGTCT TACTGTAAC T 100
AGCACAAACG CACCGATCTC TGTTCCAGTT GGTACAGCCA CTCTTGGCCG 150
TATCATGGAC GTTTTAGGTC GTCCTATCGA TGAAGCAGGT CCTGTTGCGA 200
25 CTGAAGAACG TTTGCCGATT CACCGTCAAG CGCCTTCTTA TGCTGAACAA 250
GCAGCTTCTA CTGACCTTTT AGAAACTGGT ATTAAAGTCA TCGACTTACT 300
TTGCCCGTTT GCGAAAGGTG GTAAAGTTGG TTTATTTCGGT GGTGCTGGTG 350
TTGGTAAAAC CGTTAACATG ATGGAATTGA TCAACAACAT CGCGAAAGCA 400
CACTCAGGTT TATCTGTGTT TGCTGGTGTT GGTGAGCGTA CTCGTGAAGG 450
30 TAATGACTTC TATCAGAAA TGAAAGATTC TAACGTCTT GACAAAGTAG 500
CAATGGTCTA CGGTCAGATG AACGAGCCAC CAGGTAACCG TTTACGCGTA 550
GCGTTAACTG GTTTGACTAT GGCTGAATAC TTCCGTGATG AAAAAGACGA 600
AAACGGTAAA GGTCTGTACG TATTATTATT CGTCGACAAC ATCTACCGTT 650
ATACACTTGC AGGTACTGAA GTATCAGCAT TGTTAGGTCG TATGCCATCT 700
35 GCGGTAGGTT ACCAACCTAC ACTTGCAGAA GAAATGGGTG TTCTTCAAGA 750
GCGTATTACA TCTACTAAAT CTGGTTCGAT CACTTCG 787

40 2) INFORMATION FOR SEQ ID NO: 244

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 825 bases
(B) TYPE: Nucleic acid
45 (C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

50 (vi) ORIGINAL SOURCE:
(A) ORGANISM: *Acinetobacter lwoffii*
(B) STRAIN: CDCF 3697

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 244
55 GTTCCTAAGA TCTATGACGC TCTCCACGTT GATGGCACTG AAACCTACATT 50
AGAAGTTCAG CAACAACCTG GTGATGGCGT AGTTCGTACT ATTGCAATGG 100
GTTCTACTGA AGGCCTTAAG CGTGTTTGA ACGTAACTAA CACTAACGCG 150
CCGATTTCTG TACCAGTAGG TACAGCGACT CTAGGTCGTA TCATGGACGT 200
50 TCTTGGTCGC CCAATCGACG AAGCTGGTCC AGTTGCGACT GAAGCGCGTT 250

	TGCCGATTCA	CCGTCAAGCA	CCTTCTTATG	CTGAACAAGC	AGCTTCTACT	300
	GACCTTTTAG	AAACTGGTAT	TAAAGTCATC	GACTTACTTT	GCCCGTTCGC	350
	TAAAGGTGGT	AAAGTTGGTC	TGTCGGGTGG	TGCCGGTGTT	GGTAAACTG	400
	TAAACATGAT	GGAGTTGATC	AACAACATCG	CTAAAGCGCA	CTCAGGTTTA	450
5	TCTGTATTCT	CTGGTGTGG	TGAGCGTACT	CGTGAAGGTA	ATGACTTCTA	500
	TCACGAGATG	AAAGACTCAA	ACGTTCTAGA	CAAAGTAGCA	ATGGTCTACG	550
	GTCAGATGAA	CGAGCCACCG	GGTAACCGTT	TACGCGTAGC	GTTGACTGGT	600
	TTGACCATGG	CTGAGTACTT	CCGTGACGAG	AAAGACGAAA	ACGGCAAAGG	650
	CCGTGACGTA	CTATTGTTTCG	TAGATAACAT	CTACCGTTAT	ACACTAGCAG	700
10	GTAAGTGAAGT	ATCAGCACTT	CTAGGTCGTA	TGCCGTCTGC	AGTAGGTTAC	750
	CAACCGACAC	TTGCAGAAGA	GATGGGTGTT	CTTCAAGAAC	GTATTACATC	800
	GACTAAGTCT	GGTTCGATTA	CGTCA			825

15

2) INFORMATION FOR SEQ ID NO: 245

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 837 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

25

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus saprophyticus*
 (B) STRAIN: CSG-197

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 245

	CAATGAAGTT	CCAGAAATTA	ACAATGCCTT	AGTCGTAGAC	GTTGAAAGAG	50
	ATGAAGGTAC	AGTATCTCTT	ACATTAGAAG	TGGCATTACA	ACTTGGCGAT	100
	GATGTCGTAC	GTACAATTGC	AATGGATTCT	ACTGATGGTG	TTAAACGTGG	150
35	TACAGAAGTT	CGAGATAGCG	GAGATAGCAT	CAGTGTTCCA	GTTGGTGATG	200
	CTACGTTAGG	ACGTGTGTTT	AATGTTCTTG	GTGATACAAT	TGACTTAGAC	250
	GAGAAGCTTG	ATACTTCTGT	CAAACGTGAT	CCAATTCATA	GAGAAGCACC	300
	TGCATTCGAT	CAATTATCAA	CAAAAGTTGA	AATCTTAGAA	ACAGGTATTA	350
	AAGTAATTGA	TTTACTTGCA	CCATATATTA	AAGTGGTAA	AATCGGTTTA	400
40	TTCGGTGGCG	CTGGTGTAGG	TAAAACAGTA	TTAATTCAAG	AATTAATTAA	450
	TAATATAGCT	CAAGAACATG	GTGGTATTTT	AGTATTTGCC	GGCGTAGGTG	500
	AACGTACGCG	TGAAGGTAAT	GACTTATACT	ACGAAATGAG	TGATAGTGGT	550
	GTTATTAAGA	AAACAGCTAT	GGTCTTCGGA	CAAAATGAATG	AGCCACCTGG	600
	TGCGCGTATG	CGTGTTGCTT	TATCAGGCTT	AACAATGGCT	GAACACTTCC	650
45	GTGATGTACA	AGGACAAGAT	GTTTTACTAT	TTATTGATAA	CATATTCAGA	700
	TTTACGCAAG	CTGGTTCAGA	AGTATCAGCA	CTATTAGGTC	GTATGCCATC	750
	AGCCGTTGGT	TATCAACCTA	CCCTTGCTAC	TGAAATGGGT	CAATTACAAG	800
	AACGTATTAC	ATCAACAACCT	AAAGGATCTG	TAACGTC		837

50

2) INFORMATION FOR SEQ ID NO: 246

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 851 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

60

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Alcaligenes faecalis*
 (B) STRAIN: ATCC 15554

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 246

	TTCCCCCGCG	ACAGCATCCC	TAAAGTCTAC	GAAGCATTGA	CGCTCGTTGA	50
	CGAAAGTTCG	GCTTTCGCAG	AAAAAGGCCT	GACTTTTGAA	GTACAGCAAC	100
10	AATTGGGTGA	CGGTGTAGTT	CGCACCATCG	CCATGGGTTC	CAGCGACGGC	150
	CTGCGCCGCG	GTATGGAAGT	GGCCGGTTCG	GGCGCTCCCA	TCTCCGTTCC	200
	CGTGGGTGTC	GGCACCTG	GTCGCATTAT	GGACGTTCTG	GGTCGCCCTA	250
	TTGACGAAGT	CGGTCCTATT	CAGTCCGACG	AGCGTCGCGC	CATTCAACAG	300
	CCTGCGCCTA	CTTTCGACGA	ACTGTCGCCT	TCCGTAGAGC	TGCTGGAAAC	350
15	CGGTATTAAA	GTGATTGACC	TGGTTTGCCC	GTTTCGCCAAG	GGTGGTAAGG	400
	TTGGTCTGTT	CGGTGGTGCC	GGTGTGGGCA	AGACCGTGAA	CATGCTGGAG	450
	CTGATCAACA	ACATCGCCAA	GGCACACAGC	GGTCTGTCCG	TGTTTGCCGG	500
	TGTGGGTGAG	CGTACCCGTG	AAGGTAACGA	CTTCTACCAC	GAAATGGCCG	550
	ATGCTGGCGT	TATCCAGATG	GACAACCTGA	GCGAGTCCAA	AGTGGCCATG	600
20	GTGTTCCGTC	AGATGAACGA	ACCTCCAGGC	AACCGTCTGC	GTGTGGCACT	650
	GTCCGGCCTG	ACCATGGCCG	AGAAGTTCCG	TGACGAAGGC	CGTGACATCC	700
	TGTTCTTTGT	GGACAACATC	TACCGCTACA	CGCTGGCCGG	TACAGAAGTG	750
	TCCGCTCTGC	TGGGTCGTAT	GCCTTCCGCA	GTGGGTTACC	AGCCTACGCT	800
	GGCCGAGGAA	ATGGGTAAGC	TGCAAGAGCG	CATTACCTCC	ACCAAGACCG	850
25	G					851

2) INFORMATION FOR SEQ ID NO: 247

30

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 846 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacillus anthracis*
 (B) STRAIN: 4229

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 247

45	GATGGCGGAA	AGCTACCAGA	AATCTACAAC	GCCCTTACGG	TAAAACAGAG	50
	CAACGAAAAC	GGAACAAGCA	TTAACTTAAC	ATTTGAAGTT	GCACTTCATT	100
	TAGGTGATGA	CACAGTTCGT	ACAGTTGCAA	TGTCTTCCAC	AGATGGACTT	150
	GTTCGTGGCA	CAGAAGTAGA	AGATACTGGT	AAAGCAATCT	CTGTACCAGT	200
	TGGTGATGCA	ACACTTGGTC	GTGTATTTAA	CGTATTAGGT	GATGCAATTG	250
50	ACTTAGATGG	TGAGGTTCTT	GCGGATGTAC	GTCGTGATCC	AATTCACCGT	300
	CAAGCACCTG	CATTCAAGA	ATTATCTACT	AAAGTAGAAA	TTCTTGAAAC	350
	TGGTATTAAA	GTAGTAGACT	TACTTGCTCC	TTACATTAAG	GGTGGTAAGA	400
	TCGGTCTATT	CGGTGGTGCC	GGTGTAGGTA	AAACGGTATT	AATTCAGGAA	450
	TTAATCAATA	ACATCGACA	AGAACACGGT	GGTATCTCTG	TATTCGCTGG	500
55	TGTAGGTGAG	CGTACTCGTG	AGGGTAATGA	CTTATACCAC	GAAATGAGCG	550
	ATTCTGGCGT	AATTAAGAAA	ACTGCGATGG	TATTCGGACA	AATGAACGAG	600
	CCACCTGGAG	CACGTCAACG	TGTTGCGTTA	ACAGGTTTAA	CAATGGCTGA	650
	GCATTTCCGT	GATGAGCAAG	GACAAGATGT	ACTTCTGTTC	ATCGATAATA	700
	TCTTCCGTTT	CACGCAAGCA	GGTTCCTGAAG	TATCTGCCCT	TCTTGGCCGT	750
50	ATGCCATCTG	CGGTAGGTTA	CCAACCAACA	CTTGCAACAG	AAATGGGTCA	800

ATTACAAGAG CGTATTACAT CTACAAATAA AGGGTCTATC ACGTCT

846

5 2) INFORMATION FOR SEQ ID NO: 248

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 810 bases
 (B) TYPE: Nucleic acid
 10 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

15 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacillus cereus*
 (B) STRAIN: ATCC 14579

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 248

20 CCAGAAATCT ACAATGCCCT TACGGTAAAA CAAAGCAACG AAAACGGAAG 50
 CATGAACTTA ACATTTGAAG TTGCACTTCA TTTAGGTGAT GATACAGTTC 100
 GTACAGTTGC GATGTCTTCC ACAGATGGAC TTGTTCTGTGG CACAGAAGTA 150
 GAAGATACTG GTAAAGCAAT CTCTGTACCA GTTGGTGATG CAACACTTGG 200
 25 ACGTGTATTC AACGTATTAG GTGATGCAAT TGA CT TAGAT GGTGAACTTC 250
 CTGCGGATGT ACACCGTGAT CCAATTCACC GTCAAGCACC TGCATTGAA 300
 GAATTATCTA CTAAAGTAGA AATTCTTGAA ACTGGTATTA AAGTAGTAGA 350
 CTTACTTGCT CCTTACATTA AGGGTGGTAA GATCGGCCTA TTCGGTGGTG 400
 CCGGCGTAGG TAAAACAGTA TTAATTCAGG AGTTAATCAA TAACATCGCA 450
 30 CAAGAGCACG GTGGTATCTC TGTATTCGCT GGTGTAGGTG AGCGTACTCG 500
 TGAGGGTAAT GACTTATACC ACGAAATGAG CGATTCTGGC GTAATCAAGA 550
 AAAGTGCAT GGTATTCGGA CAAATGAACG AGCCACCTGG AGCACGTCAA 600
 CGTGTTCAT TAACAGGTTT AACAAATGGCT GAGCATTTC GTGATGAGCA 650
 AGGACAAGAC GTACTTCTGT TCATCGATAA CATCTTCCGT TTCACGCAAG 700
 35 CGGGTTCTGA AGTATCTGCC CTTCTTGGTC GTATGCCATC TGCGGTAGGT 750
 TACCAACCAA CACTTGCAAC AGAAATGGGT CAATTACAAG AGCGTATTAC 800
 ATCTACAAAT 810

40

2) INFORMATION FOR SEQ ID NO: 249

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 944 bases
 45 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

50

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacteroides distasonis*
 (B) STRAIN: ATCC 8503

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 249

CTTTGATTAT GGGACAGAAG AAACAGTAAC CCTCCCCCGT ATCCACGACG 50
 CCATGGAGAT TTCCCGCCCA AACGGAAAGA TCTTGATCGT CGAAGTTCAG 100
 CAACACATCG GGGAAAACAC CGTCCGTACC GTAGCGATGG ATACGACCGA 150
 50 CGGATTGAGA CGAGGCATGG AGGCCGTGTC ATACGGAATG CCCATCACCA 200

	TGCCGACCGG	CGACCAAGTC	AAAGGACGTT	TAATGAATGT	CACCGGCGAC	250
	CCTATCGATG	GCATGGCCCA	GCTTACTAAA	GACGGGGCTC	TTCCCATCCA	300
	TCGTGAGCCT	CCTAAATTCG	AGGATCTGAC	AACGACCCAA	GAGGTCTTGT	350
	ACACGGGTAT	TAAAGTAATC	GATTTATTGG	AACCTTACGC	CAAAGGAGGC	400
5	AAGATCGGAC	TTTTCGGAGG	AGCCGGAGTC	GGCAAAACGG	TATTGATCAT	450
	GGAATTGATC	AACAACATCG	CAAAGAAAAA	CAACGGATTC	TCCGTCTTCG	500
	CCGGTGTGGG	TGAACGTACA	CGTGAAGGAA	ATGACCTATT	GCGTGAAATG	550
	ATCCAATCCG	GTGTCATCCG	ATACGGCGAG	GAGTTTAAGA	AGAGTATGGA	600
	GGCAGGCAAC	TGGGACTTGT	CGAAGATCGA	TTACGATGAA	TTGGCTAAGT	650
10	CGCAGGCTAC	CTTGGTATTG	GGGCAGATGA	ACGAACCGCC	GGGCGCCCGC	700
	TCGTCCGTGG	CCTTATCCGG	TTTGACGATC	GCCGAATCCT	TCCGTGACAA	750
	AGCCTCTGAG	GGAGAAAGAA	AAGATATATT	ATTCTTTCATC	GATAATATCT	800
	TCCGTTTCAC	CCAAGCCGGT	TCCGAGGTTT	CCGCCTTGCT	GGGGCGTATG	850
	CCTTCCGCCG	TAGGTTACCA	ACCGACATTG	GCCACGGAAA	TGGGAGCTAT	900
15	GCAAGAGCGT	ATCACTTCAA	CCAAGAAGGG	CTCCATCACC	TCCG	944

2) INFORMATION FOR SEQ ID NO: 250

20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 939 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 25 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 30 (A) ORGANISM: *Bacteroides ovatus*
 (B) STRAIN: ATCC 8483

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 250

35	TTGAGGGTAC	GGATGCAGAA	TTGGTGCTGC	CAAGCATCCA	CGACGCACTG	50
	GAGATAAAGA	GGCCAAACGG	CAAAATACTG	GTTGTAGAAG	TTCAGCAACA	100
	TATCGGCGAA	AATACGGTGC	GTACCGTAGC	GATGGACAGT	ACTGACGGAC	150
	TTCAGAGAGG	CATGAAAGTG	TATCCCACCG	GAGGCCCCGAT	CACGATGCCG	200
	ATTGGCGAAC	AGATTAAAGG	ACGACTGATG	AACGTAGTCG	GTGATTTCGAT	250
40	CGACGGTATG	AAAGGACTCG	ACCGCAAAGG	TGCATATTCC	ATTCATCGCG	300
	ACCCCCCTAA	GTTTGAGGAT	TTGACTACTG	TGCAAGAGGT	GCTCTTCACA	350
	GGTATCAAAG	TGATCGACCT	GCTCGAACCG	TATGCCAAAG	GTGGTAAAAT	400
	CGGTTTGTTC	GGCGGTGCCG	GTGTAGGAAA	GACTGTATTG	ATTCAGGAAC	450
	TTATCAATAA	TATCGCCAAG	AAACATAATG	GATTCTCTGT	ATTTGCCGGA	500
45	GTAGGTGAAC	GTACCCGTGA	AGGTAACGAC	TTGCTGCGCG	AAATGATTGA	550
	ATCCGGTGTA	ATCCGTTACG	GCGAAGCATT	CAAAGAAGGA	ATGGAGAAAG	600
	GTCACGGGA	TCTTTCGAAA	GTGGATTATA	ACGAACTGGA	GAAATCGCAA	650
	GTGTCTCTGA	TTTTCGGTCA	GATGAACGAG	CCTCCGGGCG	CACGTGCCTC	700
	TGTGGCATTG	TCCGGACTGA	CGGTGGCGGA	ATCTTTCCGC	GACGCAGGAA	750
50	AAGAAGGTGA	GAAACGCGAT	ATTCTGTTCT	TTATTGATAA	TATCTTCCGT	800
	TTCACGCAAG	CAGGTTTACA	AGTGTCCGCC	CTTTTGGGAC	GTATGCCCTC	850
	CGCTGTTGGT	TACCAGCCCA	CGTTGGCTAC	GGAAATGGGT	GCGATGCAGG	900
	AACGTATCAC	GTCTACCCGC	AAAGGTTCTA	TCACCTCCG		939

55

2) INFORMATION FOR SEQ ID NO: 251

(i) SEQUENCE CHARACTERISTICS:

- 50 (A) LENGTH: 833 bases

- (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

5 (ii) MOLECULE TYPE: DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Leclercia adecarboxylata*
 (B) STRAIN: ATCC 23216

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 251

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CGAATTCCCT CAGGATGCCG TACCGCGCGT GTACGATGCT CTTGAGGTTC      50
AGAATGGTAA TGAGAGCCTG GTGCTGGAAG TTCAGCAGCA GCTCGGCGGC      100
15 GGTATTGTGC GTACCATCGC CATGGGTTCT TCCGACGGTC TGCGTCGTGG      150
TCTGGAAGTT AAAGACCTCG AGCACCCAAT CGAAGTACCA GTAGGTAAAG      200
CAACCCTGGG CCGTATCATG AACGTCCTGG GTCAGCCGAT CGACATGAAA      250
GGCGACATCG GCGAAGAAGA GCGTTGGGCT ATCCACCGTT CAGCACCTTC      300
CTATGAAGAG CTGTCCAGCT CTCAGGAACT GCTGGAAACC GGCATCAAAG      350
20 TTATCGACCT GATGTGTCCG TTCGCGAAGG GCGGTAAAGT TGGTCTGTTC      400
GGCGGTGCGG GTGTAGGTAA AACCGTAAAC ATGATGGAGC TGATCCGTAA      450
CATCGCGATC GAGCACTCCG GTTACTCCGT GTTTGCAGGC GTGGGTGAGC      500
GTACTCGTGA GGGTAACGAC TTCTACCACG AAATGACCGA CTCCAACGTT      550
CTGGACAAAG TATCCCTGGT TTACGGCCAG ATGAACGAGC CACCAGGAAA      600
25 CCGTCTGCGC GTTGCCTGTA CCGGCCTGAC CATGGCTGAG AAGTTCCTGTG      650
ACGAAGGTCG TGACGTACTG CTGTTTCGTTG ACAACATCTA CCGTTACACC      700
CTGGCCGGTA CGGAAGTATC CGCACTGCTG GGTGCTATGC CATCAGCAGT      750
AGGCTACCAG CCGACCCTGG CGGAAGAGAT GGGTGTTCTG CAGGAACGTA      800
TCACCTCTAC CAAAACCGGT TCTATCACCT CCG                          833
30

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2) INFORMATION FOR SEQ ID NO: 252

35 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 819 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

40

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Stenotrophomonas maltophilia*
 (B) STRAIN: CDC F3338

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 252

```

GTGTACGACG CACTGAAGGT GGAAAACACC GAGATCACCC TCGAAGTCCA      50
50 GCAGCAGCTG GGCACGCGCG TGGTGCCTAC CATCGCCCTC GGTTCACCG      100
ACGGCCTGAA GCGCAACCTG GTTGCCGTCA ACACCGGCCG TGGCATCTCG      150
GTGCCGGTCG GCGCCGGCAC CCTGGGCCCG ATCATGGACG TGCTGGGCCG      200
TCCGATCGAC GAAGCCGGCC CGGTCGCTGC CAGCGACAAC TGGGAAATCC      250
ACCGCGCTGC GCCGTCGTAT GAAGACCAGT CCCCAGCCAC CGAGCTGCTG      300
55 GAAACCGGCA TCAAGGTCAT CGACCTGATG TGCCCGTTCT CCAAGGGCGG      350
CAAGGTCGGC CTGTTCCGGC GCGCCGGCGT CGGCAAGACC GTCAACATGA      400
TGGAAGTATG CAACAACATC GCCAAGGCCG ACAGCGGCCT GTCCGTGTTC      450
GCCGGCGTGG GTGAGCGTAC CCGTGAGGGC AACGACTTCT ACCACGAGAT      500
GAAGGACTCC AACGTCCTGG ACAAGGTGGC GATGGTGTAC GGCCAGATGA      550
60 ACGAGCCGCC GGGCAACCGT CTGCGCGTCG CCCTGACCGG CCTGACCATG      600

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	GCCGAGTACT	TCCGCGATGA	GAAGGACGAA	AACGGCAAGG	GCAAGGACGT	650
	CCTGCTGTTC	GTCGACAACA	TCTACCGCTA	CACCCTGGCC	GGTACCGAAG	700
	TGTCGGCACT	GCTGGGCCGC	ATGCCGTCCG	CGGTGGGTTA	CCAGCCGACC	750
	CTGGCCGAGG	AAATGGGCGT	CCTGCAGGAG	CGCATCACCT	CGACCAAGAA	800
5	TGGTTCGATC	ACCTCGATC				819

2) INFORMATION FOR SEQ ID NO: 253

10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 864 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 15 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 20 (A) ORGANISM: *Bartonella henselae*
 (B) STRAIN: ATCC 49882

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 253

25	AGTTTGAAGG	CCCTTTGCCA	AATATTCTCA	ATGCATTAGA	AACAGATAAT	50
	TTGGGCAATC	GGCTAGTTTT	AGAAGTTGCT	CAGCATTG	GTGAAAATAC	100
	CGTGCGTACC	ATTGCCATGG	ATACTACCGA	TGGTCTTGTC	CGTGGTCAAA	150
	AAGTTTTTGA	TACAGGAACA	CAGATCAGTG	TTCCCGTGGG	AGAAGCAACA	200
	CTTGGTCGTA	TTATGAATGT	GATTGGAGAG	CCGGTTGATA	ATGTTGGCCC	250
30	AATTGCTACA	AGCAAAACCC	GTTCCATTCA	CCAAGAGGCT	CCTGAATATG	300
	TGGAGCAATC	AACCGCATCA	GAAATCCTTG	TGACTGGTAT	TAAAGTCGTT	350
	GATCTGTTAG	CTCCTTATTC	TAAAGGGGGG	AAGGTTGGTT	TGTTTGGAGG	400
	TGCCGGTGTT	GGTAAAACCG	TTCTCATTAT	GGAGCTTATC	AACAATATTG	450
	CAAAGGCGCA	TGGTGGCTAT	TCAGTGTTTG	CCGGTGTG	TGAACGTACA	500
35	CGTGAGGGAA	ATGATCTTTA	TTATGAAATG	ATCGAAAGCC	GTGTGAATGT	550
	GAATCCAAAA	GACAACAATG	GTTCAACAGA	AGGATCAAAA	TGTGCACTCG	600
	TTTATGGGCA	AATGAATGAA	CCACCAGGGG	CGCGTGCACG	TGTGGCTCTT	650
	TCAGGATTGA	CCATTGCAGA	AAGTTTCCGT	GATGAGGGAC	AAGATGTTTT	700
	GTTCTTCGTA	GATAATATTT	TCCGTTTTAC	GCAAGCAGGC	GCTGAAGTGT	750
40	CAGCTCTTTT	AGGGCGTATT	CCTTCTGCTG	TAGGGTATCA	GCCAACTTTG	800
	GCAACTGATA	TGGGGGCTTT	GCAAGAGCGT	ATTACCAGTA	CAAGAACAGG	850
	CTCTATTACC	TCTG				864

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2) INFORMATION FOR SEQ ID NO: 254

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 866 bases
 50 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

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(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bifidobacterium adolescentis*
 (B) STRAIN: ATCC 15703

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 254

	TTCCCGGTGG	GCCACCTGCC	CGACATTTAC	AATGCACTTA	CCGTTGAACT	50
	GKCCAAACACC	GGYGTCCACG	AASAGGGCGA	GACCACCAAG	AAGATCACCC	100
	TTGMMGGTTGA	ACAGCATCTT	GGCGATTCCA	CCGTGCGTAC	CGTCGCTCTG	150
5	AAGCCGACTG	ACGGCCTTGT	GCGTGGCGCC	ACCGTGTATG	ACACCGGCGG	200
	CCCGATCTCT	GTGCCGGTTG	GCGATGTCAC	CAAGGGCCAC	GTATTCGACG	250
	TGTCCGGCAA	CATCCTCAAC	AAGAAGGCCG	ACGAGACCGT	TAAGGTTACC	300
	GAACGTTGGT	CTATCCACCG	TAACCCGCCG	GCATTCGACC	AGCTGGAGTC	350
	CAAGACCCAG	ATGTTGAAA	CCGGTATCAA	GGTCATCGAT	TTGCTGACCC	400
10	CGTATGTGCA	GGGCGGCAAG	ATCGGTCTGT	TCGGCGGCGC	AGGCGTCGGC	450
	AAGACCGTGC	TGATCCAGGA	AATGATTTCAG	CGTGTGGCTC	AGAACCACGG	500
	CGGTGTGTCC	GTGTTCCGAG	GCGTCGGCGA	GCGTACCCGT	GAGGGTAACG	550
	ATCTGATCGG	CGAAATGGAC	GAAGCCGGCG	TGCTCGAGAA	GACCGCACTG	600
	GTCTTCGGCC	AGATGGATGA	GCAGCCGGGT	ACCCGTCTGC	GCGTGCCGCT	650
15	GACCGCACTG	ACCATGGCAG	AGTACTTCCG	TGACGTACAG	AATCAGGACG	700
	TGCTGCTGTT	CATCGATAAC	ATCTTCCGTT	TCACCCAGGC	TGGTTCCGAG	750
	GTGTCCACCC	TGCTCGGCCG	TATGCCGTCC	GCAGTGGGCT	ACCAGCCGAA	800
	CCTGGCCGAT	GAGATGGGCG	CGCTGCAGGA	GCGAATCACT	TCGACCCGTG	850
	GACACTCCAT	CACCTC				866
20						

2) INFORMATION FOR SEQ ID NO: 255

- 25 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 842 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Double
 - (D) TOPOLOGY: Linear
- 30 (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Brucella abortus*
 - (B) STRAIN: S2308
- 35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 255

	AAGGCCAGCT	GCCGCTGATC	CTGAACGCGC	TTGAAGTGGA	CAATCAGGGC	50
40	CATCGTCTGG	TTCTCGAAGT	TGCCCAGCAC	CTCGGCGAAG	ACACCGTGCG	100
	CACCATCGCC	ATGGACGCGA	CCGAAGGTCT	CGTTCGCGGT	CAGGAAGCAC	150
	GCGACACTGG	CGAACCGATC	ATGGTGCCGG	TCGGCGTCGA	AACGCTTGGC	200
	CGCATCATGA	ACGTCATCGG	CGAGCCGGTT	GACGAAGCAG	GCCCCATCAA	250
	GACCAAGGCA	ACCCGCGCCA	TCCACCAGAA	CGCGCCGGAA	TATATCGAAC	300
45	AGTCGACCGA	AGCCGAAATT	CTGGTCACGG	GCATCAAGGT	CGTCGACCTT	350
	CTGGCGCCTT	ACGCCAAGGG	CGGCAAGATC	GGCCTCTTCG	GCGGTGCAGG	400
	CGTCGGCAAG	ACCGTTCTCA	TCATGGAAC	CATCAACAAC	GTCGCCAAGG	450
	CGCACGGCGG	TTATTCCGTG	TTCGCAGGCG	TCGGTGAGCG	TACCCGTGAG	500
	GGCAACGACC	TTTACCACGA	AATGATCGAG	TCGGGCGTGA	ACAAGCTCGG	550
50	CGGCGGCGAA	GGCTCCAAGG	CAGCCCTCGT	TTACGGCCAG	ATGAACGAAC	600
	CCCCGGGTGC	CCGCGCCCGC	GTTGCCCTTT	CCGGTCTGAC	GGTTGCTGAA	650
	AACTTCCGTG	ACCAGGGCCA	GGACGTTCTG	TTCTTCGTGG	ACAACATCTT	700
	CCGCTTCACG	CAGGCAGGTT	CGGAAGTGTC	GGCTCTTCTC	GGCCGTATTC	750
	CTTCCGCTGT	GGGTTATCAG	CCGACGCTGG	CAACCGACAT	GGGCGCCATG	800
55	CAGGAACGCA	TCACCACGAC	GACCAAGGGT	TCGATCACCT	CG	842

2) INFORMATION FOR SEQ ID NO: 256

60

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 833 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Cedecea davisae*
 (B) STRAIN: ATCC 33431

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 256

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15  CGAGTTCCTT CAGGACGGCG TACCGCGCGT TKATGATGCG CTTGAAGTAC      50
    AAAATAACAG CGAGCAGCTG GTGCTGGAAG TTCAGCAGCA GCTCGGCGGC      100
    GGTATCGTGC GTACCATCGC TATGGGTTC TCCGACGGTC TGCGTCGTGG      150
    TCTGGAAGTT AAAGACCTCG AGCACCCGAT CGAAGTCCCG GTAGGTAAAG      200
    CGACCCTTGG CCGTATCATG AACGTGCTGG GTCAGCCGAT CGACATGAAA      250
20  GGCATATATCG GCGAAGAAGA CCGTTGGGCT ATTACCGCG CTGCACCTTC      300
    CTATGAAGAG CTGTCCAGCT CTCAGGAACT GCTGGAAACC GGCATCAAAG      350
    TAATCGACCT TATCTGTCCG TTCGCTAAGG GCGGTAAAGT AGGTCTGTTC      400
    GGTGGTGCGG GCGTGGGTAA AACCGTAAAC ATGATGGAGC TTATCCGTAA      450
    CATCGCGATC GAGCACTCCG GCTACTCCGT GTTTGCGGGC GTGGGTGAGC      500
25  GTAATCGTGA GGGTAACGAC TTCTATCAGC AAATGACCGA CTCCAACGTT      550
    CTGGACAAAG TTGCCCTGGT TTACGGCCAG ATGAACGAGC CACCGGGTAA      600
    CCGTCTGCGC GTAGCGCTGA CCGGTCTGAC CATCGCGGAG AAATTCCGTG      650
    ACGAAGGTCG TGACGTTCTG CTGTTTCGTTG ATAACATCTA CCGTTACACC      700
    CTGGCCGGTA CTGAAGTATC CGCGCTGCTG GGTCTGATGC CTTCTGCGGT      750
30  AGGTTACCAG CCAACTCTGG CGGAAGAGAT GGGTGTCTT CAGGAGCGTA      800
    TTACCTCCAC CAAGACCGGT TCCATCACCT CCG                               833
  
```

35 2) INFORMATION FOR SEQ ID NO: 257

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 829 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Cedecea lapagei*
 (B) STRAIN: ATCC 33432

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 257

```

50  TTCCCTCAGG ACGGCGTACC GCGCGTATAT GACGCGCTTG AGGTACAGAA      50
    TAACAGCGAG AAGCTGGTGC TGGAAGTTCA GCAGCAGCTC GGCGGCGGTA      100
    TCGTACGTAC CATCGCAATG GGTTCCTCCG ACGGTCTGCG TCGTGGTCTG      150
    GAAGTGAAAG ACCTCGAGCA CCCGATCGAA GTCCCGGTAG GTAAAGCGAC      200
55  TCTGGGTCTG ATCATGAACG TGCTGGGTCA GCCAATTGAT ATGAAAGGCG      250
    ACATCGGCGA AGAAGATCGT TGGGCGATTG ACCGCGCAGC ACCTTCCTAT      300
    GAAGAGCTGT CCAGCTCTCA GGAAGTCTG GAAACCGGCA TCAAAGTTAT      350
    CGACCTGATT TGTCCGTTCT CTAAGGGCGG TAAAGTTGGT CTGTTCCGGT      400
    GTGCGGGCGT AGGTAAACCG GTAAACATGA TGGAGCTGAT CCGTAACATC      450
50  GCGATCGAGC ACTCCGGTTA CTCCGTGTTT GCAGGCGTGG GTGAGCGTAC      500
  
```

	TCGTGAGGGT	AACGACTTCT	ACCACGAGAT	GACCGACTCC	AACGTTCTGG	550
	ACAAAGTTGC	ACTGGTTTAC	GGCCAGATGA	ACGAGCCGCC	AGGTAACCGT	600
	CTGCGCGTAG	CGCTGACCGG	TCTGACCATC	GCGGAGAAAT	TCCGTGACGA	650
	AGGCCGTGAC	GTTCTGCTGT	TCGTCGATAA	CATCTATCGT	TATACCCTGG	700
5	CCGGTACAGA	AGTTTCTGCA	CTGCTGGGTC	GTATGCCATC	TGCGGTAGGT	750
	TATCAGCCTA	CTCTGGCAGA	AGAGATGGGT	GTTCTTCAGG	AGCGTATTAC	800
	CTCCACCAAG	ACCGGTTCCA	TCACTTCCG			829

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2) INFORMATION FOR SEQ ID NO: 258

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 830 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

20

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Cedecea neteri*
(B) STRAIN: ATCC 33855

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 258

	TCCCTCAGGA	CGGCGTACCG	CGCGTTTATG	ACGCGCTTGA	GGTACAGAAC	50
	AACAATGAGA	AGCTGGTGCT	GGAAGTTCAG	CAGCAGCTCG	GCGGCGGTAT	100
	CGTGCGTACC	ATCGCAATGG	GTTCTTCCGA	CGGTCTGCGT	CGTGGTCTGG	150
30	TAGTAACAGA	CCTCGAGCAC	CCGATCGAAG	TCCCGGTAGG	TAAAGCGACC	200
	CTTGCCCGTA	TCATGAACGT	GCTGGGTCAG	CCGATCGACA	TGAAAGGCCGA	250
	CATCGGCGAA	GAAGACCGTT	GGGCGATTCA	CCGCGCAGCA	CCTTCCTACG	300
	AAGAGCTGTC	CAGCTCTCAG	GAATTGCTGG	AAACCGGCAT	CAAAGTTATC	350
	GACCTGATTT	GTCCGTTTCG	TAAGGGCGGT	AAAGTAGGTC	TGTTCCGTGG	400
35	TGCGGGCGTA	GGTAAAACCG	TAAACATGAT	GGAGCTGATC	CGTAACATTG	450
	CGATCGAGCA	CTCCGGTTAT	TCCGTGTTTG	CGGGCGTGGG	TGAGCGTACT	500
	CTTGAGGGTA	ACGACTTCTA	CCACGAAATG	ACCGACTCCA	ACGTTCTGGA	550
	TAAAGTAGCA	CTGGTTTACG	GCCAGATGAA	CGAGCCACCA	GGTAACCGTC	600
	TGCGCGTAGC	GCTGACCGGT	CTGACCATCG	CGGAAAAATT	CCGTGACGAA	650
40	GGCCGCGACG	TTTTGCTGTT	CGTTGATAAC	ATCTACCGTT	ATACCCTGGC	700
	CGGTACCGAA	GTATCTGCAC	TGCTGGGTCTG	TATGCCCTTCT	GCGGTAGGTT	750
	ATCAGCCAAC	TCTGGCAGAA	GAGATGGGTG	TTCTTCAGGA	GCGTATTACC	800
	TCCACCAAGA	CCGGTTCTAT	CACCTCCGTA			830

45

2) INFORMATION FOR SEQ ID NO: 259

(i) SEQUENCE CHARACTERISTICS:

- 50 (A) LENGTH: 931 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

55

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Chryseobacterium meningosepticum*
(B) STRAIN: CDC B7681

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 259

	TTTCAGGAAG	TAGAGGAACT	ACCAAAACATT	TATGACGCAC	TTGAAGTTGT	50
	CAGAGAAGGC	CAGAAAGGTC	TGATCTTAGA	AGTTGAACAA	CACATCGGTG	100
5	AGGATACAGT	GAGATGTATC	GCTATGGATG	CAACAGACGG	ACTTCAAAGA	150
	GGACAATCTG	TAATAGGACA	TGGAAGACAA	ATTACTATGC	CTATTGGTGA	200
	AGAAGTAAAT	GGTAGATTGT	TCAACGTGGT	AGGAGATGCT	ATCGACGGAC	250
	TTCAGGAATT	ATCTAAAGAC	AATGGTTTGC	CAATCCACAG	AGAAGCACCT	300
	AAATTTCGATC	AGTTATCAAC	TTCTGCTGAA	GTACTATATA	CAGGTATCAA	350
10	AGTAATCGAC	CTTATCGAGC	CTTATGCAAA	AGGTGGTAAA	ATTGGTTTGT	400
	TCGGTGGTGC	TGGTGTAGGT	AAAACAGTAT	TGATCCAGGA	ATTGATTAAT	450
	AACATTGCTA	AAGGACACGG	TGGTCTTTCT	GTATTCCGAG	GAGTAGGTGA	500
	GAGAACAAGA	GAAGGAAATG	ACCTTCTTCG	TGAGATGTTA	GAGTCTGGTA	550
	TTATTAAATA	TGGTGACGAA	TTCATGCATT	CTATGGAGAA	CGGTGGATGG	600
15	GATCTTTCTA	AAGTTGACAG	TGAGTTGATG	AAAGAGTCTA	AAGCTGCTTT	650
	CGTTTTTCGGA	CAGATGAACG	AGCCACCAGG	TGCAAGAGCA	CGTGTAGCCC	700
	TTTCTGGTCT	TACTTTAGCT	GAATACTACC	GTGATGGTGG	CGAAAGCGGA	750
	CAAGGTAGAG	ACGTTCTTTT	CTTCGTAGAC	AACATCTTCC	GTTTTACACA	800
	GGCTGGTTCT	GAGGTGTCTG	CACCTCTAGG	TCGTATGCCT	TCAGCGGTAG	850
20	GTTACCAACC	AACTCTAGCT	TCTGAGATGG	GTGCAATGCA	GGAGAGAATT	900
	ACTTCAACTA	AAAACGGATC	TATTACATCT	G		931

25 2) INFORMATION FOR SEQ ID NO:260

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 726 bases
 (B) TYPE: Nucleic acid
 30 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

35 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Citrobacter amalonaticus*
 (B) STRAIN: ATCC 25405

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 260

40	GTATCGTACG	TACCATCGCA	ATGGGTTCTT	CCGACGGTCT	GCGTCGTGGT	50
	CTGGAAGTCA	AAGACCTCGA	GCACCCGATC	GAAGTCCCGG	TAGGTAAAGC	100
	AACCCTGGGT	CGTATCATGA	ACGTCCTGGG	TCACCCGATC	GACATGAAAG	150
	GCGATATCGG	TGAAGAAGAG	CGTTGGGCTA	TCCACCGCGC	AGCACCGTCC	200
45	TATGAAGAGC	TGTCCAGCTC	TCAGGAACTG	CTGGAAACCG	GTATCAAAGT	250
	TATCGACCTG	ATGTGTCCGT	TCGCGAASGG	CGGTAAAGTG	GGTCTGTTCC	300
	GTGGTGCGGG	TGTAGGTAAA	ACCGTAAACA	TGATGGAGCT	TATCCGTAAC	350
	ATCGCGATCG	AGCACTCCGG	TTACTCCGTG	TTTGCGGGCG	TAGGTGAACG	400
	TACTCGTGAG	GGTAACGACT	TCTACCACGA	AATGACCGAC	TCCAACGTTT	450
50	TGGATAAAGT	ATCCCTGGTA	TATGGCCAGA	TGAACGAGCC	GCCGGGAAAC	500
	CGTCTGCGCG	TTGCACTGAC	CGGTCTGACC	ATGGCAGAGA	AATTCCGTGA	550
	CGAAGGTCGT	GACGTACTGC	TGTTCTGTCG	TAACATCTAT	CGTTACACCC	600
	TGGCCGGTAC	GGAAGTTTCC	GCACTGCTGG	GTCGTATGCC	ATCAGCGGTA	650
	GGTTACCAGC	CGACCCTGGC	GGAAGAGATG	GGTGTTCTGC	AGGAACGTAT	700
55	CACTTCTACC	AAAACCGGTT	CTATCA			726

50 2) INFORMATION FOR SEQ ID NO: 261

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 812 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Citrobacter braakii*
 (B) STRAIN: ATCC 43162

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 261

```

15  GCCGTACCGC GCGTGTACGA TGCTCTTGAG GTTATGAATG GTAAAGAGAG      50
    CCTGGTGCTG GAAGTTCAGC AGCAGCTCGG CGGCGGTATC GTACGTACCA      100
    TCGCCATGGG TTCTTCCGAC GGTCTGCGTC GTGGTCTGGA AGTTAAAGAT      150
    CTCGAGCACC CGATCGAAGT CCCGGTAGGT AAAGCAACTC TGGGTCGTAT      200
    CATGAACGTC CTGGGTCACC CGATCGACAT GAAAGGCGAT ATCGGTGAAG      250
20  AAGAGCGTTG GGCTATCCAC CGCGCGGCAC CTTCTATGA AGAGCTGTCC      300
    AGCTCTCAGG AACTGCTGGA AACCGGCATC AAAGTTATCG ACCTGATGTG      350
    TCCGTTTCGCT AAGGGCGGTA AAGTTGGTCT GTTCGGTGGT GCGGGTGTAG      400
    GTAAACCGT AAACATGATG GAGCTGATCC GTAACATCGC GATCGAACAC      450
    TCCGGTTACT CCGTGTTTGC GGGCGTGGGT GAACGTAATC GTGAGGGTAA      500
25  CGACTTCTAC CACGAAATGA CCGACTCCAA CGTTCTGGAT AAAGTATCCC      550
    TGGTATATGG CCAGATGAAC GAGCCGCCGG GAAACCGTCT GCGCGTTGCT      600
    CTGACCGGTC TGACCATGGC AGAGAAGTTC CGTGACGAAG GTCGTGACGT      650
    TCTGCTGTTC GTTGATAACA TCTATCGTTA CACCCTGGCC GGTACAGAAG      700
    TATCCGCTCT GCTGGGTCGT ATGCCATCAG CGGTAGGCTA CCAGCCGACC      750
30  CTGGCGGAAG AGATGGGTGT TCTTCAGGAA CGTATCACCT CTACCAAAC      800
    CGGTTCTATC AC                                     812
  
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2) INFORMATION FOR SEQ ID NO: 262

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 811 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Citrobacter koseri*
 (B) STRAIN: ATCC 27156

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 262

```

50  GCGCGTGTAC GACGCCCTTG AGGTGCAGAA TGGTAATGAA CATCTGGTGC      50
    TGGAAGTTCA GCAGCAGCTC GGTGGCGGTA TCGTACGTAC CATCGCCATG      100
    GGTTCCTCCG ACGGCCCTGC TCGTGGTCTG GATGTGAAAG ACCTTGAGCA      150
    CCCGATCGAA GTCCCGGTAG GTAAAGCAAC GCTGGGTCGT ATCATGAACG      200
55  TACTGGGCGA ACCAGTAGAC ATGAAAGGCG AGATCGGTGA AGAAGAGCGT      250
    TGGGCTATCC ACCGTGCGGC ACCGTCCTAC GAAGAGTTGT CAAACTCTCA      300
    GGAAGTCTG GAAACCGGTA TCAAAGTTAT CGACCTGATG TGCCCGTTCTG      350
    CGAAGGGCGG TAAAGTGGGT CTGTTCCGGT GTGCGGGTGT AGGTAAAACC      400
    GTAAACATGA TGGAGCTGAT CCGTAACATC GCGATCGAAC ACTCCGGTTA      450
60  CTCCGTGTTT GCGGGCGTAG GTGAACGTAC TCGTGAGGGT AACGACTTCT      500
  
```

ACCACGAAAT GACCGACTCC AACGTTATCG ACAAAGTATC CCTGGTTTAC 550
 GGCCAGATGA ACGAGCCGCC GGGAAACCGT CTGCGCGTTG CGCTGACCGG 600
 CCTGACCATG GCGGAGAAAT TCCGTGACGA AGGTCGTGAC GTTCTGCTGT 650
 TCGTCGACAA CATCTACCGT TACACCCTGG CCGGTACGGA AGTATCCGCA 700
 5 CTGCTGGGTC GTATGCCTTC AGCGGTAGGT TACCAGCCGA CCCTGGCGGA 750
 AGAGATGGGT GTTTTGCAGG AACGTATCAC CTCCACCAA ACCGGTTCTA 800
 TCACCTCCGT A 811

10

2) INFORMATION FOR SEQ ID NO: 263

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 816 bases
 15 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

20

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Citrobacter farmeri*
 (B) STRAIN: ATCC 51112

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 263

GATGCCGTAC CGCGCGTGTA CGATGCTCTT GAGGTTATGA ATGGTAAAGA 50
 GAGTCTGGTG CTGGAAGTTC AGCAGCAGCT CGGCGGCGGT ATCGTACGTA 100
 CCATCGCGAT GGGTTCTTCC GACGGTCTGC GTCGTGGTCT GGAAGTAAAA 150
 30 GACCTCGAAC ACCCGATCGA AGTCCCGGTA GGTAAGCAA CTCTGGGTCTG 200
 TATCATGAAC GTCCTGGGTC ACCCGATCGA CATGAAAGGC GATATCGGTG 250
 AAGAAGAGCG TTGGGCTATC CACCGCGCAG CGCCATCCTA TGAAGAGCTG 300
 TCCAGCTCTC AGGAACTGCT GGAAACCGGT ATCAAAGTTA TCGACCTGAT 350
 GTGTCCGTTT GCGAAGGGCG GTAAAGTCGG TCTGTTCCGT GGTGCGGGTG 400
 35 TAGGTAAAC CGTAAACATG ATGGAAGTCA TCCGTAACAT CGCGATCGAG 450
 CACTCCGGTT ACTCCGTGTT TGCGGGCGTA GGTGAACGTA CTCGTGAGGG 500
 TAACGACTTC TACCACGAAA TGACCGATTC CAACGTTCTG GATAAAGTAT 550
 CCCTGGTATA TGGCCAGATG AACGAGCCGC CGGGAAACCG TCTGCGCGTT 600
 GCGCTGACCG GTCTGACCAT GGCAGAGAAA TTCCGTGACG AAGGTCGTGA 650
 40 CGTACTGCTG TTCGTCGATA ACATCTATCG TTACACCCTG GCCGTACGG 700
 AAGTATCCGC ACTGCTGGGC CGTATGCCAT CAGCGGTAGG CTACCAGCCA 750
 ACCCTGGCGG AAGAGATGGG TGTTCGTCAG GAACGTATCA CTTCTACCAA 800
 AACCGGTTCT ATTACC 816

45

2) INFORMATION FOR SEQ ID NO: 264

(i) SEQUENCE CHARACTERISTICS:

- 50 (A) LENGTH: 819 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

55

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Citrobacter freundii*
 (B) STRAIN: ATCC 8090

60

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 264

	AGGATGCCGT	ACCGCGCGTG	TACGATGCTC	TTGAGGTTAT	GAATGGTAAA	50
	GAGAGCCTGG	TGCTGGAAGT	TCAGCAGCAG	CTCGGCGGCG	GTATCGTACG	100
5	TACCATCGCC	ATGGGTTCTT	CTGACGGTCT	GCGTCGTGGT	CTGGAAGTTA	150
	AAGACCTCGA	GCACCCGATC	GAAGTCCCGG	TAGGTAAAGC	AACGCTGGGT	200
	CGTATCATGA	ACGTTCTGGG	TCACCCGATC	GACATGAAAG	GCGATATCGG	250
	TGAAGAAGAG	CGTTGGGCTA	TCCACCGTGC	AGCACCTTCC	TACGAAGAGC	300
	TGTCAAGCTC	TCAGGAACCTG	CTGGAAACCG	GTATCAAAGT	TATCGACCTG	350
10	ATGTGTCCGT	TCGCTAAGGG	CGGTAAAGTT	GGTCTGTTTCG	GTGGTGCGGG	400
	TGTAGGTAAA	ACCGTAAACA	TGATGGAGCT	GATCCGTAAC	ATCGCGATCG	450
	AACACTCCGG	TTACTCCGTG	TTTGCGGGCG	TAGGTGAACG	TACTCGTGAG	500
	GGTAACGACT	TCTACCACGA	AATGACCGAC	TCCAACGTTC	TGGACAAAGT	550
	ATCCCTGGTA	TATGGCCAGA	TGAACGAGCC	GCCTGGAAAC	CGTCTGCGTG	600
15	TTGCGCTGAC	CGGTCTGACC	ATGGCTGAGA	AGTTCCGTGA	CGAAGGTCGT	650
	GACGTTCTGC	TGTTCTGTTGA	TAACATCTAT	CGTTACACCC	TGGCCGGTAC	700
	AGAAGTATCT	GCACTGCTGG	GTCGTATGCC	ATCAGCGGTA	GGCTACCAGC	750
	CGACCCTGGC	GGAAGAGATG	GGTGTCTGCTG	AGGAACGTAT	CACCTCCACC	800
	AAAACCGGTT	CTATCACCT				819

2) INFORMATION FOR SEQ ID NO: 265

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 822 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Citrobacter koseri*

(B) STRAIN: ATCC 27028

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 265

	GATGCCGTAC	CGCGCGTGTA	CGACGCCCTT	GAGGTGCAGA	ATGGTAATGA	50
40	ACATCTGGTG	CTGGAAGTTC	AGCAGCAGCT	CGGTGGCGGT	ATCGTACGTA	100
	CCATCGCCAT	GGGTTCTTCC	GACGGCCTGC	GTCGTGGTCT	GGATGTGAAA	150
	GACCTTGAGC	ACCCGATCGA	AGTCCCGGTA	GGTAAAGCAA	CGCTGGGTCTG	200
	TATCATGAAC	GTA CTGGGCG	AACCAGTAGA	CATGAAAGGC	GAGATCGGTG	250
	AAGAAGAGCG	TTGGGCTATC	CACCGTGCGG	CACCGTCCTA	CGAAGAGTTG	300
45	TCAAACCTCTC	AGGAACTGTT	GGAAACCGGT	ATCAAAGTTA	TCGACCTGAT	350
	GTGTCCGTTC	GCGAAGGGCG	GTAAAGTGGG	TCTGTTCGGT	GGTGCGGGTG	400
	TAGGTAAAAC	CGTAAACATG	ATGGAGCTGA	TCCGTAACAT	CGCGATCGAA	450
	CACTCCGGTT	ACTCCGTGTT	TGCGGGCGTA	GGTGAACGTA	CTCGTGAGGG	500
	TAACGACTTC	TACCACGAAA	TGACCGACTC	CAACGTTATC	GACAAAGTAT	550
50	CCTTGTTTGA	CGGCCAGATG	AACGAGCCGC	CGGGAAACCG	TCTGCGCGTT	600
	GCGCTGACCG	GCCTGACCAT	GGCGGAGAAA	TTCCGTGACG	AAGGTCGTGA	650
	CGTTCCTGCTG	TTCGTCGACA	ACATCTACCG	TTACACCCTG	GCCGGTACGG	700
	AAGTATCCGC	ACTGCTGGGT	CGTATGCCTT	CAGCGGTAGG	TTACCAGCCG	750
	ACCCTGGCGG	AAGAGATGGG	TGTTTTGCAG	GAACGTATCA	CCTCCACCAA	800
55	AACCGGTTCT	ATCACCTCCG	TA			822

2) INFORMATION FOR SEQ ID NO: 266

60

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 820 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 5 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 10 (A) ORGANISM: *Citrobacter sedlakii*
 (B) STRAIN: ATCC 51115

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 266

```

15 GATGCCGTAC CGCGCGTGTA CGACGCCCTT GAGGTACAGA ATGGTAATGA      50
   GCGTCTGGTG CTGGAAGTTC AGCAGCAGCT CGGTGGCGGT ATTGTACGTA      100
   CCATCGCCAT GGGTTCTTCC GACGGTCTGC GTCGTGGTCT GGAAGTAAAA      150
   GACCTTGAGC ACCCGATCGA AGTCCCGGTA GGTAAAGCAA CGCTGGGTCG      200
   TATCATGAAC GTACTGGGCG AACCAGTAGA CATGAAAGGC GACATCGGTG      250
20 AAGAAGAGCG TTGGGCTATC CACCGTGCCG CGCCGTCCTA TGAAGAGTTG      300
   TCTAACTCTC AGGAACTGCT GGAACCCGGC ATCAAAGTTA TCGACCTGAT      350
   GTGTCCGTTT GCGAAGGGCG GTAAAGTCGG TCTGTTCGGT GGTGCGGGCG      400
   TAGGTAAAAC CGTAAACATG ATGGAGCTGA TCCGTAACAT CGCGATCGAG      450
   CACTCCGGTT ACTCTGTGTT TGCGGGCGTG GGTGAACGTA CTCGTGAGGG      500
25 TAACGACTTC TACCACGAAA TGACCGACTC CAACGTTATC GACAAAGTAT      550
   CCCTGGTGTA CGGCCAGATG AACGAGCCGC CTGGAAACCG TCTGCGCGTC      600
   GCACTGACCG GTCTGACCAT GGCTGAGAAG TTCCGTGACG AAGGTCGTGA      650
   CGTTCTGCTG TTCGTCGATA ACATCTATCG TTACACCCTG GCCGGTACGG      700
   AAGTATCCGC ACTGCTGGGT CGTATGCCTT CAGCGGTAGG TTATCAGCCG      750
30 ACTCTGGCGG AAGAGATGGG TGTTCTGCAG GAACGTATCA CCTCAACCAA      800
   AACCGGTTCT ATCACCTCCG                                     820

```

35 2) INFORMATION FOR SEQ ID NO: 267

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 806 bases
 (B) TYPE: Nucleic acid
 40 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 45 (A) ORGANISM: *Citrobacter werkmanii*
 (B) STRAIN: ATCC 51114

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 267

```

50 GCCGTACCGC GCGTGTACGA TGCTCTTGAG GTTATGAATG GTAAAGAGAG      50
   CCTGGTGCTG GAAGTTCAGC AGCAGCTCGG CGGCGGTATC GTACGTACCA      100
   TCGCCATGGG TTCTTCCGAC GGTCTGCGTC GTGGTCTGGA AGTTAAAGAC      150
   CTTGAGCACC CGATCGAAGT CCCGGTAGGT AAAGCAACCC TGGGTCGTAT      200
55 CATGAACGTC CTGGGTCATC CGATCGACAT GAAAGGCGAT ATCGGTGAAG      250
   AAGAGCGTTG GGCTATCCAC CGCGCAGCAC CTACCTATGA AGAACTGTCC      300
   AGTTCTCAGG AACTGCTGGA AACCGGCATC AAAGTTATCG ACCTGATGTG      350
   TCCGTTGCGG AAGGGCGGTA AAGTTGGTCT GTTCGGTGGT GCGGGTGTAG      400
   GTAAAACCGT AAACATGATG GAGCTGATCC GTAACATCGC GATCGAACAC      450
50 TCCGGTTACT CAGTGTTTGC GGGCGTTGGT GAACGTACTC GTGAGGGTAA      500

```

	CGACTTCTAC	CACGAAATGA	CCGACTCCAA	CGTTCTGGAC	AAAGTATCCC	550
	TGGTATATGG	CCAGATGAAC	GAGCCGCCGG	GAAACCGTCT	GCGCGTTGCG	600
	CTGACCGGTC	TGACCATGGC	TGAGAAGTTC	CGTGACGAAG	GTCGTGACGT	650
	TCTGCTGTTC	GTTGATAACA	TCTATCGTTA	CACCCTGGCC	GGTACTGAAG	700
5	TATCTGCACT	GCTGGGTCGT	ATGCCATCAG	CGGTAGGCTA	CCAGCCAACC	750
	CTGGCGGAAG	AGATGGGTGT	TCTGCAGGAA	CGTATCACCT	CTACCAAAC	800
	CGGTTC					806

10

2) INFORMATION FOR SEQ ID NO: 268

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 810 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

20

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Citrobacter youngae*
(B) STRAIN: ATCC 29935

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 268

	GCCGTACCGC	GCGTGACGA	TGCTCTTGAG	GTTATGAATG	GTAAAGAGAG	50
	CCTGGTGCTG	GAAGTTCAGC	AGCAGCTCGG	CGGCCGGTATC	GTACGTACCA	100
	TCGCCATGGG	TTCTTCCGAC	GGTCTGCGTC	GTGGTCTGGA	AGTTAAAGAC	150
30	CTCGAGCACC	CGATCGAAGT	CCCGGTAGGT	AAAGCAACGC	TGGGTCGTAT	200
	CATGAACGTT	CTGGGTCACC	CGATCGACAT	GAAAGGCGAT	ATCGGAGAAG	250
	AAGAGCGTTG	GGCTATTAC	CGCGCAGCAC	CTTCCTATGA	AGAGCTGTCC	300
	AGCTCTCAGG	AACTGCTGGA	AACCGGCATC	AAAGTTATCG	ACCTGATGTG	350
	TCCGTTGCT	AAGGGCGGTA	AAGTTGGTCT	GTTGCGGTGGT	GCGGGTGTAG	400
35	GTAAAACCGT	AAACATGATG	GAGCTTATTC	GTAACATCGC	GATCGAGCAC	450
	TCCGGTTACT	CTGTGTTTGC	GGGTGTAGGT	GAACGTACTC	GTGAGGGTAA	500
	CGACTTCTAC	CACGAAATGA	CCGATTCCAA	CGTTCTGGAT	AAAGTATCCC	550
	TGGTTTATGG	CCAGATGAAC	GAGCCGCCGG	GAAACCGTCT	GCGCGTTGCG	600
	CTGACCGGTC	TGACCATGGC	TGAGAAATTC	CGTGACGAAG	GTCGTGACGT	650
40	ACTGCTGTTC	GTCGATAACA	TCTATCGTTA	TACCCTGGCC	GGTACGGAAG	700
	TATCCGCACT	GCTGGGTCGT	ATGCCATCAG	CGGTAGGTTA	CCAGCCGACC	750
	CTGGCGGAAG	AGATGGGTGT	TCTGCAGGAA	CGTATCACTT	CTACCAAAC	800
	CGGTTCTATC					810

15

2) INFORMATION FOR SEQ ID NO: 269

(i) SEQUENCE CHARACTERISTICS:

- 50 (A) LENGTH: 827 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

55

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Clostridium innocuum*
(B) STRAIN: ATCC 14501

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 269

```

5  TTGAGAACGG AGATTTGCCG CAGCTATTGA CCGCTATTGA AATTCCTCTG      50
   AAAGACAGTG AATCTCTGAT TGTGGAAGTT GCTCAGCATA TCGGTGATGA      100
   ACGTGTCCGC TGTATCGCTA TGGGCGGTAC AGATGGTCTG GTTCGTGGAA      150
   TGGAAGCCAT TGATACAGGA TCCGCAATCC GTGTACCGGT GGGAAAAGAA      200
   ATTCTGGGAA GAATGTTCAA TGTCTCGGA CGTGAAATTG ATGGTCTGGG      250
   ACCTGTAGGA ACGGATAACA CACTGCCGAT CCACAGACAG GCACCGGGCT      300
   TTGAGGAGCA GCAGACATCC GCAGAAATGC TGGAAACAGG AATTAAGGTC      350
10 ATTGACCTGT TATGTCCATA TTCCAAGGGT GGTAAGATTG GTTTGTTTGG      400
   TGGTGC GGGA GTAGGTAAAA CCGTACTGAT TCAGGAGCTG ATTCATAATA      450
   TCGCCAAGGA ACATGGTGGA ATGTCCGTCG TTACCGGTGT AGGGGAGAGA      500
   ACCCGTGAAG GAAACGACAT GTATCATGAA ATGAAGGACA GCGGTGTCCT      550
   TGATAAGACC GTACTGGTTT ACGGACAGAT GAATGAATCA CCGGGTGCCA      600
15 GAATGCGTGT CGGTCTGACC GGGCTGACGA TGGCGGAATA TTTCCGTGAT      650
   CACGACCATC AGGATGTATT GCTGTTTATT GATAATATTT TCCGTTTTAC      700
   CCAGGCGGGA AGTGAAGTAA GTGCCCTGCT GGGACGTATG CCAAGTGCAG      750
   TAGGCTATCA GCCGACACTT GCGACAGAAA TGGGACAGCT GCAGGAGCGC      800
   ATTACATCCA CGAAGGATGG TTCCATT                                827
20

```

2) INFORMATION FOR SEQ ID NO: 270

25 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 829 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

30

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Clostridium perfringens*
 35 (B) STRAIN: ATCC 13124

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 270

```

40 GCAAATGATG AACTTCCTAA TATATTTAAT GCAATACACA TAAAAATGGA      50
   CGATGGAAAA ATCTTAGTTT GTGAGGTAGA GCAACACGTA GGAGACGATA      100
   TAGTTAGAAC TATAGCTATG GAAGCTACTG AAGGACTAAG AAGAGGTGTA      150
   GAAGCTGTTG ATACAGGAGC ACCTATATCA GTACCAGTTG GTGAATGCGT      200
   ATTAGGAAGA ATATTTAACG TATTAGGTAA ACCACTAGAT AGTGGAGCTG      250
   AAGTTAATAA CGAAGAAAAA TATCCAATTC ATAGACCAGC TCCATCATTT      300
15 GAAGAACAAT CAGTTGTTCC TCAAATGTTT GAGACAGGAA TAAAGGTTAT      350
   CGACCTTTTA GCACCTTACC AAAGAGGGGG AAAAATCGGT CTATTTGGAG      400
   GTGCAGGTGT TGGTAAAACA GTTCTTATCC AAGAGCTTAT AAACAACATA      450
   GCTAAAGAGC ACGGTGGACT TTCTGTATTC ACAGGAGTTG GAGAAAGATC      500
   AAGAGAAGGT AATGACCTTT ACTATGAAAT GATGGAATCA GGAGTTATAA      550
20 AAAATACAGC ATTAGTATTT GGACAAATGA ACGAACCACC TGGAGCAAGA      600
   ATGAGAGTTG CTTTAACAGG ACTTACTATG GCTGAGTACT TCAGAGACCA      650
   AGGTCAAGAC GTGTTATTAT TCATAGATAA CATATTCAGA TTCTCACAAG      700
   CTGGATCAGA GGTTCAGCT TTATTAGGAA GAATACCATC AGCTGTTGGT      750
   TACCAACCAA CTCTTGCTAC AGAGATGGGA GCTCTTCAAG AGAGAATCAC      800
35 ATCAACTACC CATGGATCAA TTACATCAG                                829

```

2) INFORMATION FOR SEQ ID NO: 271

50

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 22 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 271

10

TTGTCCACGT TGGATRTCTT CA

22

15 2) INFORMATION FOR SEQ ID NO: 272

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 818 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

25 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Corynebacterium diphtheriae*
(B) STRAIN: ATCC 27010

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 272

30

CCCCGCGTGGC	GAGCTGCCCG	CACTGTACAA	CGCGTTGACT	GTCGAGGTCA	50
CCCTCGAGGC	AGTCGCTAAG	ACCATTACCC	TTGAGGTTGC	CCAGCACTTG	100
GGCGACAACC	TCGTTTCGCG	CGTGTCCATG	GCCCCTACCG	ACGGCCTCGT	150
CCGTGGTGCT	GTTGTGACCG	ACTCGGGCAA	GCCAATCTCC	GTGCCAGTTG	200
35 GCGACGTTGT	TAAAGGCCAC	GTTTTCAACG	CACTGGGCGA	TTGCTTGGAT	250
GAGCCAGGTC	TCGGCCGCGA	TGGTGAGCAG	TGGGGAATTC	ACCGCGATCC	300
ACCACCATTG	GATCAGCTCG	AAGGTAAGAC	CGAAATCCTC	GAGACCGGTA	350
TTAAGGTCAT	CGACTTGCTC	ACCCCTTACG	TTAAGGGCGG	CAAGATTGGT	400
CTGTTTCGGT	GTGCAGGTGT	GGGTAAGACC	GTGCTCATCC	AGGAGATGAT	450
40 CACTCGTATT	GCTCGCGAGT	TCTCCGGTAC	CTCCGTCTTC	GCTGGCGTTG	500
GTGAGCGTAC	CCGTGAGGGC	ACCGACCTCT	TCCTCGAAAT	GGAAGAAATG	550
GGCGTTCTTC	AGGACACCGC	TCTCGTGTTT	GGCCAGATGG	ACGAGCCACC	600
AGGAGTCCGT	ATGCGCGTTG	CTCTGTCCGG	TCTGACCATG	GCGGAGTACT	650
TCCGCGATGT	TCAGCACCAG	GACGTGCTTC	TGTTTCATCGA	TAACATTTTC	700
45 CGTTTACCCC	AGGCCGGTTC	CGAGGTTTCG	ACCCCTTCTG	GTCGTATGCC	750
TTCCGCCGTG	GGTTACCAGC	CAACCTTGGC	TGACGAGATG	GGTGTTCTCC	800
AGGAGCGTAT	TACCTCTA				818

50

2) INFORMATION FOR SEQ ID NO: 273

(i) SEQUENCE CHARACTERISTICS:

- 55 (A) LENGTH: 833 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

60

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Corynebacterium pseudodiphtheriticum*
 (B) STRAIN: ATCC 10700

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 273

```

CGATGCCTGC TCTGTACAAC GCGCTGACTG TCGAGGTCAC CCTCGAGGCA      50
GTCGCCAAGA CCATCACGCT TGAGGTTGCA CAGCACCTCG GCGATAACCT      100
GATCCGGACC ATTGCGTTGG CACCTACGGA CGGTCTCGTC CGTGGCGCTG      150
10 AGGTTATCGA CACTGGTAAG CCAATTACTG TTCCCGTCGG CGATGCCGTC      200
AAAGGACACG TCTTCAATGC GCTCGGTGAG TGTTTGGACG AACCAGGATT      250
GGGCCGCGAC GCGGAACAGT GGGGAATCCA CCGCGATCCG CCACCATTCTG      300
ATGCGCTGGA GGGCAAAACC GAGATTCTGG AGACTGGAAT CAAGGTTATC      350
GACCTCCTTA CCCCTTACGT TAAGGGTGGC AAAATTGGTC TGTTCGGTGG      400
15 CGCCGGCGTC GGCAAGACCG TTCTTATCCA GGAAATGATC ACTCGTATCG      450
CTCGTAACTT CTCCGGTACT TCCGTGTTCC CCGGCGTCGG TGAGCGTACC      500
CGTGAGGGTA CTGACCTGTT CCTGGAATG GAAGAGATGG GCGTGTTGCA      550
AGACACCGCC CTTGTCTTCG GTCAAATGGA CGAACCACCA GGGGTTTCGTA      600
TGCGCGTGGC CTTGTCTGGT CTAACCATGG CTGAATATTT CCGCGACGTT      650
20 CAAAACCAGG ACGTTTTGTT GTTCATTGAC AACATCTTCC GTTTACTCA      700
GGCAGGTTCC GAGGTTTCCA CGCTGTGGG CCGTATGCCT TCCGCCGTGG      750
GTTATCAGCC AACATTGGCT GATGAGATGG GTGTTTTCGA GGAACGGATT      800
ACCTCTACAC GTGGTAAGTC AATTACTTCC CTG                          833

```

25

2) INFORMATION FOR SEQ ID NO: 274

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 417 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

35 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Corynebacterium ulcerans*
 (B) STRAIN: NCTC 8665

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 274

```

CCGTGCTCAT CCAGGAGATG ATCACCCGTG TGGCCCGCAA CTTCGGCGGC      50
ACCTCTGTGT TCGCCGGCGT CGGCGAGCGC ACCCGTGAGG GCAACGACCT      100
15 CTGGGTCGAG ATGGACGAGG CCGACGTGCT CAAGGACACC GCCCTGGTGT      150
TCGGCCAGAT GGACGAGCCG CCGGGAACCC GTCTGCGCGT GGCCCTGTCC      200
GCGCTGACCA TGGCGGAGTA CTTCCGCGAT GTGCAGAACC AGGACGTGCT      250
GCTGTTCATC GACAACATCT TCCGCTTCTC CCAGGCCGGC TCCGAGGTCT      300
CCACCCTGCT GGGCCGCATG CCCTCCGCGG TGGGCTACCA GCCGAACCTG      350
50 GCGGACGAGA TGGGTGTGCT GCAGGAGCGC ATCACCTCGA CTCGCGGCCA      400
CTCCATCACC TCGATGC                          417

```

55 2) INFORMATION FOR SEQ ID NO: 275

(i) SEQUENCE CHARACTERISTICS:

- 50 (A) LENGTH: 835 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double

164

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

5 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Corynebacterium urealyticum*

(B) STRAIN: ATCC 43042

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 275

10

	GGGCAGCAGC	CAGCACTATT	CAACGCGCTG	CACGTCGAGG	TTGACCTCGA	50
	GGCAGTTGCG	AAGACCATTA	CCCTGGAGGT	CGCACAGCAC	CTGGGTGACA	100
	ACCTGGTGCG	CACCGTCTCC	ATGGCCCCGA	CCGACGGCCT	GGTCCGCGGT	150
	GCAGAGGTCA	AGGACACCGG	TAAGCCGATC	TCTGTGCCAG	TCGGCGATGT	200
15	TGTCAAGGGG	CACGTCTTCA	ACGCCCTGGG	CGACTGCCTG	GATGAGCCAG	250
	GTCTCGGCCG	CGACGGCGAG	CAGTGGGGCA	TCCACCGCGA	GCCACCGGCA	300
	TTCGACGAGC	TCGAGGGTAA	GACCGAGATC	CTGGAGACCG	GCGTTAAGGT	350
	CATCGACCTG	CTGACCCCTT	ACGTCAAGGG	CGGCAAGATT	GGCCTCTTCG	400
	GTGGTGCAAG	TGTGGGTAAG	ACCGTCCTGA	TTCAGGAGAT	GATTACCCGT	450
20	ATCGCCCCG	AGTTCTCCG	TACCTCCGTG	TTCGCCGGCG	TCGGCGAGCG	500
	TACCCGTGAG	GGTACGGACC	TCTTCCTCGA	GATGGAGGAG	ATGGGCGTGC	550
	TCCAGGACAC	CGCGCTGGTG	TTCGGTCAGA	TGGATGAGCC	GCCGGGAGTC	600
	CGTATGCGCG	TGGCTCTGTC	CGGTCTGACC	ATGGCGGAGT	ACTTCCGCGA	650
	TGTTTCAGGGC	CAGGACGTGC	TGCTGTTTCA	CGACAACATC	TTCCGTTTCA	700
25	CCCAGGCAGG	TTCTGAGGTC	TCCACGCTGC	TCGGCCGCAT	GCCGTCCGCA	750
	GTGGGTTACC	AGCCGACCCT	GGCTGACGAG	ATGGGTGTTT	TGCAGGAGCG	800
	CATTACCTCC	ACGAAGGGTA	AGTCCATTAC	CTCCC		835

30

2) INFORMATION FOR SEQ ID NO: 276

(i) SEQUENCE CHARACTERISTICS:

35 (A) LENGTH: 818 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

40

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Coxiella burnetii*

(B) STRAIN: Nine Mile phase II

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 276

	CCCGTCACGC	TGTCCCGAAA	GTGTACGATG	CTTTGCAGGT	GGATGAAAAT	50
	AATTTAACGC	TCGAAGTCCA	ACAGCAACTC	GGGGACGGTG	TCGTGCGCAC	100
	AATTGCCATG	GGCAGCACTG	AGGGCTTAAA	ACGCGATATC	GCCGTAAAAA	150
50	ATACGGAAAA	ACCGATTGAA	GTTCCCGTAG	GAAAAGAAAC	TTTAGGTCGT	200
	ATCATGAACG	TGCTGGGTGA	GCCGATCGAT	GAGTTAGGTC	CCATTAATTC	250
	AAAAGAAAAA	CTCCCTATTC	ATCGTCCTGC	GCCGAGCTTT	ATTGAGCAAT	300
	CTGGCGCTAC	CGAATTATTA	GAAACCGGTA	TTAAAGTGGT	CGATTTGCTT	350
	TGCCCCTTTG	CTAAGGGAGG	CAAAGTGGGT	CTTTTTGGAG	GCGCGGGCGT	400
55	TGGAAAAACG	GTTAATATGA	TGGAATTAAT	CCGTAATATC	GCCATTGAAC	450
	ACAGCGGTTA	TTCTGTTTTT	GCGGGTGTGG	GAGAAAGAAC	GCGAGAAGGC	500
	AATGATTTTT	ATCATGAAAT	GAAAGAATCC	AATGTCTTGG	ATAAAGTGCC	550
	GTTGGTGTAC	GGACAAATGA	ACGAGCCGCC	AGGGAACCGC	TTGCGGGTGG	600
	GTTTGACGGG	GCTTACGCTG	GCGGAAGCCT	TCCGTGACGA	AGGACGCGAC	650
60	GTTCTGTTAT	TTATCGATAA	TATCTTTCGT	TACACTTTGG	CAGGGGTTGA	700

AGTCTCTGCC	CTCCTCGGTC	GGATGCCATC	GGCTGTGGGT	TATCAGCCGA	750
CGTTGGCCGA	AGAGATGGGG	GCCCTGCAAG	AACGCATTAC	TTCCACTAAA	800
AAAGGGTCCA	TTACGTCG				818

5

2) INFORMATION FOR SEQ ID NO: 277

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 829 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

15 (ii) MOLECULE TYPE: Genomic DNA.

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Edwardsiella hoshinae*
 (B) STRAIN: ATCC 33379

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 277

TTCCCGCAGG	ACGCCGTGCC	GAAGGTGTAT	AACGCACTGG	AAGTAAAAGG	50
CGGTGCCACG	AAACTGGTAC	TGGAAGTGCA	GCAGCAGCTG	GGTGGCGGCG	100
25 TAGTTCGCTG	CATCGCGATG	GGCTCTTCCG	ACGGTCTGCG	CCGTGGGCTA	150
GAGGTTGAAG	ACCAAGACCA	TCCGATCGAG	GTTCTGTGTG	GCAAGGCGAC	200
TCTGGGCCGT	ATCATGAACG	TACTGGGTGA	TCCGGTCGAC	ATGAAGGGCG	250
AGATCGGTGA	AGAAGAGCGT	TGGGCTATCC	ATCGTGCTGC	ACCGAGCTAT	300
GAAGATCTGT	CTAACTCTCA	GGAAGTGTG	GAGACCGGCA	TTAAGGTTAT	350
30 CGACCTGATT	TGCCCCGTTG	CTAAAGGCGG	TAAAGTGGGC	CTGTTCGGTG	400
GGGCCGGTGT	GGGTAAGACC	GTTAACATGA	TGGAGCTTAT	CCGTAACATC	450
GCTATCGAGC	ACTCCGGTTA	CTCAGTCTTC	GCCGGTGTGG	GTGAGCGTAC	500
CCGTGAGGGT	AACGACTTCT	ACCACGAGAT	GACCGATTCC	AACGTATTGG	550
ATAAAGTTTC	TCTGGTGTAT	GGTCAGATGA	ACGAGCCACC	GGGAAACCGT	600
35 CTGCGCGTGG	CGCTGACCGG	TCTGACCATG	GCGGAGAAAT	TCCGTGATGA	650
AGGTCGTGAT	GTAATGTTGT	TCATCGATAA	CATCTACCGT	TATACCTTGG	700
CCGGTACTGA	AGTCTCCGCT	CTGCTGGGCC	GTATGCCGTC	GGCGGTAGGT	750
TATCAGCCGA	CTCTGGCGGA	GGAAATGGGG	GTGCTGCAAG	AGCGTATTAC	800
40 CTCCACTAAG	ACCGGGTCCA	TCACCTCTG			829

2) INFORMATION FOR SEQ ID NO: 278

(i) SEQUENCE CHARACTERISTICS:

- 45 (A) LENGTH: 809 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 55 (A) ORGANISM: *Edwardsiella tarda*
 (B) STRAIN: ATCC 15947

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 278

GCCGTGCCGA	AGGTGTATAA	CGCACTGGAA	GTAAAAGGCG	GTGCCACGAA	50
50 ACTGGTACTG	GAAGTGCAGC	AGCAGCTGGG	TGGCGGCGTC	GTTTCGCTGCA	100

	TCGCGATGGG	CTCCTCCGAC	GGTCTGCGCC	GTGGGCTGGT	GTTTGAAGAC	150
	CAAGACCATC	CGATCGAGGT	TCCGGTCGGT	AAGGCGACCC	TGGGCCGTAT	200
	CATGAACGTA	CTGGGTGATC	CGGTCGACAT	GAAGGGCGAG	ATCGGCCAAG	250
	AAGAGCGTTG	GGCTATCCAC	CGCGCGGCGC	CGAGCTATGA	AGATCTGTCC	300
5	AACTCTCAGG	AGCTGCTGGA	GACCGGCATC	AAGGTTATCG	ACCTGATTTG	350
	CCCCTTCGCC	AAAGGCGGTA	AAGTTGGCCT	GTTCCGGTGGT	GCCGGTGTGG	400
	GTAAGACCGT	TAACATGATG	GAGCTTATCC	GTAACATCGC	TATCGAGCAC	450
	TCCGGTTACT	CCGTATTTCG	CGGTGTAGGC	GAGCGTACCC	GTGAGGGTAA	500
	CGACTTCTAC	CACGAGATGA	CCGACTCCAA	CGTATTGGAT	AAAGTTTCTC	550
10	TGGTATACGG	CCAGATGAAT	GAGCCGCCGG	GAAACCGTCT	GCGTGTGGCG	600
	TTGACGGGTC	TGACCATGGC	GGAGAAATTC	CGTGATGAAG	GTCGCGATGT	650
	GTTGTTGTTC	ATCGATAACA	TTTATCGTTA	TACCTTGGCT	GGTACCGAAG	700
	TTTCTGCTCT	GCTGGGTCGT	ATGCCGTCGG	CGGTAGGTTA	TCAGCCGACC	750
	CTGGCGGAAG	AGATGGGTGT	GTTGCAAGAG	CGTATCACCT	CAACGAAGAC	800
15	GGGCTCTAT					809

2) INFORMATION FOR SEQ ID NO: 279

20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 840 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

25

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

30

- (A) ORGANISM: *Eikenella corrodens*
- (B) STRAIN: ATCC 23834

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 279

35	TTTCCGCGTA	CCGCCATTCC	GCGTGTTTAC	GATGCACTCA	AACTGGTTGA	50
	TACTGATTTC	ACGCTGGAAG	TACAGCAGCA	GCTTGGTGAC	GGCGTTGTCC	100
	GTACCATTGC	GATGGGTAGT	ACAGACGGTT	TGAAACGTGG	CTTGGCTGTG	150
	CAAAATACTG	GTGCACCGAT	TACTGTGCCG	GTGGGGAAAG	CCACCCTAGG	200
	CCGCATCATG	GACGTTCTGG	GCAACCCCGT	GGACGAACAA	GGTCCGATCG	250
40	GTTCTGACCA	AACCCGTGCT	ATTTCATCAAT	TTGCACCTAA	GTTTCGACGAA	300
	CTCTCCAGCA	CTACCGAATT	GTTGGAAACA	GGCATTAAAG	TGATCGATTT	350
	GCTTTGTCCG	TTTGCTAAAG	GTGGTAAAGT	GGGTCTGTTT	GGCGGTGCCG	400
	GTGTGGGCAA	AACCGTGAAC	ATGATGGAGC	TGATTAACAA	CATTGCCAAA	450
	GCGCACAGTG	GTCTTTCCGT	ATTGCCCGGT	GTGGGTGAGC	GTACTCGTGA	500
45	AGGTAACGAC	TTCTACCACG	AAATGAAAGA	CTCCAACGTG	TTGGATAAAG	550
	TGGCAATGGT	GTATGGCCAG	ATGAACGAGC	CGCCTGGTAA	CCGCTTGCGT	600
	GTTGCTCTAA	CTGGTTTGTC	GATGGCTGAA	TACTTCCGTG	ACGAAAAAGA	650
	CGAAAACGGC	AAAGGCCGTG	ACGTATTATT	CTTTGTGGAT	AATATCTACC	700
	GCTATACTCT	GGCGGGTACC	GAAGTGTCGG	CTCTGCTTGG	CCGTATGCCT	750
50	TCTGCTGTGG	GTTATCAGCC	AACTTTGGCT	GAAGAAATGG	GTCGTTTGCA	800
	GGAGCGTATT	ACCTCCACCC	AAACTGGTTC	CATTACCTCT		840

55 2) INFORMATION FOR SEQ ID NO: 280

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 803 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double

50

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

5 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Enterobacter agglomerans*

(B) STRAIN: ATCC 27989

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 280

10
 -----GCCGTACCAC GAGTGTACGA TGCACCTGAG GTAAAGAATG GTGAAGAGCG 50
 TCTGGTGCTG GAAGTTCAGC AACAGCTCGG CGGTGGCGTT GTACGTACCA 100
 TCGCAATGGG TTCTTCTGAT GGTCTGCGTC GTGGTCTGGA AGTAACGGAC 150
 CTGGCTCACC CGATCGAAGT CCCGGTAGGT AAAGCAACAC TGGGTCGTAT 200
 15 CATGAACGTA CTGGGCGAAC CAGTAGACAT GAAAGGCGAC ATCGGTGAAG 250
 AAGAGCGTTG GGCATCCAC CGTGCAGCAC CGTCCTACGA AGAGTTGTCA 300
 AACTCTCAGG AACTGCTGGA AACCGGTATC AAAGTTATCG ACCTGATGTG 350
 TCCGTTGCTG AAGGGCGGTA AAGTGGGTCT GTTCGGTGGT GCGGGTGTAG 400
 GTAAAACCGT AAACATGATG GAGCTTATTC GTAACATCGC GATCGAGCAC 450
 20 TCCGTTACT CTGTGTTTGC GGGCGTAGGT GAACGTACTC GTGAGGGTAA 500
 CGACTTCTAC CACGAAATGA CCGACTCCAA CGTTATCGAC AAAGTATCCC 550
 TGGTGTATGG TCAGATGAAC GAGCCGCCGG GAAACCGTCT GCGCGTTGCG 600
 CTGACCGGTC TGACCATGGC TGAGAAGTTC CGTGACGAAG GTCGTGACGT 650
 ACTGTTGTTT GTTGACAACA TCTACCGTTA CACCCTGGCC GGTACGGAAG 700
 25 TATCCGCACT GCTGGGCCGT ATGCCTTCTG CGGTAGGTTA TCAGCCGACG 750
 CTGGCGGAAG AGATGGGCGT TCTGCAGGAA CGTATCACCT CCACCAAAC 800
 CCG 803

30

2) INFORMATION FOR SEQ ID NO: 281

(i) SEQUENCE CHARACTERISTICS:

35 (A) LENGTH: 833 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

40

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Enterobacter amnigenus*

(B) STRAIN: ATCC 33072

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 281

CGAATTCCT CAGGATGCCG TACCGCGCGT GTACGATGCT CTTGAGGTAC 50
 AGAATGGTAA CGAGAGTCTG GTGCTGGAAG TTCAGCAGCA GCTCGGTGGT 100
 GGTATCGTAC GTACTATCGC CATGGGTTCT TCCGACGGTC TCGCTCGTGG 150
 50 TCTGGCTGTT AAAGATCTCG AACACCCGAT CGAAGTCCCG GTAGGTAAAG 200
 CAACACTGGG TCGTATCATG AACGTTTTGG GTCAACCAAT CGACATGAAA 250
 GGCGACATCG GTGAAGAAGA CCGTTGGGCA ATCCACCGTG CAGCACCTTC 300
 CTATGAAGAG CTGTCTAGCT CTCAGGAAGT GCTGGAAACC GGCATCAAAG 350
 TTATCGACCT GATGTGTCCG TTCGCTAAGG GCGGTAAAGT TGGTCTGTTC 400
 55 GGCGGTGCGG GCGTGGGTAA AACTGTAAAC ATGATGGAGC TGATCCGTAA 450
 CATCGCGATC GAGCACTCCG GTTACTCCGT GTTTGCAGGC GTGGGTGAGC 500
 GTACTCGTGA GGGTAACGAC TTCTACCACG AAATGACCGA TTCCAACGTT 550
 CTGGATAAAG TATCCCTGGT TTATGGCCAG ATGAACGAGC CACCAGGAAA 600
 CCGTCTGCGC GTTGCCTGTA CCGGTCTGAC TATGGCTGAG AAGTTCCGTG 650
 50 ACGAAGGTCTG TGACGTACTG CTGTTCTGAG ATAACATCTA CCGTTACACC 700

CTGGCCGGTA	CTGAAGTATC	TGCGCTGCTG	GGCCGTATGC	CTTCAGCGGT	750
AGGTTACCAG	CCGACCCTGG	CGGAAGAGAT	GGGCGTTCTG	CAGGAACGTA	800
TCACTTCTAC	CAAAACCGGT	TCTATCACCT	CCG		833

5

2) INFORMATION FOR SEQ ID NO: 282

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 810 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

15 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterobacter asburiae*
 (B) STRAIN: ATCC 35953

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 282

	GCCGTACCAC	GCGTGTACGA	CGCGCTTGAG	GTACAGAATG	GTAACGAGAG	50
	CCTGGTGCTG	GAAGTTCAGC	AGCAGCTCGG	CGGCGGTATC	GTGCGTACCA	100
25	TCGCGATGGG	TTCTTCCGAC	GGTCTGCGTC	GTGGTCTGGA	AGTCAAAGAC	150
	CTTGAGCACC	CGATCGAAGT	CCCGGTAGGT	AAAGCAACAC	TGGGTCGTAT	200
	CATGAACGTA	TTGGGTCAAC	CAATCGACAT	GAAAGGCGAC	ATCGGTGAAG	250
	AAGAGCGTTG	GGCTATCCAC	CGCGCGGCAC	CTTCCTACGA	AGAGCTGTCC	300
	AGCTCTCAGG	AACTGCTGGA	AACCGGTATC	AAAGTTATCG	ACCTGATGTG	350
30	TCCGTTTCGG	AAGGGCGGTA	AAGTCGGTCT	GTTCCGGTGGT	GCGGGTGTTG	400
	GTAACACCGT	AAACATGATG	GAGCTGATCC	GTAACATCGC	GATCGAGCAC	450
	TCCGGTTACT	CCGTGTTTGC	GGGCGTAGGT	GAACGTACTC	GTGAGGGTAA	500
	CGACTTCTAC	CACGAAATGA	CCGACTCCAA	CGTTCTGGAC	AAAGTATCCC	550
	TGGTTTACGG	CCAGATGAAC	GAGCCACCAG	GAAACCGTCT	GCGCGTTGCG	600
35	CTGACCGGTC	TGACGATGGC	TGAGAAGTTC	CGTGATGAAG	GCCGTGACGT	650
	TCTGCTGTTC	GTTGATAACA	TCTATCGTTA	CACCCTGGCC	GGTACGGAAG	700
	TATCTGCACT	GCTGGGTCGT	ATGCCTTCAG	CGGTAGGTTA	CCAGCCTACG	750
	CTGGCGGAAG	AGATGGGTGT	TCTTCAGGAA	CGTATCACCT	CTACCAAAAC	800
	CGGTTCTATC					810

40

2) INFORMATION FOR SEQ ID NO: 283

(i) SEQUENCE CHARACTERISTICS:

- 45 (A) LENGTH: 811 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterobacter cancerogenus*
 55 (B) STRAIN: ATCC 35317

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 283

	GCCGTACCGC	GCGTGTACGA	TGCTCTTGAG	GTACAGAATG	GTAACGAGAG	50
60	CCTGGTGCTG	GAAGTTCAGC	AGCAGCTCGG	CGGCGGTATC	GTACGTACTA	100

	TCGCCATGGG	TTCTTCCGAC	GGTCTGCGTC	GTGGTCTGGA	AGTAAAAGAC	150
	CTTGAGCACC	CGATCGAAGT	CCCGGTAGGT	AAAGCAACAC	TGGGTCGTAT	200
	CATGAACGTA	TTGGGTCAAC	CAATCGACAT	GAAAGGCGAC	ATCGGTGAAG	250
	AAGAGCGTTG	GGCTATCCAC	CGCGCAGCAC	CTTCCTACGA	AGAGCTGTCC	300
5	AGCTCTCAGG	AACTGCTGGA	AACCGGCATC	AAAGTTATCG	ACCTGATGTG	350
	TCCGTTTCGG	AAGGGCGGTA	AAGTCGGTCT	GTTTCGGTGGT	GCGGGTGTAG	400
	GTAACACCGT	AAACATGATG	GAGCTGATCC	GTAACATCGC	GATCGAGCAC	450
	TCCGTTTATT	CCGTGTTTGC	GGGCGTGGGT	GAACGTACTC	GTGAGGGTAA	500
	CGACTTCTAC	CACGAAATGA	CCGACTCCAA	CGTTCTGGAT	AAAGTATCCC	550
10	TGGTGTACGG	CCAGATGAAC	GAGCCACCAG	GAAACCGTCT	GCGCGTTGCG	600
	CTGACCGGCC	TGACCATGGC	TGAGAAGTTC	CGTGACGAAG	GTCGTGACGT	650
	ACTGCTGTTC	GTTGATAACA	TCTACCGTTA	CACCCTGGCC	GGTACCGAAG	700
	TATCTGCACT	GCTGGGTCGT	ATGCCTTCAG	CGGTAGGTTA	TCAGCCTACG	750
	CTGGCGGAAG	AGATGGGTGT	TCTTCAGGAA	CGTATCACCT	CAACCAAAC	800
15	CGGTTCTATC	A				811

2) INFORMATION FOR SEQ ID NO: 284

20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 817 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 25 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 30 (A) ORGANISM: *Enterobacter cloacae*
 (B) STRAIN: ATCC 13047

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 284

35	GCCGTACCAC	GCGTGTACGA	CGCGCTTGAG	GTACAGAATG	GTAACGAGAG	50
	CCTGGTGCTG	GAAGTTCAGC	AGCAGCTCGG	CGGCGGTATC	GTGCGTACCA	100
	TCGCGATGGG	GTCTTCCGAC	GGTCTGCGTC	GTGGTCTGGA	AGTTAAAGAC	150
	CTTGAGCACC	CGATCGAAGT	CCCGGTAGGT	AAAGCAACAC	TGGGTCGTAT	200
	CATGAACGTA	TTGGGTCAAC	CAATCGACAT	GAAAGGCGAC	ATCGGTGAAG	250
40	AAGAGCGTTG	GGCTATCCAC	CGCGCGGCAC	CTTCCTACGA	AGAGCTGTCC	300
	AGCTCTCAGG	AACTGCTGGA	AACCGGTATC	AAAGTTATCG	ACCTGATGTG	350
	TCCGTTTTCG	AAGGGCGGTA	AAGTTGGTCT	GTTTCGGTGGT	GCGGGTGTAG	400
	GTAACACCGT	AAACATGATG	GAGCTGATCC	GTAACATCGC	GATCGAGCAC	450
	TCCGTTTACT	CCGTATTTGC	GGGCGTAGGT	GAACGTACTC	GTGAGGGTAA	500
45	CGACTTCTAC	CACGAAATGA	CCGACTCCAA	CGTTCTGGAC	AAAGTATCCC	550
	TGGTTTACGG	CCAGATGAAC	GAGCCACCAG	GAAACCGTCT	GCGCGTTGCG	600
	CTGACTGGTC	TGACGATGGC	TGAGAAGTTC	CGTGACGAAG	GCCGTGACGT	650
	TCTGCTGTTC	GTTGATAACA	TCTACCGTTA	CACCCTGGCC	GGTACGGAAG	700
	TATCTGCACT	GCTGGGTCGT	ATGCCTTCAG	CGGTAGGTTA	TCAGCCTACG	750
50	CTGGCGGAAG	AGATGGGTGT	TCTTCAGGAA	CGTATCACCT	CTACCAAAC	800
	CGGTTCTATC	ACTTCCG				817

55 2) INFORMATION FOR SEQ ID NO: 285

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 766 bases
 (B) TYPE: Nucleic acid
 50 (C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

5 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Enterobacter gergoviae*

(B) STRAIN: ATCC 33028

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 285

10

AATGAGAGCC	TGGTGCTGGA	AGTTCAGCAG	CAGCTCGGCG	GCGGTATCGT	50
GCGTACCATC	GCAATGGGTT	CTTCTGACGG	TCTGCGTCGC	GGTCTGGAAG	100
TTAAAGATCT	CGAACATCCG	ATCGAAGTCC	CGGTAGGTAA	AGCGACCCTC	150
GGCCGTATTA	TGAACGTGCT	GGGTCAGCCG	GTTGATATGA	AAGGCGATAT	200
15 CGGCGAAGAA	GAGCGTTGGG	CGATCCACCG	CGCTGCGCCG	TCCTATGAAG	250
AGCTCTCCAG	CTCTCAGGAA	CTGCTGGAAA	CCGGTATCAA	GGTAATGGAC	300
CTGATTTGCC	CGTTCGCGAA	GGGCGGTAAA	GTCGGTCTGT	TCGGCGGTGC	350
GGGCGTTGGT	AAAACCGTAA	ACATGATGGA	GCTGATCCGT	AACATCGCGA	400
TCGAGCACTC	CGGCTACTCC	GTGTTTGC GG	GCGTGGGTGA	ACGTACTCGT	450
20 GAGGGTAACG	ACTTCTACCA	CGAAATGACC	GACTCCAACG	TTATCGACAA	500
AGTATCCCTG	GTGTACGGCC	AGATGAACGA	GCCGCCGGGA	AACCGTCTGC	550
GCGTGGCGCT	GACCGGTCTG	ACCATGGCTG	AGAAATTCCG	TGACGAAGGT	600
CGTGACGTTT	TGCTGTTCGT	CGATAACATC	TACCGCTATA	CCCTCGCCGG	650
TACTGAAGTA	TCCGCACTGC	TGGGCCGTAT	GCCTTCTGCA	GTAGGTTACC	700
25 AGCCGACGCT	GGCGGAAGAG	ATGGGTGTTC	TGCAGGAACG	TATCACCTCC	750
ACCAAAACCG	GTTCTA				766

30 2) INFORMATION FOR SEQ ID NO: 286

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 805 bases

(B) TYPE: Nucleic acid

35 (C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

40 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Enterobacter hormaechei*

(B) STRAIN: ATCC 49162

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 286

45

GCCGTACCAC	GCGTGACGA	CGCGCTTGAG	GTACAGAATG	GTAACGAGAG	50
CCTGGTGCTG	GAAGTTCAGC	AGCAGCTCGG	CGGCGGTATC	GTGCGTACCA	100
TCGCCATGGG	TTCTTCCGAC	GGTCTGCGTC	GTGGTCTGGA	AGTGAAAGAC	150
CTTGAGCACC	CGATCGAAGT	CCCGGTAGGT	AAAGCAACGC	TGGGTCGTAT	200
50 CATGAACGTA	TTGGGTCAGC	CAATCGACAT	GAAAGGCGAC	ATCGGTGAAG	250
AAGAGCGTTG	GGCTATCCAC	CGCGCGGCAC	CTTCCTACGA	AGAGCTGTCC	300
AGCTCTCAGG	AAGTCTGGA	AACCGGCATC	AAAGTTATCG	ACCTGATGTG	350
TCCGTTTTCG	AAGGGCGGTA	AAGTTGGTCT	GTTTCGGTGGT	GCGGGTGTAG	400
GTAACACCGT	AAACATGATG	GAGCTGATCC	GTAACATCGC	GATCGAGCAC	450
55 TCCGGTTACT	CCGTGTTTGC	GGGCGTGGGT	GAACGTACTC	GTGAGGGTAA	500
CGACTTCTAC	CACGAAATGA	CCGACTCCAA	CGTTCTGGAC	AAAGTATCCC	550
TGGTTTACGG	CCAGATGAAC	GAGCCACCAG	GAAACCGTCT	GCGCGTTGCG	600
CTGACTGGCC	TGACGATGGC	TGAGAAGTTC	CGTGACGAAG	GCCGTGACGT	650
TCTGCTGTTC	GTCGATAACA	TCTACCGTTA	CACCCTGGCC	GGTACGGAAG	700
60 TATCTGCACT	GCTGGGTCGT	ATGCCTTCAG	CGGTAGGTTA	TCAGCCAACG	750

CTTGCGGAAG AGATGGGTGT TCTTCAGGAA CGTATCACCT CGACCAAAAC 800
CGGTT 805

5

2) INFORMATION FOR SEQ ID NO: 287

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 791 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

15

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterobacter sakasaki*
(B) STRAIN: ATCC 29544

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 287

25 TACGACGCCC TTGAGGTAAC GAATGGTAAT GAGCGTCTGG TGCTGGAAGT 50
CCAGCAGCAG CTCGGCGGCG GTATCGTACG TACCATCGCG ATGGGCTCTT 100
CCGACGGTCT GCGTCGCGGT CTGCCTGTTG CAGACCTTGA GCACCCGATC 150
GAAGTGCCGG TAGGTAAAGC GACGCTGGGT CGTATCATGA ACGTCCTGGG 200
TCAGCCTATC GACATGAAAG GCGACATCGG CGAAGAAGAG CGTTGGGCGA 250
TTCATCGCGC GGCGCCGTCC TATGAAGAGC TGTCCAGCTC TCAGGAACTG 300
CTGGAAACCG GCATCAAAGT TATCGACCTG ATGTGTCCGT TCGCGAAGGG 350
CGGTAAAGTC GGTCTGTTCG GTGGTGCAGG TGTAAGTAAA ACCGTAAACA 400
30 TGATGGAGCT TATTCGTAAC ATCGCGATTG AGCACTCCGG TTACTCCGTG 450
TTTGCGGGCG TGGGCGAACG TACCCGTGAA GGTAACGACT TCTACCACGA 500
AATGACCGAC TCCAACGTAC TGGATAAAGT ATCCCTGGTG TACGGCCAGA 550
TGAACGAGCC GCCGGGAAAC CGTCTGCGCG TTGCGCTGAC CGGCCTGACC 600
ATGGCTGAGA AATTCCGTGA CGAAGGTCGT GACGTTCTGC TGTTCGTCGA 650
35 CAACATCTAC CGTTACACCC TGGCCGGTAC TGAAGTATCC GCACTGCTGG 700
GCCGTATGCC TTCAGCGGTA GGTATCAGC CGACCCTGGC GGAAGAGATG 750
GGTGTCTG C AGGAGCGTAT CACCTCCACC AAAACCGGTT C 791

40

2) INFORMATION FOR SEQ ID NO: 288

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 839 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

50

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus avium*
(B) STRAIN: ATCC 14025

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 288

50 TTTCTTTAGA TCAATCCTTA CCAGACATCA ACAATGCGTT GATTGTTTAC 50
AAAAAAGATA AAACAAAAGT TGTTCTTGAA GTTGCTTTGG AACTTGGTGA 100
TG GTGTTATC CGCACAATCG CTATGGAGGC TACTGATGGA TTGCAACGTG 150
60 GAATGGAAGT TGTCGATACT GGCAATCAA TCTCCGTTCC TGTAAGTAAA 200

	GATACTCTAG	GTCGTGTGTT	TAACGTATTA	GGTGAAACGA	TTGATAAAGA	250
	AGCACCTTTT	CCAGAAGATG	CAGAAAGAAG	CGGCATTCAT	AAAAAGGCGC	300
	CTGCTTTTGA	AGACCTTAGT	ACAAGTAACG	AGATTTTGA	AACAGGGATC	350
	AAGGTTATCG	ACTTATTAGC	CCCTTATTTA	AAAGGTGGGA	AAGTCGGACT	400
5	ATTCGGTGGT	GCCGGTGTG	GTAAAACCGT	TTTGATCCAA	GAATTAATTC	450
	ATAATATCGC	CCAAGAACAC	GGTGGTATTT	CAGTGTTTAC	CGGTGTTGGG	500
	GAACGTACTC	GTGAAGGGAA	CGACCTTTAT	TATGAAATGA	AAGACTCTGG	550
	CGTTATTGAT	AAAACAGCCA	TGGTGTTCGG	ACAAATGAAC	GAGCCGCCTG	600
	GTGCACGTAT	GCGTGTGGCC	TTGACTGGTT	TGACATTAGC	TGAATATTTT	650
10	CGTGATGAAG	AAGGACAAGA	TGTGTTGCTA	TTTATTGACA	ACATCTTCCG	700
	CTTTACTCAA	GCCGGATCAG	AAGTTTCTGC	CTTATTAGGA	CGTATGCCAT	750
	CAGCCGTTGG	GTATCAACCA	ACTTTGGCAA	CTGAAATGGG	GCAATTACAA	800
	GAACGAATCA	CTTCAACCAA	AAAAGGTTTC	ATCACTTCA		839

15

2) INFORMATION FOR SEQ ID NO: 289

- (i) SEQUENCE CHARACTERISTICS:
- 20 (A) LENGTH: 847 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

- 25 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus casseliflavus*
- (B) STRAIN: ATCC 25788

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 289

	TTCTCTCTAG	ACCAATCATT	ACCAGATATC	AACAATGCGT	TGATTGTTTA	50
	CAAAAAAGAT	GAGCAGAAAA	CAAAAGTTGT	GTTAGAAGCT	GCCTTAGAAC	100
35	TTGGCGACGG	CGTTATCCGT	ACGATTGCCA	TGGAATCAAC	AGATGGCTTA	150
	CAACGAGGAA	TGGAAGTAAT	CGATACAGGC	GCCTCCATTT	CTGTTCCAGT	200
	TGGGACAGAA	ACCTTAGGAC	GGGTGTTTAA	TGTCTTAGGG	GACACCATCG	250
	ATTTAGAAGC	GCCGTTCCCT	GAAGAAGCAC	CCCGCAGTGG	GATTCACAAA	300
	AAAGCACCTG	ACTTTGATGA	ATTGTCAACA	AGTACGGAGA	TCCTTGAAAC	350
40	TGGGATCAAA	GTTATCGATT	TGTTAGCCCC	TTATTTAAAA	GGGGGGAAAG	400
	TTGGACTTTT	CGGTGGTGCC	GGTGTGTTGTA	AAACCGTCTT	GATCCAAGAA	450
	TTGATCCACA	ACATCGCCCA	AGAGCATGGT	GGGATCTCTG	TCTTCACAGG	500
	TGTTGGTGAA	CGGACACGTG	AAGGAAATGA	CCTTTATAAT	GAAATGAAAG	550
	AATCTGGCGT	TATCGAAAAA	ACAGCCATGG	TGTTTGGACA	AATGAACGAA	600
45	CCACCAGGTG	CTCGGATGCG	GGTAGCCTTG	ACTGGTTTGA	CATTAGCCGA	650
	GTACTTCCGT	GATGTGGAAG	GACAAGACGT	GCTCTTGTTT	ATCGATAATA	700
	TCTTCCGCTT	CACTCAAGCA	GGTTCTGAAG	TATCTGCCTT	ACTAGGTCGG	750
	ATGCCGTCTG	CCGTTGGGTA	TCAGCCAACA	TTAGCAACTG	AGATGGGGCA	800
50	ATTACAAGAA	CGGATCACAT	CGACGAAGAA	AGGTTCCGTT	ACGTCTA	847

50

2) INFORMATION FOR SEQ ID NO: 290

- 55 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 845 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 5 (A) ORGANISM: *Enterococcus durans*
(B) STRAIN: ATCC 19432

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 290

```

10 TTTCTTTAGA CCAATCCTTA CCAGATATCA ACAACGCTTT AGTTGTTTAT 50
   AAAAATGATG AGAAGAAATC GAAAGTTGTT CTTGAAACAG CGCTAGAATT 100
   AGGTGACGGT GTCATCCGTA CAATCGCGAT GGAATCAACA GATGGTTTAC 150
   AACGCGGAAT GGAAGTCATT GATACAGAAA AAGCAATTTC TGTACCAGTG 200
   GGTAAAGAAA CGTTAGGTCG TGTATTCAAT GTATTAGGAG ATACGATCGA 250
   TTTATCTGCA CCTTTCCCAG AAGATGCAAA ACGTAGCGAA ATCCATAAAA 300
15 AAGCACCAAA CTTTGATGAG TTAAGTACAA GTACTGAGAT CCTTGAAACT 350
   GGGATCAAAG TTATTGACTT GCTTGCTCCT TACTTAAAAG GTGGGAAAGT 400
   TGGATTATTC GGTGGTGCCG GTGTAGGTAA AACTGTATTG ATCCAAGAAT 450
   TGATCCATAA TATCGCTCAA GAACACGGTG GTATTTCTGT ATTTACTGGT 500
   GTTGGTGAAC GTACACGTGA AGGTAATGAC CTTTATTATG AAATGAAAGA 550
20 TTCAGGAGTT ATTGAAAAA CAGCCATGGT GTTTGGTCAA ATGAACGAAC 600
   CACCAGGTGC ACGTATGCGT GTTGCCCTGA CTGGTTTGAC GATTGCTGAA 650
   TACTTCCGTG ATGTTGAAGG GCAAGACGTG CTATTGTTTA TTGATAATAT 700
   TTTCCGTTTC ACTCAAGCCG GTTCAGAAGT TTCTGCCCTA TTAGGTCGTA 750
   TGCCTTCTGC CGTTGGGTAC CAACCAACGC TAGCAACAGA AATGGGTCAA 800
25 TTACAAGAAC GGATCACTTC AACGAAAAA GGTTCATCA CTTCA 845

```

2) INFORMATION FOR SEQ ID NO: 291

30

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 840 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
35 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 40 (A) ORGANISM: *Enterococcus faecalis*
(B) STRAIN: ATCC 29212

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 291

```

45 TTAGATCAAT CCTTACCCGA TATTAACAAC GCTTTAGTCG TTTATAAAAA 50
   TGGCGAAGCA AAACAAAAAG TAGTACTTGA AGTCGCTTTA GAACTAGGTG 100
   ATGGAGTGAT TCGTTCTATC GCCATGGAAT CGACAGATGG TTTACAACGT 150
   GGAATGGAAG TTATCGATAC AGGAAAATCA ATTTCA GTTC CTGTTGGTAA 200
   AGATACATTA GGTCGTGTGT TTAACGTTTT AGGAGACACA ATTGACTTAG 250
50 AAGCGCCATT CCCTGCAGAT GCTGAACGTA GTGGGATTCA TAAAAAAGCG 300
   CCAGCATTTG ATGAATTAAG TACCAGTAAT GAAATTTTAG AAACAGGGAT 350
   TAAAGTTATT GACTTATTAG CACCTTATCT AAAAGGTGGT AAAGTCGGAC 400
   TTTTCGGTGG TGCCGGTGTT GGTAAAACCG TCTTAATTCA AGAATTAATT 450
   CATAATATTG CCAAGAACA TGGAGGGATT TCCGTCTTTA CTGGTGTTGG 500
55 TGAACGGACA CGTGAAGGGA ACGATCTGTA CTATGAAATG AAAGATTTCAG 550
   GCGTTATTGA AAAAACAGCC ATGGTTTTTG GTCAAATGAA CGAACCGCCA 600
   GGTGCACGGA TGCGTGTGGC CTTAACTGGG TTAACGATTG CTGAATATTT 650
   CCGTGATGTG GAAGGACAAG ACGTGCTATT ATTTATTGAT AACATTTTCC 700
   GTTTCACCCA AGCCGGTTCA GAAGTTTCTG CCCTTTTAGG TCGGATGCCG 750
60 TCAGCCGTTG GTTACCAACC AACCTTAGCG ACTGAAATGG GACAATTACA 800

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AGAACGGATT ACTTCAACGA AAAAAGGATC AATTACCTCT

840

5 2) INFORMATION FOR SEQ ID NO: 292

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 831 bases
(B) TYPE: Nucleic acid
10 (C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

15 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus faecium*
(B) STRAIN: ATCC 19434

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 292

20 TTTCTTTAGA CCAATCCTTA CCAGATATCA ACAACGCATT AGTTGTTTAT 50
AAAAATGACG AAAATAAATC AAAAGTTGTT CTTGAAGCAG CGTTAGAATT 100
AGGGGACGGA GTGATCCGGA CCATTGCGAT GGAATCAACA GATGGTTTAC 150
AAAGAGGAAT GGAAGTCATT GATACAGGCA AAGCAATCTC TGTTCTGTGA 200
25 GGTAAAGAAA CATTAGGTCG CGTATTCAAC GTACTAGGAG ATACGATCGA 250
TTTAGAAACA CCTTTCCCAG AAGATGCGGA AAGAAGCGAA ATTCATAAAA 300
AAGCACCAGC CTTTGACGAA TTAAGTACAA GTACAGAAAT TTTGGAAACA 350
GGGATCAAAG TTATCGATTT GCTTGCCCCA TATTTAAAAG GTGGGAAAGT 400
CGGACTATTC GGTGGTGCCG GTGTTGGTAA AACCGTACTG ATCCAAGAAC 450
30 TGATCCATAA TATCGCCCAA GAACATGGTG GTATTTCTGT ATTTACCGGT 500
GTAGGTGAAC GTAATCGTGA AGGTAATGAC TTGTATTATG AAATGAAAGA 550
TTCAGGAGTT ATCGAAAAAA CAGCCATGGT GTTCGGACAA ATGAACGAAC 600
CACCAGGTGC ACGTATGCGT GTTGCTTTGA CTGGTTTGAC GATTGCGGAA 650
TATTTCCGTG ATGTAGAAGG TCAAGATGTA CTGTTGTTTA TCGACAACAT 700
35 TTTCCGTTTC ACTCAAGCTG GATCTGAAGT ATCAGCCTTG TTAGGACGGA 750
TGCCTTCTGC GGTGTTGTTAT CAACCAACAT TGGCAACAGA AATGGGTCAA 800
TTGCAAGAAC GTATCACATC TACGAAAAAA G 831

40

2) INFORMATION FOR SEQ ID NO: 293

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 826 bases
45 (B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

50

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus gallinarum*
(B) STRAIN: ATCC 49573

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 293

CCTTACCAGA TATCAACAAT GCGTTGATCG TTTACAAAAA AGACGAGAAA 50
AAAACAAAAG TAGTATTGGA AGCCGCTTTA GAACTAGGGG ATGGTGTGAT 100
CCGCACCATC GCAATGGAAT CTACAGACGG TTTGCAACGA GGAATGGAAG 150
60 TCATCGATAC CGGTGCCTCA ATCTCTGTCC CTGTAGGAAC AGATACTCTA 200

	GGCCGAGTAT	TTAATGTACT	AGGCGATACT	ATCGACTTGG	AAGCACCATT ^U	250
	CCCAGAAGAT	GCCAAACGTA	GTGGCATCCA	CAAAAAAGCC	CCAGATTTTCG	300
	ATGAATTGTC	AACAAGTACA	GAAATCCTTG	AAACTGGGAT	CAAAGTTATC	350
	GATTTATTAG	CTCCTTACTT	AAAAGGTGGT	AAAGTCGGCT	TGTTTCGGTGG	400
5	TGCCGGTGTT	GGTAAAACCG	TATTGATTCA	AGAATTGATT	CACAATATCG	450
	CTCAAGAGCA	TGGGGGAATT	TCAGTATTTA	CCGGTGTTGG	CGAACGGACG	500
	CGTGAAGGTA	ATGACTTGTA	TTATGAAATG	AAAGAATCAG	GCGTTATCGA	550
	AAAGACAGCC	ATGGTTTTTCG	GTCAAATGAA	TGAACCACCA	GGTGCCCGGA	600
	TGCGGGTTGC	TTTGACTGGT	TTGACCATTG	CTGAGTATTT	CCGTGACGTT	650
10	GAAGGACAAG	ATGTGCTCTT	GTTTATCGAT	AATATTTTCC	GTTTCACACA	700
	AGCGGGTTCT	GAAGTATCTG	CCTTGTTAGG	CCGGATGCCA	TCAGCCGTTG	750
	GTTATCAACC	AACTCTAGCA	ACTGAAATGG	GTCAATTACA	AGAACGAATC	800
	ACTTCTACGA	AAAAAGGATC	TGTAAC			826

15

2) INFORMATION FOR SEQ ID NO: 294

- (i) SEQUENCE CHARACTERISTICS:
- 20 (A) LENGTH: 846 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

- 25 (ii) MOLECULE TYPE: Genomic DNA

- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Enterococcus saccharolyticus*
- (B) STRAIN: ATCC 43076

30

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 294

	TTTCTTTGGA	CCAATCCTTA	CCAGACATCA	ACAATGCGTT	GGTGGTCTAT	50
	AAAAAGAATG	ATGAAAAAAC	AAAAGTGCTA	CTTGAAACAG	CTTTAGAACT	100
35	TGGTGATGGT	GTCGTACGTA	CGATTGCTAT	GTCGTCAACA	GACGGTTTGC	150
	AACGTGGGAT	GGAAGTCATC	GATACAGGAG	CATCAATTTC	TGTTCTGTGT	200
	GGGAAAGAGA	CATTAGGACG	TGTATTTAAC	GTTTTAGGGG	AGACTATCGA	250
	CTTAGATGGT	CCATTCCCAG	AAGAAGTAGC	ACGAGATGGT	ATTCTATAAA	300
	AGGCACCTGA	TTTTGATGAA	TTAAGTACAA	GTACGGAGAT	TCTTGAAACA	350
40	GGGATTAAAG	TAATCGATTT	ATTAGCGCCT	TACTTAAAAG	GTGGGAAAGT	400
	TGGTTTTATTC	GGTGGTGCCG	GTGTAGGTAA	AACGGTATTA	ATTCAAGAAT	450
	TGATTAACAA	TATTGCGCAA	GAACATGGTG	GTATTTTCAGT	ATTTGCGGGT	500
	GTTGGTGAGC	GTAATCGTGA	AGGAAATGAC	CTTTATTATG	AAATGAAAGA	550
	GTCGGGCGTT	ATTGAGAAAA	CAGCGATGGT	TTTTGGACAA	ATGAACGAAC	600
45	CACCAGGTGC	ACGTATGCGA	GTTGCTTTAA	CTGGTTTAAC	CATTGCAGAA	650
	TACTTCCGTG	ATGTTGAAGG	ACAAGATGTA	TTACTATTTA	TTGATAACAT	700
	TTTCCGTTTT	ACTCAAGCTG	GTTTCAAGAGT	TTCAGCTTTA	TTAGGACGTA	750
	TGCCTTCAGC	GGTAGGGTAT	CAACCGACAT	TAGCAACAGA	AATGGGACAA	800
50	TTACAAGAAC	GTATTACGTC	AACGAAAAAA	GGCTCAATTA	CATCAA	846

2) INFORMATION FOR SEQ ID NO: 295

- 55 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 803 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- 50 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Escherichia fergusonii*
 5 (B) STRAIN: ATCC 35469

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 295

	GCCGTACCGC	GCGTGTACGA	TGCTCTTGAG	GTGCAAAATG	GTAATGAGCG	50
10	TCTGGTGCTG	GAAGTTCAGC	AGCAGCTCGG	CGGTGGTATC	GTGCGTACCA	100
	TCGCAATGGG	GTCCTCCGAC	GGTCTGCGTC	GCGGTCTGGA	TGTAAAAGAC	150
	CTCGAACACC	CGATCGAAGT	CCCGGTAGGT	AAAGCGACTC	TGGGCCGTAT	200
	CATGAACGTA	CTGGGTGAAC	CGGTGACAT	GAAAGGCGAG	ATCGGTGAAG	250
	AAGAGCGTTG	GGCGATTCAC	CGCGCAGCAC	CTTCCTACGA	AGAGCTGTCA	300
15	AACTCTCAGG	AACTGCTGGA	AACCGGTATC	AAAGTTATCG	ACCTGATGTG	350
	TCCGTTTCGCT	AAGGGCGGTA	AAGTCGGTCT	GTTTCGGTGGT	GCGGGTGTAG	400
	GTAAACTGT	AAACATGATG	GAGCTTATTC	GTAACATCGC	GATCGAGCAC	450
	TCCGGTTACT	CTGTGTTTGC	GGGCGTAGGT	GAACGTACTC	GTGAGGGTAA	500
	CGACTTCTAC	CACGAAATGA	CTGACTCCAA	CGTTATCGAC	AAAGTATCCC	550
20	TGGTATATGG	CCAGATGAAC	GAGCCGCCGG	GAAACCGTCT	GCGCGTTGCA	600
	CTGACCGGCC	TGACCATGGC	TGAGAAATTC	CGTGACGAAG	GTCGTGACGT	650
	TCTGCTGTTT	GTTGACAACA	TCTATCGTTA	CACCCTGGCC	GGTACGGAAG	700
	TATCCGCACT	GCTGGGCCGT	ATGCCTTCAG	CGGTAGGTTA	TCAGCCGACT	750
	CTGGCGGAAG	AGATGGGCGT	TCTTCAGGAA	CGTATCACCT	CCACCAAAC	800
25	TGG					803

2) INFORMATION FOR SEQ ID NO: 296

30

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 822 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 35 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 40 (A) ORGANISM: *Escherichia hermannii*
 (B) STRAIN: ATCC 33650

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 296

45	GATGCCGTAC	CGCGCGTGTA	CGATGCTCTT	GAGGTGCAAA	ATGGTGATGA	50
	GCGTCTGGTG	CTGGAAGTGC	AGCAGCAGCT	CGGCGGCGGT	ATCGTGCGTA	100
	CCATCGCAAT	GGGTTCTTCC	GACGGTCTGC	GTCGTGGTCT	GACTGTCGTC	150
	GACCTCGAGC	ACCCGATCGA	AGTCCCGGTA	GGTAAAGCGA	CCCTGGGCCG	200
	TATCATGAAC	GTGCTGGGTC	AGCCGATCGA	CATGAAAGGC	GATATCGGTG	250
50	AAGAAGAGCG	TTGGGCGATT	CACCGCGCGG	CGCCGTCCTA	TGAAGAGCTG	300
	TCCAGCTCTC	AGGAACTGCT	GGAAACCGGC	ATCAAAGTTA	TCGACCTGAT	350
	GTGTCCGTTT	GCGAAGGGCG	GTAAAGTCGG	TCTGTTCGGT	GGTGCGGGCG	400
	TAGGTAAAAC	CGTAAACATG	ATGGAGCTGA	TCCGTAACAT	CGCGATCGAG	450
	CACTCCGGTT	ACTCTGTGTT	TGCGGGCGTG	GGTGAACGTA	CTCGTGAGGG	500
55	TAACGACTTC	TACCATGAAA	TGACCGACTC	CAACGTTCTG	GACAAAGTAT	550
	CCCTGGTTTA	CGGCCAGATG	AACGAACCGC	CGGGAAACCG	TCTGCGCGTT	600
	GCACTGACCG	GCCTGACCAT	GGCTGAGAAA	TTCCGTGACG	AAGGTCGTGA	650
	CGTTCTGTTG	TTCGTCGACA	ACATCTACCG	TTACACCCTG	GCCGGTACTG	700
	AAGTATCCGC	ACTGCTGGGC	CGTATGCCTT	CTGCGGTAGG	TTACCAGCCG	750
60	ACCCTGGCGG	AAGAGATGGG	CGTTCTGCAC	GAGCGTATCA	CCTCCACCAA	800

5 2) INFORMATION FOR SEQ ID NO: 297

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 808 bases
(B) TYPE: Nucleic acid
10 (C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

15 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Escherichia vulneris*
(B) STRAIN: ATCC 33821

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 297

20 CCGAACGTGT ACGACGCCCT CGAAGTGACA AATGGTAATG AGCGTCTGGT 50
GCTGGAAGTT CAGCAGCAGC TCGGCGGCGG TATCGTACGT ACCATCGCTA 100
TGGGTTCTTC CGACGGTCTG CGTCGTGGTC TGGAAGTTCA GGACCTCGAG 150
CACCCGATCG AAGTGCCGGT AGGTAAAGCG ACCCTGGGTC GTATCATGAA 200
25 CGTACTGGGT CAGCCGATCG ATATGAAAGG CGACATCGGT GAAGAAGAGC 250
GTTGGGCTAT TCACCGTGCA GCACCGTCCT ATGAAGAGCT CTCCAGCTCT 300
CAGGAAGTGC TGGAAACCGG CATCAAGGTT ATCGACCTGA TGTGTCCGTT 350
CGCCAAGGGC GGTAAAGTCG GCCTGTTCGG CGGCGCGGGC GTGGGTAAAA 400
CCGTAAACAT GATGGAGCTG ATCCGTAACA TCGCGATCGA GCACTCCGGT 450
30 TACTCCGTGT TTGCAGGCGT GGGTGAGCGT ACTCGTGAGG GTAACGACTT 500
CTACCACGAG ATGACCGACT CCAACGTTCT GGACAAAGTA TCCCTGGTGT 550
ACGGCCAGAT GAACGAGCCG CCGGGAAACC GTCTGCGCGT GGCCTGACC 600
GGCCTGACCA TGGCTGAGAA GTTCCGTGAC GAAGGTCGTG ACGTTCTGCT 650
GTTCTGTTGAC AACATCTATC GTTACACCC TGGCCGGTACG GAAGTATCTG 700
35 CACTGCTGGG CCGTATGCCT TCAGCGGTAG GTTACCAGCC GACGCTGGCG 750
GAAGAGATGG GCGTTCTGCA GGAGCGTATC ACCTCCACCA AAACCGGTTC 800
TATCACCT 808

40 2) INFORMATION FOR SEQ ID NO: 298

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 843 bases
45 (B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

50 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Eubacterium lentum*
(B) STRAIN: ATCC 43055

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 298

TTTCCCCCTG ATCAGCTGCC GGCGATTTAC AACGCGCTGA CGGTTGATGC 50
CAAGACCCTG GCGGGCGACT TGCACCTCGT GCTCGAGGTC GAGACGCACC 100
TGCCGGGCAA CCTTGTCCGC TCGGTGGCCA TGAGCTCGAC GGACGGTCTC 150
50 GTCCGCGGCC TCGAGGTCGT CGACACGGGC AACCCGATCA TGATGCCCGT 200

	GGGTCCCGAG	ACCCTGGGTC	GCATCTGGAA	CGTCATGGGC	GAGCCCGTGG	250
	ACGAGAAGCC	GATGCCCAG	GTGAAGGGCT	ACATGCCCAT	CCACCGTCCG	300
	GCTCCGGACT	ACGACGAGCT	GTCCACCACC	ACCGAGATCT	TCGAGACCGG	350
	CATCAAGGCC	ATCGACCTCG	TCGAGCCCTT	CGTCAAGGGC	GGCAAGACGG	400
5	GTCTGTTTCG	CGGCGCCGGC	GTGGGCAAGA	CGGTTATCAT	CCAGGAGCTC	450
	ATCAACAACC	TGGCCCAGGA	GCACGGCGGC	ACGTCGGTGT	TCACGGGCGT	500
	GGGCGAGCGT	ACCCGCGAGG	GTACCGACCT	CTACCTGGAG	ATGAGCGACT	550
	CGGGCGTCAT	CAACAAGACC	TGCCTCGTGT	ACGGTCAGAT	GAACGAGCCT	600
	CCGGGAGCGC	GTCTGCGCGT	GGGTCTCGCG	GGCCTCACCG	AGGCGGAGTA	650
10	CTTCCGCGAT	CAGGGCCAGG	ACGTGCTTCT	GTTCTGTGGAC	AACATCTTCC	700
	GCTTCACGCA	GGCCGGCTCC	GAGGTGTCCG	CTCTGCTGGG	CCGCATGCCC	750
	TCTGCCGTGG	GTTACCAGCC	GACGCTGCAC	ACCGAGATGG	GCGACCTGCA	800
	GGAGCGCATC	ACGTCGACGT	CCACCGGCTC	CATCACGTCC	GTG	843

15

2) INFORMATION FOR SEQ ID NO: 299

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 829 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

25 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Ewingella americana*
 (B) STRAIN: ATCC 33852

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 299

	TCCCTCAGGA	TGCAGTACCG	AACGTGTACA	ATGCTCTTGA	GGTAGAAAAC	50
	GGTGCCTCCA	AACTGGTTCT	GGAAGTTCAG	CAACAGTTAG	GCGGCGGCGT	100
35	TGTTTCGTTGT	ATCGCAATGG	GTACCTCAGA	CGGCCTTCGT	CGCGGTCTGA	150
	AAGTGAACAA	CCTGGAACAC	CCAATTGAAG	TTCCGGTTGG	TAAAGCGACT	200
	CTGGGTCGTA	TCATGAACGT	ATTGGGTGAA	CCAATCGACA	TGAAAGGTGA	250
	AATCGGCGAA	GAAGAACGTC	GTGCAATTCA	CCGTCCAGCG	CCTTCTTATG	300
	AAGAGCTGGC	TAACTCCCAA	GAATTGCTGG	AAACCGGTAT	CAAAGTTATG	350
40	GACCTGATGT	GTCCGTTTCG	TAAGGGCGGT	AAAGTCGGTC	TGTTTCGGTGG	400
	TGCGGGTGTT	GGTAAACTG	TAAACATGAT	GGAGCTGATC	CGTAACATCG	450
	CGATCGAGCA	CTCCGGTTAC	TCAGTGTTTG	CAGGCGTGGG	TGAGCGTACT	500
	CGTGAGGGTA	ACGACTTCTA	CCACGAAATG	ACTGACTCCA	ACGTTATCGA	550
	CAAAGTTTCC	CTGGTCTATG	GTCAGATGAA	TGAGCCACCA	GGTAACCGTC	600
45	TGCGCGTTGC	ACTGACCGGC	CTGACCATGG	CGGAGAAATT	CCGTGATGAA	650
	GGTCGTGACG	TACTGCTGTT	CGTTGACAAC	ATTTACCGTT	ACACCCCTGGC	700
	AGGTACCGAA	GTGTCCGCAC	TTCTGGGCCG	TATGCCATCG	GCGGTAGGTT	750
	ATCAGCCAAC	GCTGGCGGAA	GAGATGGGTG	CTCTGCAAGA	GCGTATCACC	800
50	TCTACCAAAA	GTGGTTCTAT	CACCTCCGT			829

50

2) INFORMATION FOR SEQ ID NO: 300

(i) SEQUENCE CHARACTERISTICS:

- 55 (A) LENGTH: 805 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

60

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Francisella tularensis*
 (B) STRAIN: LVS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 300

```

10 AACACGCCTA AAGTATATGA TGCTTTTAAAT GTAGTAGAAG CTGGTTT TAGT      50
   ATTAGAAGTT CAGCAACAAA TTGGTGATGG CGTAGTTCGT ACAATTGCTA      100
   TGGGATCTAG TGATGGTCTT AGACGTGGTA TGGAAAGTTAA GAACACAAAT      150
   GCGCCTATTT CTGTTCCAGT TGGACATGGC ACACTTGGAC GTATCATGAA      200
   TGTTTTAGGT GAACCAATTG ATGAAGCTGG TCCAATTGAA TATACTGAGA      250
   AAAGATCTAT CCATCAAGCT CCTCCTGCAT ATGATGAGTT AGCATTAAGT      300
15 ACAGAAATAT TAGAAACAGG TATCAAAGTA GTTGACCTTA TTTGTCCATT      350
   TGCTAAGGGC GGTAAAGTTG GTTTATTGGG CGGTGCAGGT GTTGGTAAAA      400
   CTGTAACGAT GATGGAACCT ATCAACAATA TTGCAAAAGA ACATAGTGGC      450
   TACTCTGTAT TTTCCGGTGT TGGTGAAAGA ACTCGTGAAG GTAATGACTT      500
   CTACTATGAG ATGAAATATT CTAATGTATT GGATAAAGTA TCATTAGTAT      550
20 ATGGTCAGAT GAATGAGCCG CCTGGAAACA GATTAAGAGT AGCTCTTAGT      600
   GGCTTAACAA TAGCAGAAGG ATTCCGTGAT GAAAAGCGTG ATGTTTTGAT      650
   GTTTATCGAT AACATCTATC GTTATACATT AGCAGGTACA GAGGTATCGG      700
   CGCTACTTGG TCGTATGCCA TCTGCTGTGG GTTATCAGCC AACGCTTGCA      750
   GCTGAGATGG GTGCTTTACA GGAGCGTATT ACATCTACTA AGACAGGATC      800
25 TATTA                                         805

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2) INFORMATION FOR SEQ ID NO: 301

30

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 825 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Fusobacterium gonidiaformans*
 (B) STRAIN: ATCC 25563

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 301

```

45 GACGAATTGC CAAAAATATA CAATGCATTA AAGGTGCAAG TTGGAGAAAA      50
   AGAACTTGTA TTGGAAGTGC AACAACATTT GGGAAATAAT GTTGTGAGAA      100
   CAGTAGCGAT GGA CTCAACA GATGGATTGC TTCGAGGAAT GGAAGTAATG      150
   GATACCGGAG CACCGATTAC TGTTCCAGTA GGGAAAGGCGG TTTTAGGAAG      200
   AATATTGAAT GTTTTGGGAG AGCCTGTGGA TCAAAAAGGG CCTGTGGAAA      250
50 CAGAAGAATA TTTACCTATC CATAGAGAAG CACCAAAATT TGAAGAACAA      300
   GAAACAGTAA CAGAAATTTT TGAAACAGGA ATTAAGTCA TAGATTTGTT      350
   AGCCCCTTAT ATCAAAGGAG GAAAGACAGG TCTATTCGGT GGAGCCGGAG      400
   TAGGGAAAAC AGTTTTAATT ATGGAATTAA TTAATAACAT TGCAAAGGGC      450
   CACGGAGGAA TTTCTGTGTT TGCAGGAGTT GGAGAAAGAA CAAGAGAAGG      500
55 AAGAGATTTA TACAACGAAA TGACAGAGTC CGGAGTTTGT AATAAGACCT      550
   CGTTGGTGTA TGGTCAAAATG AATGAGCCGC CCGGAGCAAG ACTTCGTGTG      600
   GCGTTGACAG GATTAACGGT TGCTGAAAAC TTTAGAGATA AAGAAGGGCA      650
   AGATGTATTG TTGTTTATCG ACAATATCTT CCGTTTCACA CAAGCAGGAT      700
   CAGAAGTATC GGCTCTATTG GGAAGAATTC CATCGGCAGT AGGATATCAA      750
60 CCGAACTTAG CGACAGAAAT GGGAACTTTA CAAGAAAGAA TTACTTCTAC      800

```

5 2) INFORMATION FOR SEQ ID NO: 302

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 806 bases
(B) TYPE: Nucleic acid
10 (C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

15 (vi) ORIGINAL SOURCE:
(A) ORGANISM: *Fusobacterium necrophorum* subsp.
necrophorum
(B) STRAIN: ATCC 25286

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 302

ACAATGCATT	AAAGGTACAG	GTGGGAGAAA	GGGAACTTGT	GTTGGAAGTG	50
CAGCAACATT	TAGGAAATAA	TGTTGTCAGA	ACAGTAGCAA	TGGATTCAAC	100
AGACGGATTA	CTTCGGGGAA	TGGAAGTGAG	AGATACAGGA	GTTCCCATTA	150
25 CTGTTCCGGT	AGGAAAGGCG	GTTTTGGGAA	GAATATTAAA	TGTCTTAGGG	200
GAGCCTGTGG	ACGAAAAGG	TCCGATAGAG	ACAGAAGAAT	ATTTACCAAT	250
ACATAGAGAA	GCACCGAAAT	TTGAAGAACA	GGAAACGGTG	ACAGAAATTT	300
TTGAAACAGG	AATTAAAGTC	ATTGATTTGT	TAGCTCCTTA	TATTAAAGGA	350
GGAAAAACAG	GCCTATTCGG	AGGAGCCGGA	GTAGGAAAAA	CCGTTTTGAT	400
30 TATGGAAGTG	ATCAATAATA	TTGCAAAAGG	TCATGGAGGA	ATTTCTGTTT	450
TTGCAGGAGT	TGGAGAAAGA	ACGAGAGAGG	GAAGAGATCT	ATACAACGAA	500
ATGACAGAGT	CCGGAGTTTT	GAATAAAACT	TCTTTGGTAT	ATGGGCAAAT	550
GAATGAGCCG	CCCGGAGCAA	GACTTCGAGT	GGCTTTAACC	GGACTTACTG	600
TTGCCGAAAA	TTTCAGAGAT	AAAGAGGGAC	AGGATGTCTT	ATTGTTTCATT	650
35 GACAATATTT	TCCGTTTCAC	ACAAGCAGGT	TCGGAAGTAT	CGGCACTTTT	700
GGGGAGAATT	CCTTCTGCAG	TGGGATATCA	ACCGAACTTG	GCGACAGAAA	750
TGGGAAGCTT	ACAAGAAAGA	ATTACTTCTA	CAAAATCCGG	TTCTATCACT	800
TCCGTG					806

40

2) INFORMATION FOR SEQ ID NO: 303

(i) SEQUENCE CHARACTERISTICS:
45 (A) LENGTH: 821 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

50 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Fusobacterium nucleatum* subsp. *polymorphum*
(B) STRAIN: ATCC 10953

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 303

GATGAATTGC	CTGCAATATA	TAATGCTTTA	AAAGTAAAAT	TAGAAGATAA	50
GGAAGTTGTT	CTAGAAGTTG	AACAACATCT	TGGTAACAAT	GTTGTAAAGAA	100
50 CTGTTGCTAT	GGATTCAACT	GATGGATTAA	AAAGAGGAAT	GGAAGTTATA	150

	GATACAGGTA	AACCAATTAC	AGTACCAGTT	GGTAAAGCTG	TTCTTGGTAG	200
	AATATTAAAT	GTTTTAGGAG	AACCTGTTGA	TAATCAAGGT	CCTATAAATG	250
	CTGAAACATT	TTTACCTATT	CATAGAGAAG	CACCAGAATT	TGATGACTTA	300
	GAAACTGAAA	CTGAAATATT	TGAAACAGGA	ATAAAAAGTTA	TAGACTTATT	350
5	AGCACCATAT	ATTAAAGGTG	GAAAAATAGG	ATTATTTGGT	GGAGCTGGAG	400
	TAGGAAAAAC	AGTTTTAATA	ATGGAACCTTA	TCAACAACAT	TGCAAAAGGA	450
	CATGGAGGAA	TTTCAGTTTT	TGCAGGAGTT	GGAGAAAGAA	CAAGAGAAGG	500
	TAGAGACTTA	TATGGTGAAA	TGACTGAATC	AGGAGTTATC	ACAAAAACAG	550
	CTCTTGTTTA	TGGACAAATG	AATGAGCCAC	CTGGAGCAAG	ACTTAGAGTT	600
10	GCTTAACAG	GGCTTACTGT	TGCAGAAAAC	TTTAGAGATA	AAGATGGGCA	650
	AGATGTTCTT	CTATTTATAG	ATAATATATT	TAGATTTACA	CAAGCAGGTT	700
	CAGAAGTTTC	AGCTTTACTT	GGAAGAATAC	CATCAGCTGT	TGGATATCAA	750
	CCAAACCTAG	CAACTGAAAT	GGGTGCTTTA	CAAGAAAGAA	TAACATCTAC	800
	AAAATCTGGT	TCAATTACAT	C			821

15

2) INFORMATION FOR SEQ ID NO: 304

20 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 864 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

25

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Gardnerella vaginalis*
- (B) STRAIN: ATCC 49145

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 304

	TTCCCAGTTG	GCTATCTTCC	AGATATTTAT	AATGCTCTCA	AGGTTGATAT	50
35	CAACACCGTT	GGAAACACGG	AGGGAGATAC	CGTCCACGAG	ATTACATTGG	100
	AAGTTGAGCA	GCACCTTGGT	GATTCAACTG	TGCGAGCAGT	GGCACTTAAG	150
	CCTACGGACG	GCTTGGTCCG	TGGTGCTTTA	GTGCGAGATA	CTGGTGGCCC	200
	AATTTCTGTG	CCTGTTGGAG	ATGTTACAAA	AGGTCACGTT	TTTGACGTAA	250
	CTGGTAACAT	TTTAAACGCT	AAACCAGGCG	AAAACATTGA	GGTGACCGAG	300
40	CGCTGGCCAA	TCCACCGCAA	CCCACCTGCT	TTGATCAGC	TTGAGTCTAA	350
	GACTCAAATG	TTTGAAACAG	GCATTAAGGT	TATCGATTTG	CTTACGCCTT	400
	ACGTTTCAGG	CGGAAAGATT	GGTCTGTTCG	GTGGTGCAGG	CGTTGGTAAA	450
	ACTGTGTTGA	TTCAGGAGAT	GATTCAGCGC	GTTGCACAGA	ACCACGGCGG	500
	TGTGTCTGTG	TTTGCTGGCG	TTGGCGAACG	TACTCGTGAG	GGTAACGATT	550
45	TGATTGGCGA	AATGGCTGAG	GCTGGCGTTT	TGGAGAAAAC	AGCGCTTGTC	600
	TTTGGTCAGA	TGGATGAGCC	TCCTGGGACT	CGTCTTCGTG	TGCCTCTTAC	650
	TGCTTTGACT	ATGGCTGAGT	ATTTCCGTGA	TGTTCAGAAT	CAGGATGTGT	700
	TGCTGTTTAT	CGACAACATC	TTCCGCTTTA	CTCAGGCAGG	TTCTGAGGTT	750
	TCCACGTTGC	TTGGTCGTAT	GCCTTCTGCA	GTTGGTTATC	AGCCAAACTT	800
50	GGCGGATGAA	ATGGGTGCGT	TGCAGGAGCG	CATTACTTCT	ACGCGCGGTC	850
	ATTCTATTAC	GTCG				864

55 2) INFORMATION FOR SEQ ID NO: 305

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 848 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double

60

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

5 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Gemella haemolysans*

(B) STRAIN: ATCC 10379

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 305

10

TCGAATCAGG	GCATATGCCA	AATCTATTAA	ACGCTTTAGA	AGTTTACATA	50
GAAAAAGGCG	ATGGGAAAAA	AGAAAAATTA	GTTCTTGAAG	TTTCTCTTGA	100
AATTGGTGAT	AACGTAGTAA	GAACAATCGC	TATGTCATCT	ACTGATGGAT	150
TAAATAGGGG	AGCAGAAGTA	GTAGATACAG	GAGCACCAAT	TACAGTTCCT	200
15 GTAGGTAAC	ACACATTAGG	TCGTGTGTTC	AACGTATTAG	GTGAAGCAGT	250
TGACCACGGT	GAAGAAGCAG	GAGCAGAAGT	TCGTAAAGAT	TCAATTCACA	300
AAGAAGCTCC	AACATTCGAT	GAATTATCAA	CTCACGTTGA	GGTTCTTGAA	350
ACAGGTATTA	AAGTTATCGA	CTTACTTGCA	CCATATATTA	AAGGTGGTAA	400
AATCGGTCTT	TTCGGTGGTG	CGGGAGTTGG	TAAAACGGTT	CTTATCCAAG	450
20 AACTTATCAA	CAACGTTGCG	CAACAACACG	GTGGATTATC	AGTATTCACA	500
GGTGTAGGTG	AGCGTACTCG	TGAAGGAAAT	GACTTATACT	ATGAAATGAA	550
AGATTCTGGT	GTTATTAACA	AAACAGCCAT	GGTATTCGGA	CAAATGAACG	600
AACCACCAGG	TGCTCGTATG	CGTGTAGCAT	TAACAGGATT	AACAATGGCG	650
GAATACTTCC	GTGATGAAGA	AGGACAAGAC	GTGCTTCTAT	TCATCGATAA	700
25 CATTTTCCGT	TTCACACAAG	CAGGTTCTGA	GGTTTCTGCG	TTATTAGGAC	750
GTATGCCATC	AGCCGTTGGT	TACCAACCAA	CATTGCTAC	AGAGATGGGA	800
CGTTTACAAG	AACGTATAAC	ATCAACTAAA	AAAGGTTCTG	TTACATCT	848

30

2) INFORMATION FOR SEQ ID NO: 306

(i) SEQUENCE CHARACTERISTICS:

35 (A) LENGTH: 848 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

40

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Gemella morbillorum*

(B) STRAIN: ATCC 27824

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 306

50

TCGAATCAGG	GCATATGCCT	AATCTACTAA	ACGCTTTAGA	AGTTTATATA	50
GAAAAAGGCG	ATGGAAAAAA	AGAAAAATTA	GTTCTTGAAG	TTTCTCTTGA	100
AATCGGGGAT	AATGTCGTAA	GAACATTATG	GATGTCATCT	ACTGATGGAT	150
50 TAAACAGAGG	GGCAGAAGTA	GTTGATACTG	GAGCGCCAAT	TACAGTGCCA	200
GTAGGTAAC	ATACATTAGG	ACGTGTGTTC	AACGTATTAG	GTGAAGCAGT	250
TGACCACGGA	GAAGAAGCTG	GAGCAGAAGT	TCAAAAAGAA	TCTATTCATA	300
AAGAAGCTCC	AACTTTCGAA	GAATTATCAA	CACATGTTGA	GGTATTAGAA	350
ACAGGTATTA	AAGTTATCGA	CCTTCTTGCA	CCATATATTA	AAGGTGGTAA	400
55 GATTGGACTA	TTCGGTGGTG	CTGGAGTTGG	GAAAACAGTT	CTTATCCAAG	450
AACTTATTAA	CAACGTAGCA	CAACAACACG	GAGGACTTTC	AGTATTTACT	500
GGGGTAGGTG	AACGTACTCG	TGAGGGTAAC	GACTTGTACT	ATGAAATGAA	550
AGACTCTGGA	GTTATTAATA	AAACTGCCAT	GGTATTTGGT	CAAATGAATG	600
AGCCACCAGG	TGCACGTATG	CGTGTTCGCT	TAACAGGATT	AACAATGGCA	650
50 GAGTACTTCC	GTGATGAAGA	AGGACAAGAC	GTACTATTAT	TTATCGATAA	700

TATCTTCCGT	TTCACACAAG	CAGGGTCTGA	GGTATCTGCA	TTATTAGGGC	750
GTATGCCTTC	AGCCGTTGGA	TATCAACCAA	CTCTTGCAAC	AGAAATGGGA	800
CGTCTTCAAG	AACGTATTAC	ATCAACTAAA	AAAGGATCTG	TTACATCT	848

5

2) INFORMATION FOR SEQ ID NO: 307

(i) SEQUENCE CHARACTERISTICS:

10 (A) LENGTH: 813 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

15 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Haemophilus ducreyi*

(B) STRAIN: DSM 8925

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 307

GATGCAGTAC	CAAAAGTATA	TGATGCTTTA	AAAGTTGAAT	CAGGTTTAAAC	50
CTTAGAAGTT	CAACAACAAT	TAGGTGGTGG	TTTAGTACGT	TGTATCGCAT	100
25 TAGGTACCTC	AGATGGTTTA	AAGCGTAGCT	TAAAGGTTGT	AAATACAGGT	150
AACCCTATTC	AAGTTCCTGT	AGGCACTAAA	ACATTAGGCC	GTATTATGAA	200
TGTATTAGGC	GAACCAATTG	ATGAAAAAGG	ACCTATTAGC	GAAGAAGCTC	250
GTTGGGATAT	TCATCGTGCG	GCTCCAAATT	ATGAAGAACA	GTCAAATAGT	300
ACTGAATTAC	TTGAAACCGG	TATCAAAGTT	ATTGACTTAA	TTTGTCCATT	350
30 TGCAAAAGGT	GGTAAAGTCG	GCTTATTTGG	TGGAGCTGGT	GTAGGTAAAA	400
CCGTTAATAT	GATGGAATTG	ATCCGTAATA	TTGCTATTGA	GCACTCAGGT	450
TATTCGGTTT	TTGCTGGTGT	AGGTGAGCGT	ACTCGTGAAG	GTAATGATTT	500
TTATCATGAA	ATGACGGATT	CTAATGTATT	AGATAAAGTA	TCACTAGTAT	550
ATGGTCAAAT	GAATGAACCA	CCAGGTAACC	GCCTACGTGT	TGCGTTAACA	600
35 GGTTTAACTA	TGGCTGAAAA	ATTCCGTGAT	GAAGGTCGTG	ATGTATTATT	650
TTTCGTAGAT	AATATTTATC	GTTATACTTT	AGCCGGTACA	GAAGTTTCTG	700
CTTTATTAGG	CCGTATGCCA	TCAGCGGTAG	GTTATCAACC	AACCCTTGCA	750
GAAGAAATGG	GTGTATTACA	AGAACGTATT	ACCTCAACTA	AAACTGGTTC	800
AATCACGGCA	GTA				813

10

2) INFORMATION FOR SEQ ID NO: 308

15 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 826 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Haemophilus haemolyticus*

55 (B) STRAIN: ATCC 33390

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 308

TGAATTTCCA	CAAGATGCAG	TGCCAAAAGT	TTACGATGCA	TTAAAAGTTG	50
50 AATCAGGTTT	AACACTTGAG	GTGCAACAAC	AATTAGGTGG	CGGTGTGGTA	100

	CGTTGTATCG	CATTAGGTGC	TTCTGACGGT	TTAAAACGTG	GTTTAAAAGT	150
	AGAAAACACG	AATGATCCGA	TTCAAGTACC	GGTAGGCACA	AAAACCCTTG	200
	GTCGTATCAT	GAATGTATTG	GGTGAACCAA	TTGACGAACA	AGGTCCAATC	250
	GGTGAAGAAG	AGCGTTGGGC	TATCCATCGT	TCTGCACCAA	GCTATGAAGA	300
5	ACAATCAAAC	AGTACGGAAT	TATTAGAGAC	TGGTATCAAA	GTTATCGACT	350
	TAATTTGTCC	ATTTCGAAAA	GGTGGTAAAG	TTGGTCTATT	CGGTGGTGCG	400
	GGTGTAGGTA	AAACCGTTAA	CATGATGGAA	TTAATCCGTA	ACATCGCGAT	450
	CGAGCACTCA	GGTTACTCCG	TATTTGCGGG	TGTAGGTGAA	CGTACTCGTG	500
	AAGGTAACGA	CTTCTATCAT	GAAATGAAAG	ATTCTAACGT	ATTAGATAAA	550
10	GTATCTTTGG	TTTATGGTCA	GATGAATGAG	CCACCAGGTA	ACCGTTTACG	600
	TGTTGCGTTA	ACTGGTTTAA	CCATGGCAGA	AAAATTCCGC	GATGAAGGTC	650
	GTGATGTATT	ATTCTTCTGT	GATAATATCT	ATCGTTATAC	CCTTGCTGGT	700
	ACGGAAGTAT	CTGCGTTATT	AGGTCGTATG	CCATCTGCGG	TAGGTTACCA	750
	ACCAACTCTT	GCTGAAGAAA	TGGGTGTGTT	ACAAGAACGT	ATCACTTCAA	800
15	CCAAAACAGG	TTCTATTACA	TCTGTA			826

2) INFORMATION FOR SEQ ID NO: 309

20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 809 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 25 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 30 (A) ORGANISM: *Haemophilus parahaemolyticus*
 (B) STRAIN: ATCC 10014

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 309

35	GATGCAGTAC	CAAAAGTATA	TGATGCGTTA	AAAGTTGAAT	CAGGTTTAAC	50
	GCTTGAAGTT	CAACAACAAT	TAGGCGGTGG	CTTAGTGCGC	TGTATCGCAT	100
	TAGGTACGTC	TGATGGTTTA	AAACGTGGCT	TAAAAGTAGA	AAATACAGGC	150
	AACCCAATTG	AAGTGCCAGT	GGGCACTAAA	ACCCTTGGTC	GTATTATGAA	200
	CGTATTGGGT	GAGCCGATTG	ACGAAAAAGG	TCCTATCGGT	GAAGAAGCAC	250
40	GCTGGGCAAT	CCACCGTGCA	GCACCAAGCT	ACGAAGAGCA	ATCAAATAGC	300
	ACGGAATTAC	TCGAAACAGG	TATCAAAGTT	ATCGACTTAA	TCTGCCCAT	350
	CGCAAAAGGG	GGTAAAGTTG	GTTTATTGTT	TGGTGCAGGT	GTAGGTAAAA	400
	CCGTAAATAT	GATGGAGTTA	ATCCGTAACA	TCGCGATCGA	ACACTCTGGT	450
	TACTCTGTAT	TTGCAGGGGT	AGGTGAGCGT	ACTCGTGAAG	GTAATGACTT	500
45	CTACCACGAA	ATGACAGACT	CTAACGTATT	AGATAAAGTA	TCGTTAGTGT	550
	ATGGTCAAAT	GAACGAACCA	CCAGGTAACC	GTTTACGCGT	AGCTTTAACA	600
	GGCTTAACCA	TGGCGGAAAA	ATTCCGCGAT	GAAGGTCGTG	ACGTATTATT	650
	CTTCGTCGAT	AACATCTACC	GTTATACCCT	AGCAGGTACG	GAAGTGTGAG	700
	CACTTCTCGG	TCGTATGCCA	TCTGCGGTAG	GTTATCAGCC	AACCTTAGCA	750
50	GAAGAAATGG	GTGTATTACA	AGAGCGTATC	ACTTCAACCA	AAACTGGTTC	800
	TATCACCTC					809

55 2) INFORMATION FOR SEQ ID NO: 310

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 824 bases
 (B) TYPE: Nucleic acid
 60 (C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

5 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Haemophilus parainfluenzae*

(B) STRAIN: ATCC 7901

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 310

10
 CGAATTTCCA CAAGATGCAG TACCAAAAGT TTATGATGCA TTAAAAGTTG 50
 AATCGGGTTT AACCTTTGAA GTTCAACAAC AATTAGGTGG TGGTGTGGTA 100
 CGTTGTATCG CACTGGGAGC TTCTGACGGT TTAAAACGCA GTTTAAGCGT 150
 TGAAAATACC AATAAACCAA TTTCAGTACC GGTTGGTGTA AAAACTCTCG 200
 15 GTCGTATTAT GAACGTATTG GGCGAACCGA TTGATGAAAG AGGTCCTATC 250
 GGTGCGGAAG AAGAATGGGC AATTCACCGT TCTACTCCAA GTTATGAAGA 300
 ACAGTCCAAC AGTACCGAAT TATTAGAAAC CGGTATCAAA GTTATCGACT 350
 TAATTTGTCC ATTCGCGAAG GGTGGTAAAG TTGGTTTATT CGGTGGTGCG 400
 GGTGTAGGTA AGACCGTAAA TATGATGGAA TTAATCCGTA ATATTGCGAT 450
 20 TGAGCACTCA GGTTACTCCG TATTTGCCGG TGTAGGTGAG CGTACCCGTG 500
 AAGGTAACGA CTTCTACCAT GAAATGACAG AATCTAACGT ATTAGACAAA 550
 GTATCCCTAG TTTACGGACA AATGAATGAG CCGCCGGGTA ACCGTTTACG 600
 TGTTGCTTTA ACCGGTTTAA CCATGGCAGA AAAATTCCGT GACGAAGGTC 650
 GTGATGTATT ATTCTTCGTG GATAACATCT ATCGTTATAC CCTTGCAGGG 700
 25 ACTGAAGTAT CGGCACTTTT AGGCCGTATG CCATCAGCGG TAGGTTATCA 750
 GCCGACACTT GCAGAAGAAA TGGGTGTGTT ACAAGAACGT ATTACATCAA 800
 CCAAAACAGG TTCTATTACT TCTG 824

30

2) INFORMATION FOR SEQ ID NO: 311

(i) SEQUENCE CHARACTERISTICS:

35 (A) LENGTH: 811 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

40

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Hafnia alvei*

(B) STRAIN: ATCC 13337

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 311

GCCGTGCTTA AAGTGTATAA CGCACTTGAG GTGAAAGGCG GTGCCACTAA 50
 ACTGGTACTG GAAGTTCAGC AGCAGCTAGG CGGCGGCGTT GTACGCTGTA 100
 TCGCTATGGG TACTTCTGAC GGTCTGCGTC GCGGACTGGA CGTTGTTGAC 150
 50 CTGGAGCACC CGATTGAAGT CCCAGTAGGT AAAGCGACCT TAGGCCGCAT 200
 TATGAACGTA CTGGGTGAGC CAATTGATAT GAAGGGTGAT ATCGGCGAAG 250
 AAGATCGCTG GGCTATTCAC CGTGAAGCTC CAAGCTACGA AGAACTGTCT 300
 AACTCGCAAG AACTGCTGGA AACTGGTATC AAGGTAATGG ACCTGATTTG 350
 TCCGTTGCTT AAGGGCGGTA AAGTTGGTCT GTTCGGTGGT GCGGGTGTG 400
 55 GTAAAACAGT AAACATGATG GAGCTGATCC GTAACATCGC GATCGAGCAC 450
 TCAGGTTACT CTGTATTTGC CGGCGTGGGT GAACGTACTC GTGAGGGTAA 500
 CGACTTCTAC CACGAAATGA CCGACTCCAA CGTATTGGAC AAAGTATCAC 550
 TGGTTTATGG CCAGATGAAC GAGCCACCAG GAAACCGTCT GCGCGTTGCG 600
 CTGACCGGTC TGAATATGGC TGAGAAGTTC CGTGACGAAG GTCGTGACGT 650
 60 ACTGCTGTTC ATCGATAACA TCTACCGTTA TACCTTGCC GGTACCGAAG 700

TATCTGCACT GTTGGGTCGT ATGCCTTCTG CGGTAGGTTA TCAGCCAACG 750
 CTGGCGGAAG AGATGGGTGT TCTGCAAGAA CGTATCACCT CGACCAAAAC 800
 GGGTTCAATC A 811

5

2) INFORMATION FOR SEQ ID NO: 312

- (i) SEQUENCE CHARACTERISTICS:
 10 (A) LENGTH: 831 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

- 15 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Kingella kingae*
 (B) STRAIN: ATCC 23330

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 312

GCGATGCTAT TCCACGCGTT TACGATGCGT TGAAACTGGT TGATGTGGAC 50
 TTGACATTAG AAGTGCAACA ACAACTGGGC GATGGCGTAG TCGGTACCAT 100
 25 TCGGATGGGT AGTACCGATG GTTTGAAACG CGGCTTAGCC GTGAACAACA 150
 CAGGCGCACC TATTACAGTG CCTGTTGGTA AAGCAACATT GGGTCGTATT 200
 ATGGACGTAT TGGGTAATCC TGTTGATGAA GCAGGTCCAA TTGGTTCTGA 250
 CCAAACGCGT GCTATTCACC AACCAGCTCC TAAATTTGAT GAACTGTCTA 300
 GCGCAACCGA ATTGCTGGAA ACAGGCATCA AAGTGATTGA CTTGCTTTGC 350
 30 CCATTTGCAA AAGGTGGTAA AGTAGGTTTG TTTGGTGGTG CAGGTGTGGG 400
 CAAACTGTG AACATGATGG AGTTGATTAA CAACATTGCC AAAGCGCACA 450
 GTGGTTTGTC TGTATTTGCA GCGGTGGGTG AACGTACTCG CGAAGGTAAT 500
 GACTTCTATC ACGAGATGAA AGATTCTAAC GTGTTGGATA AAGTTGCCAT 550
 GGTGTATGGT CAAATGAATG AACCTCCTGG CAACCGTTTG CGCGTTGCAT 600
 35 TGA CTGGTTT GTCTATGGCA GAACACTTCC GTGATGAAAA AGACGAAAAT 650
 GGCAAAGGTC GCGATGTATT GTTCTTTGTG GACAACATCT ATCGCTACAC 700
 ATTGGCAGGT ACAGAAGTAT CGGCATTGCT GGGTCGTATG CCCTCTGCGG 750
 TAGGTTATCA ACCAACATTG GCAGAAGAAA TGGGTCGTTT GCAAGAGCGT 800
 ATTACTTCAA CGCAAACAGG TTCGATTACT T 831

40

2) INFORMATION FOR SEQ ID NO: 313

- 15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 812 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Klebsiella pneumoniae* subsp. *ozaenae*
 55 (B) STRAIN: ATCC 11296

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 313

ATGCCGTACC ACGCGTGATC GAAGCCCTTG AGGTACAGAA TGGTAATGAA 50
 50 GTTCTGGTGC TGGAAGTTCA GCAGCAGCTG GGCGGCGGTA TCGTACGTAC 100

	CATCGCCATG	GGTTCTTCTG	ATGGTCTGCG	CCGCGGTCTG	GATGTAAAG	150
	ACCTCGAGCA	CCCGATCGAA	GTCCCGGTAG	GTAAAGCAAC	GCTGGGTCGT	200
	ATCATGAACG	TACTGGGTCA	ACCGGTTGAC	ATGAAAGGCG	ACATCGGCCA	250
	AGAAGAGCGT	TGGGCTATCC	ACCGCGCGGC	ACCGTCCTAT	GAAGAGCTGT	300
5	CCAGCTCTCA	GGAAGTCTG	GAAACCGGCA	TCAAAGTTAT	CGACCTGATG	350
	TGTCCGTTTC	CCAAGGGCGG	TAAAGTTGGT	CTGTTTCGGC	GTGCGGGTGT	400
	AGGTAAACT	GTAAACATGA	TGGAGCTGAT	CCGTAACATC	GCGATCGAGC	450
	ACTCCGGTTA	CTCTGTGTTT	GCGGGCGTAG	GTGAGCGTAC	TCGTGAGGGT	500
	AACGACTTCT	ACCACGAAAT	GACCGACTCC	AACGTTATCG	ATAAAGTATC	550
10	CCTGGTGTAC	GGCCAGATGA	ACGAGCCGCC	GGGAAACCGT	CTGCGCGTTG	600
	CGCTGACCGG	CCTGACCATG	GCTGAGAAAT	TCCGTGACGA	AGGTCGTGAC	650
	GTACTGCTGT	TCGTCGATAA	CATCTATCGT	TACACCCTGG	CCGGTACTGA	700
	AGTATCCGCG	CTGCTGGGTC	GTATGCCTTC	AGCGGTAGGT	TATCAGCCGA	750
	CCCTGGCGGA	AGAGATGGG	GTTCTGCAGG	AACGTATCAC	CTCCACCAAA	800
15	ACCGGTTCTA	TC				812

2) INFORMATION FOR SEQ ID NO: 314

20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 812 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 25 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 30 (A) ORGANISM: *Klebsiella ornithinolytica*
 (B) STRAIN: ATCC 31898

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 314

35	ATGCCGTACC	GCGCGTGTAC	GATGCTCTTG	AGGTACAGAA	TGGTAATGAG	50
	AGCCTGGTGC	TGGAAGTTCA	GCAGCAGCTC	GGCGGTGGTA	TCGTACGTGC	100
	TATCGCCATG	GGTTCTTCCG	ACGGTCTGCG	TCGTGGTCTG	GAAGTTAAAG	150
	ACCTTGAGCA	CCCGATCGAA	GTCCCGGTTG	GTAAAGCAAC	GCTGGGTCGT	200
	ATCATGAACG	TGCTGGGTCA	GCCAATCGAT	ATGAAAGGCG	ACATCGGCCA	250
10	AGAAGAGCGT	TGGGCTATTC	ACCGTGCAGC	TCCGTCCTAT	GAAGAGCTGT	300
	CCAGCTCTCA	GGAAGTCTG	GAAACCGGCA	TCAAAGTTAT	CGACCTGATG	350
	TGTCCGTTTC	CTAAGGGCGG	TAAAGTTGGT	CTGTTTCGGT	GTGCGGGTGT	400
	AGGTAAACC	GTAAACATGA	TGGAGCTGAT	CCGTAACATC	GCGATCGAGC	450
	ACTCCGGTTA	CTCCGTGTTT	GCGGGCGTAG	GTGAACGTAC	TCGTGAGGGT	500
15	AACGACTTCT	ACCACGAAAT	GACCGACTCC	AACGTTCTGG	ATAAAGTATC	550
	CCTGGTTTAT	GGCCAGATGA	ACGAGCCGCC	GGGAAACCGT	CTGCGCGTTG	600
	CTCTGACCGG	CCTGACCATG	GCTGAGAAAT	TCCGTGACGA	AGGTCGTGAC	650
	GTTCTGCTGT	TCGTCGATAA	CATCTATCGT	TATACCCTGG	CCGGTACTGA	700
	AGTATCCGCA	CTGCTGGGTC	GTATGCCTTC	AGCGGTAGGT	TATCAGCCGA	750
50	CCCTGGCGGA	AGAGATGGGT	GTTCTGCAGG	AACGTATCAC	CTCCACCAAA	800
	ACCGGTTCTA	TC				812

55 2) INFORMATION FOR SEQ ID NO: 315

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 813 bases
 (B) TYPE: Nucleic acid
 50 (C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

5 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Klebsiella oxytoca*

(B) STRAIN: ATCC 33496

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 315

10
 GTACCGCGCG TGTACGAGGC TCTTGAGGTA CAAAATGGTA GTGAGAATCT 50
 GGTGCTGGAA GTTCAGCAGC AGCTCGGCGG CGGTATTGTT CGTACCATCG 100
 CCATGGGTTC TTCCGACGGT CTGCGTCGCG GTCTGGAAGT CAAAGACCTC 150
 GAGCATCCGA TCGAAGTCCC GGTAGGTAAA GCAACGCTGG GTCGTATCAT 200
 15 GAACGTACTG GGCCAACCGG TAGACATGAA AGGCGACATC GGCGAAGAAG 250
 AGCGTTGGGC GATTCACCGC GCAGCGCCTT CCTACGAAGA GTTGTCAAAC 300
 TCTCAGGAAC TGCTGGAAAC CGGCATCAAA GTTATCGACC TGATGTGTCC 350
 GTTTGCGAAG GGC GGTAAG TTGGTCTGTT CGGTGGTGCG GGTGTAGGTA 400
 AAACCGTAAA CATGATGGAG CTGATCCGTA ACATCGCGAT CGAGCACTCC 450
 20 GGTACTCCG TGTTCGCGG CGTAGGTGAA CGTACTCGTG AGGGTAACGA 500
 CTTCTACCAC GAAATGACCG ACTCCAACGT TATCGATAAA GTATCCCTGG 550
 TGTATGGCCA GATGAACGAG CCGCCGGGAA ACCGTCTGCG CGTTGCGCTG 600
 ACCGGCCTGA CCATGGCTGA GAAGTTCCGT GACGAAGGTC GTGACGTTCT 650
 GCTGTTCGTC GATAACATCT ATCGTTACAC CCTGGCCGGT ACTGAAGTAT 700
 25 CCGCACTGCT GGGTCGTATG CCTTCAGCGG TAGGTTACCA GCCGACTCTG 750
 GCGGAAGAGA TGGGCGTTCT GCAGGAACGT ATCACCTCCA CCAAAACGGG 800
 TTCTATCACT TCC 813

30

2) INFORMATION FOR SEQ ID NO: 316

(i) SEQUENCE CHARACTERISTICS:

35 (A) LENGTH: 822 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

40

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Klebsiella planticola*

(B) STRAIN: ATCC 33531

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 316

GATGCCGTAC CGCGCGTGTA CGATGCTCTT GAGGTACAGA ATGGTAATGA 50
 GAGCCTGGTG CTGGAAGTTC AGCAGCAGCT CGGCGGTGGT ATCGTACGTG 100
 CTATCGCCAT GGGTTCTTCT GACGGTCTGC GTCGTGGTCT GGAAGTTAAA 150
 50 GACCTTGAGC ACCCGATCGA AGTCCCGGTT GGTAAAGCAA CGCTGGGTCTG 200
 TATCATGAAC GTGCTGGGTC AGCCGATCGA TATGAAAGGC GACATCGGCG 250
 AAGAAGAGCG TTGGGCTATT CACCGCGCAG CTCCGTCTTA TGAAGAGCTG 300
 TCCAGTTCTC AGGAACTGCT GGAAACCGGC ATCAAAGTTA TCGACCTGAT 350
 GTGTCCGTTT GCTAAGGGCG GTAAAGTAGG TCTGTTTCGGT GGTGCGGGCG 400
 55 TAGGTAAAAC CGTAAACATG ATGGAGCTGA TCCGTAACAT CGCGATCGAG 450
 CACTCCGGTT ACTCCGTGTT TGCGGGCGTC GGTGAACGTA CTCGTGAGGG 500
 TAACGACTTC TACCACGAAA TGACCGACTC CAACGTTCTG GATAAAGTAT 550
 CCCTGGTTTA TGGCCAGATG AACGAGCCGC CGGGAAACCG TCTGCGCGTT 600
 GCTCTGACCG GCCTGACCAT GGCTGAGAAA TTCCGTGACG AAGGTCGTGA 650
 50 CGTTCTGCTG TTCGTCGATA ACATCTATCG TTATACCCTG GCCGGTACTG 700

AAGTATCCGC	ACTGCTGGGT	CGTATGCCTT	CAGCGGTAGG	TTATCAGCCG	750
ACCCTGGCGG	AAGAGATGGG	TGTTCTGCAG	GAACGTATCA	CCTCCACCAA	800
AACCGGTTCT	ATCACTTCCG	TA			822

5

2) INFORMATION FOR SEQ ID NO: 317

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 785 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

15 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Klebsiella pneumoniae* subsp. *pneumoniae*
 (B) STRAIN: ATCC 13883

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 317

AGAATGGTAA	TGAAGTTCTG	GTGCTGGAAG	TTCAGCAGCA	GCTGGGCGGC	50
GGTATCGTAC	GTACCATCGC	CATGGGTTCT	TCTGATGGTC	TGCGCCGCGG	100
25 TCTGGATGTA	AAAGACCTCG	AGCACCCGAT	CGAAGTCCCG	GTAGGTAAAG	150
CAACGCTGGG	TCGTATCATG	AACGTACTGG	GTCAACCGGT	TGACATGAAA	200
GGCGACATCG	GCGAAGAAGA	GCGTTGGGCT	ATCCACCGCG	CGGCACCGTC	250
CTATGAAGAG	CTGTCCAGCT	CTCAGGAACT	GCTGGAAACC	GGCATCAAAG	300
TTATCGACCT	GATGTGTCCG	TTCGCCAAGG	GCGGTAAAGT	TGGTCTGTTC	350
30 GGCGGTGCGG	GTGTAGGTAA	AACTGTAAAC	ATGATGGAGC	TGATCCGTAA	400
CATCGCGATC	GAGCACTCCG	GTTACTCTGT	GTTTGCGGGC	GTAGGTGAGC	450
GTACTCGTGA	GGGTAATGAC	TTCTACCACG	AAATGACCGA	CTCCAACGTT	500
ATCGATAAAG	TATCCCTGGT	GTACGGCCAG	ATGAACGAGC	CGCCGGGAAA	550
CCGTCTGCGC	GTTGCGCTGA	CCGGCCTGAC	CATGGCTGAG	AAATTCCGTG	600
35 ACGAAGGTCTG	TGACGTACTG	CTGTTTCGTCG	ATAACATCTA	TCGTTACACC	650
CTGGCCGGTA	CTGAAGTATC	CGCACTGCTG	GGTCGTATGC	CTTCAGCGGT	700
AGGTTATCAG	CCGACCCTGG	CGGAAGAGAT	GGGCGTTCTG	CAGGAACGTA	750
TCACCTCCAC	CAAAACCGGT	TCTATCACCT	CCGTA		785

40

2) INFORMATION FOR SEQ ID NO: 318

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 759 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

50 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Kluyvera ascorbata*
 (B) STRAIN: ATCC 33433

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 318

CTGGTGCTGG	AAGTTCAGCA	GCAGCTCGGC	GGCGGTATCG	TACGTWCCAT	50
CGCTATGGGT	TCTTCCGACG	GTCTGCGTCG	CGGTCTGGAT	GTAAAGATC	100
50 TCGAGCACCC	AATCGAAGTT	CCGGTMGGTA	AAGCAACMCT	GGGTCGTATC	150

	ATGAACGTAC	TGGGTCAKCC	AGTMGACATG	AAAGGCGAC [̄]	TCGGTGA [̄] AG [̄]	200
	AGAGCGTTGG	GCTATCCACC	GCGCTGCACC	TTCCTACGAA	GAGCTGTCTA	250
	GCTCTCAGGA	ATTGCTGGAA	ACCGGTATCA	AAGTTATCGA	CCTGATGTGT	300
	CCGTTTCGCTA	AGGGCGGTAA	AGTCGGTCTG	TTCGGTGGTG	CSGGTGTGTG	350
5	TAAAACCGTA	AACATGATGG	AGCTGATCCG	TAACATCGCG	ATCGAGCACT	400
	CCGTTACTC	CGTGTTCG	GGCGTAGGTG	AACGTACTCG	TGAGGGTAAC	450
	GACTTCTACC	ACGAAATGAC	CGACTCCAAC	GTTATCGATA	AAGTATCCCT	500
	GGTATATGGC	CAGATGAACG	AGCCACCGGG	AAACCGTCTG	CGCGTTGCTC	550
	TGACCGGTCT	GACCATGGCT	GAGAAATTCC	GTGACGAAGG	TCGTGACGTA	600
10	CTGCTGTTTCG	TCGATAACAT	CTATCGTTAC	ACCCTGGCCG	GTACTGAAGT	650
	ATCTGCWCTG	CTGGGTCGTA	TGCCTTCAGC	GGTAGGTTAC	CAGCCGACCC	700
	TGGCGGAAGA	GATGGGCGTT	CTGCAGGAAC	GTATCACCTC	CACCAAGACC	750
	GGTTCCTATC					759

15

2) INFORMATION FOR SEQ ID NO: 319

- (i) SEQUENCE CHARACTERISTICS:
- 20 (A) LENGTH: 831 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

- 25 (ii) MOLECULE TYPE: Genomic DNA

- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Kluyvera cryocrescens*
- (B) STRAIN: ATCC 33435

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 319

	TTCCCTCAGG	ATGCCGTACC	GCGTGTGTAC	GAAGCCCTTG	AGGTTTCAGAA	50
	TGGTAATGAA	GTGCTGGTGC	TGGAAGTTCA	GCAGCAGCTC	GGCGGCGGTA	100
35	TCGTACGTAC	CATCGCTATG	GGTTCTTCCG	ACGGTCTGCG	TCGTGGTCTG	150
	GATGTAAAAG	ACCTCGAGCA	CCCGATCGAA	GTCCCGGTAG	GTAAAGCAAC	200
	ACTGGGTCGT	ATCATGAACG	TACTGGGCCA	ACCGGTAGAC	ATGAAAGGCG	250
	ACATCGGTGA	AGAAGAACGT	TGGGCTATCC	ACCGTGCAGC	ACCTTCCTAC	300
	GAAGAGCTGT	CAAGCTCTCA	GGAAGTCTG	GAAACCGGCA	TCAAAGTTAT	350
40	CGACCTGATG	TGTCCGTTTG	CGAAGGGCGG	TAAAGTTGGT	CTGTTCCGGTG	400
	GTGCGGGTGT	AGGTAAAACC	GTAAACATGA	TGGAGCTTAT	TCGTAACATC	450
	GCGATTGAGC	ACTCCGGTTA	TTCTGTGTTT	GCGGGCGTAG	GTGAACGTAC	500
	TCGTGAGGGT	AACGACTTCT	ACCACGAAAT	GACCGACTCC	AACGTTATCG	550
	ATAAAGTTTC	CCTGGTTTAC	GGCCAGATGA	ACGAGCCACC	AGGAAACCGT	600
45	CTGCGCGTTG	CGCTGACTGG	TCTGACTATG	GCTGAGAAGT	TCCGTGACGA	650
	AGGTCGCGAC	GTACTGCTGT	TCGTCGATAA	CATCTATCGT	TACACCCTGG	700
	CCGGTACAGA	AGTATCTGCA	CTGCTGGGTC	GTATGCCTTC	AGCGGTAGGT	750
	TACCAGCCGA	CTCTGGCGGA	AGAGATGGGC	GTTCTGCAGG	AACGTATCAC	800
50	CTCCACCAA	ACCGTTCTA	TCACCTCCGT	A		831

50

2) INFORMATION FOR SEQ ID NO: 320

- 55 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 810 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Kluyvera georgiana*
 5 (B) STRAIN: ATCC 51603

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 320

	GCCGTACCGC	GCGTGTACGA	AGCCCTTGAG	GTACAGAATG	GTAATGAAGT	50
10	GCTGGTGCTG	GAAGTTCAGC	AGCAGCTCGG	TGGCGGTATC	GTGCGTACCA	100
	TCGCCATGGG	TTCCTCCGAC	GGTCTGCGTC	GCGGTCTGGA	AGTTAAAGAT	150
	CTCGAGCACC	CGATCGAAGT	TCCGGTAGGT	AAAGCAACAC	TGGGTCGTAT	200
	CATGAACGTA	CTGGGTCACC	CGGTAGACAT	GAAAGGCGAC	ATCGGTGAAG	250
	AAGAGCGTTG	GGCTATCCAC	CGCGCTGCGC	CTTCCTACGA	AGAGCTGTCC	300
15	AGCTCTCAGG	AACTGCTGGA	AACCGGTATC	AAAGTTATCG	ACCTGATGTG	350
	TCCGTTTCGG	AAGGGCGGTA	AAGTCGGTCT	GTTTCGGCGGT	GCGGGTGTTC	400
	GTAACACCGT	AAACATGATG	GAGCTGATCC	GTAACATCGC	GATCGAGCAC	450
	TCCGGTTACT	CTGTGTTTGC	GGGCGTAGGT	GAACGTACTC	GTGAGGGTAA	500
	CGACTTCTAC	CACGAAATGA	CCGACTCCAA	CGTTATCGAT	AAAGTATCCC	550
20	TGGTGTATGG	CCAGATGAAC	GAGCCGCCGG	GAAACCGTCT	GCGCGTTGCG	600
	CTGACCGGCC	TGACCATGGC	TGAGAAATTC	CGTGACGAAG	GTCGTGACGT	650
	ACTGCTGTTC	GTCGATAACA	TCTATCGTTA	CACCCTGGCC	GGTACTGAAG	700
	TATCTGCACT	GCTGGGTCGT	ATGCCTTCAG	CGGTAGGTTA	CCAGCCGACT	750
	CTGGCGGAAG	AGATGGGCGT	TCTGCAGGAA	CGTATCACCT	CCACCAAGAC	800
25	CGGTTCTATC					810

2) INFORMATION FOR SEQ ID NO: 321

30

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 834 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 35 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 40 (A) ORGANISM: *Lactobacillus acidophilus*
 (B) STRAIN: ATCC 4356

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 321

45	TCGATAAGAA	TTTACCTGAT	ATTAACAACG	CCTTACGTGT	AATCAAGTCC	50
	GAAGATGAAA	GCATCGTTCT	TGAAGTTACA	CTTGAACTCG	GTGATGGTGT	100
	TTTAAGAACA	ATCGCCATGG	AATCTACCGA	TGGTCTTCGT	CGTGGTATGA	150
	AAGTCGAAGA	TACTGGCGCT	CCAATTTTCA	TTCCAGTTGG	AGAAGACACT	200
	TTAGGTCGTG	TGTTTAACGT	TTTAGGACAG	CCTATTGATG	GTGGTCCAGC	250
50	CTTTCCAAAG	GATCACCAC	GTGAGGGTAT	CCACAAGGAA	GCACCTAAAT	300
	ATGAAGATTT	AACTACTAGT	CGTGAAATTC	TTGAAACTGG	TATCAAGGTT	350
	ATCGACCTTC	TTGAACCATA	TGTTTCGTGGT	GGTAAAGTTG	GTTTGTTTGG	400
	TGGTGCCGGT	GTTGGTAAAA	CTACTATTAT	TCAAGAATTA	ATTCACAACA	450
	TCGCTCAAGA	ACACGGTGGT	ATTTCCGTAT	TTACTGGTGT	TGGTGAAAGA	500
55	ACTCGTGAAG	GTAATGACCT	TTACTTTGAA	ATGAAAGCTT	CAGGCGTTTT	550
	AAGTAAGACT	GCCATGGTAT	TTGGTCAGAT	GAACGAGCCG	CCTGGTGCCA	600
	GAATGCGTGT	TGCATTAACC	GGTTTGACAC	TTGCTGAATA	CTTTAGAGAT	650
	GTTGAAGGTC	AAGACGTATT	GCTCTTTATT	GACAATATCT	TTAGATTTAC	700
	TCAGGCTGGT	TCAGAGGTAT	CTGCTTTGCT	TGGTTCGTATG	CCAAGTGCCG	750
60	TAGGTTATCA	GCCAACTTTG	GCAACAGAAA	TGGGTCAATT	GCAGGAAAGA	800

ATTACTTCTA CTAAGAAGGG TTCAATTACT TCAA

5 2) INFORMATION FOR SEQ ID NO: 322

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 824 bases
 (B) TYPE: Nucleic acid
 10 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

15 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Legionella pneumophila* subsp. *pneumophila*
 (B) STRAIN: ATCC 33152

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 322

20 TTCCTCGTGA TAGCGTGCCT AAAGTCAATG ATGCGTTAAA GCTTGTGTGAT 50
 AGTGATCTGG TTTTGAAGT GCAGCAGCAA CTTGGAGACG GAGTTGTGCG 100
 TACTATTGCC ATGGGAACAA CCGATGGTTT AAAGCGAGGA TTAAAAGCAG 150
 AAAATACAGG CCATCCTATT CAAGTGCCAG TAGGTAAGAA AACTTTGGGA 200
 25 CGCATTATGG ATGTTCTTGG GCGTCTGTGA GATGATGCTG GGCCTATCGA 250
 TGCTGAAGAG ACTTGGGCTA TTCATCGTAA AGCACCAAGT TATGAAGAGC 300
 AAGCTGGCAG CCAGGAATTA TTGGAAACTG GTATTAAAGT AATTGATTTG 350
 CTTTGCCCTT TTGCCAAGGG AGGTAAAGTT GGTCTATTCG GTGGTGCCGG 400
 TGTAGGCAA ACCGTTAACA TGATGGAATT AATACGAAAC ATTGCAATTG 450
 30 AGCATAGCGG TTATTCAGTG TTTGCAGGGG TTGGTGAACG TACCCGTGAA 500
 GGAAACGACT TCTATCATGA GATGAAAGAC TCTAATGTAT TGGATAAAGT 550
 ATCGCTTGTT TATGGTCAGA TGAATGAGCC GCCAGGAAAC CGTTTGCGTG 600
 TTGCTCTAAC CGGTTTGAAT ATGGCTGAAA AATTCGCGGA TGAAGGGCGA 650
 GACGTTCTTT TGTTTATCGA TAATATTTAT CGTTATACCT TGGCTGGGGT 700
 35 TGAAGTATCT GCGCTGTAG GCCGTATGCC TTCTGCAGTA GGATATCAGC 750
 CGACATTAGC AGAGGAAATG GGTATGCTGC AAGAGCGCAT TACCTCCACA 800
 AAAACAGGTT CTATTACTTC CATA 824

40

2) INFORMATION FOR SEQ ID NO: 323

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 818 bases
 45 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

50

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Leminorella grimontii*
 (B) STRAIN: ATCC 33999

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 323

GACGCCGTAC CGAAAGTGTA CGATGCGCTT GAAGTTCAAA TTGATGCCAA 50
 GCTGGTTCTG GAAGTTCAAC AGCAGCTCGG CGGCGGCGTT GTTCGCTGCA 100
 TCGCGATGGG TACTTCAGAC GGCTTAAGCC GCGGTCTGGA CGTGCTCGAT 150
 60 CTGGAACACC CGATTGAAGT ACCGGTGGGG AAAGCGACGC TGGGCCGCAT 200

	CATGAACGTG	CTTGGTCACC	CTATCGACAT	GAAGGGCGAC	ATCGGCGAAG	250
	AAGAGCGTTG	GGCTATTAC	CGCGCAGCGC	CGAGCTACGA	AGACCTGTCTG	300
	GGCGCAACCG	AGCTGCTGGA	GACCGGCATC	AAGGTTATCG	ACCTGATTTG	350
	TCCGTTCGCC	AAGGGCGGTA	AAGTCGGCCT	GTTTCGGCGGC	GCCGGCGTAG	400
5	GTAAAACCGT	AAACATGATG	GAGCTCATTC	GCAACATTGC	GACCGAGCAC	450
	TCCGGTTACT	CCGTGTTTGC	AGGCGTAGGT	GAACGTACCC	GTGAGGGTAA	500
	CGACTTCTAC	CACGAAATGA	CTGAATCCAA	CGTATTGGAC	AAGGTGTCTGC	550
	TGGTATACGG	TCAGATGAAC	GAGCCGCTG	GAAACCGTCT	GCGCGTAGCG	600
	TTAACGGGCT	TGACCATGGC	GGAGAAGTTC	CGTGATGAAG	GCCGTGACGT	650
10	TCTGCTGTTT	ATCGACAACA	TTTACCGCTA	TACCCTGGCC	GGTACGGAAG	700
	TATCCGCACT	GCTGGGCCGT	ATGCCTTCAG	CCGTAGGCTA	CCAGCCGACT	750
	CTGGCTGAGG	AAATGGGCGT	GCTTCAAGAG	CGTATTACCT	CTACCAAGAC	800
	GGGGTCTATC	ACCTCCGT				818

15

2) INFORMATION FOR SEQ ID NO: 324

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 835 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

- 25 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Listeria monocytogenes*

- 30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 324

	GTGGAACTT	ACCTGAAATC	TACAATGCCC	TAGTTATTGA	ATATAAATCT	50
	GATGCAGAAG	AAGCACCAAC	TAGCCAACCT	ACTTTAGAAG	TAGCCATCCA	100
	ATTAGGTGAT	GATGTTGTAC	GTACAATCGC	AATGGCATCA	ACAGATGGTG	150
35	TTCAAAGAGG	TATGGAAGTT	ATTGATACTG	GGAGCCCAAT	TACAGTTCCT	200
	GTAGGTACAG	TAACCTCTGG	TCGTGTATTT	AATGTATTAG	GAAACACCAT	250
	CGATTTGGAC	GAACCACTTC	CAAGCGATAT	TAAACGTAAT	AAAATTCACC	300
	GCGAAGCTCC	AACTTTCGAT	CAATTAGCAA	CGACAACAGA	AATTCTTGAA	350
	ACAGGAATTA	AAGTAGTTGA	CTTGCTAGCT	CCTTACTTAA	AAGGTGGTAA	400
40	AATCGGATTG	TTCGGTGTTG	CCGGTGTTGG	TAAAACCGTT	CTAATTCAAG	450
	AGCTTATCCA	TAATATCGCA	CAAGAACATG	GTGGTATTTT	TGTGTTTCGT	500
	GGCGTTGGAG	AACGTACTCG	TGAAGGTAAC	GACCTTTACT	TCGAAATGAA	550
	AGATTCAGGC	GTTATTGAAA	AAACAGCGAT	GGTATTCGGT	CAAAATGAACG	600
	AGCCACCAGG	TGCGCGTATG	CGTGTTGCCT	TAACCTGGTCT	AACAATTGCT	650
45	GAATATTTCC	GTGATGAAGA	ACATCAAGAT	GTACTTTTAT	TCATTGATAA	700
	CATTTTCCGT	TTCACACAAG	CTGGTTCAGA	GGTTTCGGCT	TTACTAGGTC	750
	GTATGCCATC	TGCGGTAGGT	TACCAACCAA	CCCTAGCTAC	TGAAATGGGT	800
	CAACTACAAG	AACGTATTAC	ATCTACTAAC	GTTGG		835

50

2) INFORMATION FOR SEQ ID NO: 325

(i) SEQUENCE CHARACTERISTICS:

- 55 (A) LENGTH: 828 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

- 60 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Micrococcus lylae*
 (B) STRAIN: ATCC 27566

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 325

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10  CCCGCGTGGC GAGTTGCCGG CACTGTTCAA CGCGCTGACT GTCGAGGTCA      50
    CCCTCGAAGC AGTCGCTAAA ACCATTACCC TTGAGGTTGC TCAGCACCTC      100
    GCGGACAACT TGGTTCGTGC CGTGTCCATG GCACCGACCG ACGGTCTCGT      150
    CCGTGGCGCT GCTGTGATCG ACAGCGGTAA GCCGATCTCA GTTCCCGTTG      200
    GTGACGTAGT CAAGGGACAC GTCTTCAACG CTCTGGGTGA TTGCCTCGAT      250
    GAGCCAGGTC TTGGCCGTGA CGGTGAGCAG TGGGGCATCC ACCGCGATCC      300
    GCCACCTTTT GACCAGCTTG AGGGTAAGAC CGAGATTCTG GAAACCGGTA      350
15  TTAAGGTCAT CGACCTGCTG ACCCCGTATG TTAAGGGCGG CAAGATCGGC      400
    CTGTTCCGTG GTGCTGGTGT GGGTAAGACC GTTCTTATCC AGGAAATGAT      450
    CACCCGTATC GCTCGCGAGT TCTCCGGTAC CTCGGTGTTC GCAGGCGTGG      500
    GTGAGCGTAC CCGTGAGGGC ACCGACCTCT TCCTGGAAAT GGAAGAGATG      550
    GGC GTTCTCC AGGACACCGC TCTTGTGTTC GGCCAGATGG ACGAGCCTCC      600
20  AGGAGTTCGT ATGCGCGTGG CGCTGTCCGG CCTGACCATG GCGGAGTACT      650
    TCCGCGATGT GCAGCACCAG GACGTGCTTC TGTTTCATCGA CAACATCTTC      700
    CGTTTACCCC AGGCAGGTTC CGAGGTTTCC ACCCTCCTAG GCCGCATGCC      750
    TTCTGCCGTG GGTTACCAGC CAACGCTGGC AGACGAGATG GGTGTTCTGC      800
    AGGAGCGTAT TACCTCCACA AAGGGTAA                                828
25

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2) INFORMATION FOR SEQ ID NO: 326

- 30 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 822 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 40 (A) ORGANISM: *Moellerella wisconsensis*
 (B) STRAIN: ATCC 35017

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 326

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45  GATGCCGTAC CAAAAGTGTA CGATGCTCTT GAGGTTCTTA ACGGTAAAGA      50
    AAAATTGGTG CTGGAAGTTC AGCAACAATT AGGCGGTGGT GTTGTTCGTT      100
    GTATCGCAAT GGGTACATCA GATGGTTTAA GCCGCGGTTT AGAAGTTAAA      150
    AATACAGATC ATCCGATCGA AGTTCCTGTC GGTGTTAAAA CGCTTGGCCG      200
    TATCATGAAC GTGCTGGGTG ACCCAATCGA CATGAAAGGT GATATCGGCG      250
    AAGAAGAACG CTGGTCAATT CACCGCGCAG CACCAAGCTA TGAAGATCTG      300
50  GCTAACTCAA CAGAACTTCT AGAAACAGGT ATCAAAGTTA TGGACCTGAT      350
    TTGCCCATTG GCTAAAGGGG GTAAAGTGGG TCTGTTCGGT GGTGCGGGTG      400
    TCGGTAAAAC AGTTAACATG ATGGAGCTTA TTCGTAATAT CGCGATTGAG      450
    CACTCAGGTT ATTCTGTATT CGCGGGTGTT GGTGAACGTA CTCGTGAAGG      500
    TAACGATTTT TACCATGAAA TGACAGACTC AAACGTTCTG GATAAAGTTT      550
    CATTGGTTTA TGGCCAGATG AATGAGCCAC CAGGAAACCG TCTGCGTGTT      600
    GCTCTGACTG GTCTGACTAT GGCAGAGAAA TTCCGTGACG AAGGTCGTGA      650
    CGTACTGTTA TTCGTAGATA ATATTTATCG TTATACCTTA GCAGGGACAG      700
    AAGTATCTGC ACTGCTGGGT CGTATGCCTT CAGCGGTGGG TTATCAGCCA      750
    ACGCTGGCGG AAGAGATGGG TGTTCTGCAA GAACGTATCA CCTCGACTAA      800
50  GACCGGCTCT ATCACTCCG TA                                822

```

2) INFORMATION FOR SEQ ID NO: 327

5

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 854 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

10

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Branhamella catarrhalis*
 (B) STRAIN: ATCC 43628

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 327

20 CCGTGGCGAT GTCCCCCAA TCTTTGATGC ACTTCATGTT GATGGTACTG 50
 AAACCACCCT TGAAGTCCAA CAACAGTTAG GTGATGGTGT GGTGCGTACC 100
 ATTGCCATGG GTTCTACCGA AGGCTTAAAG CGTGGCTTGC CTGTCTCTAA 150
 TTCAGGTGCA CCCATTTTCGG TACCAGTCGG TCAAGCAACA CTGGGTCGCA 200
 TTATGGATGT CCTAGGTCGC CCAATCGATG AAGCAGGTCC GGTAAATGCT 250
 25 GAACAAAAT GGTCCATTCA TCGTGAAGCA CCAAGTTATG ATGAACAGTC 300
 AAATAGTACA GAACTTTTAG AAACAGGCAT CAAAGTGATT GATTTGCTTT 350
 GTCCATTTGC CAAAGGTGGT AAAGTCGGTC TGTTCCGGTG TGCTGGTGTT 400
 GGTAAGACCG TTAACATGAT GGAGCTTATC AATAATATCG CCCTAAAACA 450
 CTCAGGTCTG TCGGTTTTTG CTGGTGTGGG TGAGCGTACT CGTGAGGGTA 500
 30 ATGACTTCTA CCATGAAATG CAAGAAGCAG GCGTTGTTAA TACCGAAGAT 550
 TTTACTCAGT CAAAAGTTGC CATGGTTTAT GGTCAGATGA ATGAGCCACC 600
 AGGAAACCGT CTGCGTGTG CTTAACTGG TTTGACCATG GCAGAGTATT 650
 TCCGTGATGA AAAAGACGAA GCAACGGGCA AAGGCCGTGA TGTTCTGCTG 700
 TTCGTTGATA ATATTTATCG TTACACATTG GCAGGTACTG AGGTATCAGC 750
 35 ACTTTTAGGT CGTATGCCAT CTGCGGTAGG TTATCAGCCG ACTTTGGCCG 800
 AAGAGATGGG CTTGCTACAA GAGCGTATCA CCTCCACCCA ATCAGGCTCA 850
 ATTA 854

40

2) INFORMATION FOR SEQ ID NO: 328

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 831 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

45

(ii) MOLECULE TYPE: Genomic DNA

50

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Moraxella osloensis*
 (B) STRAIN: ATCC 19976

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 328

CCGTCAAAGC GTACCAAGAA TTTATGATGC CTTAAAAGTT GAAGGCACAG 50
 AAACCTACATT AGAAGTACAA CAACAATTGG GTGATGGTAT CGTACGTACT 100
 ATTGCCATGG GTTCTACTGA AGGTCTAAAA CGTGGTCTAC CAGTTAGCAA 150
 50 CACTGGCGCA CCAATCTCTG TACCTGTGGG TAAAGGTACA CTAGGTCGTA 200

	TCATGGACGT	TTTAGGACAC	CCAATCGATG	AGGCAGGTCC	GGTAGAGCAT	250
	AGTAACACTT	GGGCGATTCA	CCGTGAAGCG	CCAAGCTATG	ATGAACAATC	300
	AAACTCTACT	GAACCTTTAG	AAACCGGTAT	TAAAGTAATT	GACTTACTAT	350
	GCCCATTTC	TAAAGGTGGT	AAAGTCGGTC	TGTTTCGGTGG	CGCGGGTGTT	400
5	GGTAAAACCG	TTAACATGAT	GGAACCTTATC	AATAACATCG	CAAAAGCACA	450
	CTCAGGTTTA	TCGGTATTTG	CTGGTGTAGG	TGAGCGTACT	CGTGAAGGTA	500
	ATGACTTCTA	CCACGAGATG	AAAGACTCAA	ACGTACTTGA	TAAAGTTGCG	550
	ATGGTGTATG	GTCAGATGAA	TGAGCCACCA	GGAAACCGTT	TACGTGTTGC	600
	CCTGACAGGT	TTAACCATGG	CAGAATACTT	CCGTGACGAA	AAAGATGAAA	650
10	ACGGTAAAGG	TCGTGACGTA	TTATTGTTTCG	TTGACAATAT	TTATCGTTAC	700
	ACGCTAGCGG	GTACCGAAGT	ATCAGCATTAA	TTAGGTCGTA	TGCCATCTGC	750
	AGTAGGGTAT	CAGCCAACGC	TTGCAGAAAG	GATGGGTGTA	CTACAAGAAC	800
	GTATTACTTC	AACCCAATCA	GGCTCTATTA	C		831

15

2) INFORMATION FOR SEQ ID NO: 329

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 835 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

25 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Morganella morganii* subsp. *morganii*
 (B) STRAIN: ATCC 25830

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 329

	CGAATTTCT	CAGGATGCAG	TACCGAAAGT	GTACGATGCG	CTTGAGGTAA	50
	CAAATGGTAA	AGAAAACTG	GTGCTGGAAG	TTCAGCAGCA	GTTAGGCGGC	100
35	GGGGTTGTCC	GTTGTATCGC	TATGGGTACA	TCTGATGGTC	TGAGCCGTAA	150
	TCTGGAAGTA	ACCGATTTAG	GCCACCCGAT	CGAAGTCCCT	GTCGGCGTGA	200
	AAACCTTAGG	ACGTATCATG	AACGTTCTGG	GTGATCCGAT	CGATATGAAA	250
	GGTGACTATCG	GCGCAGAAGA	AAAATGGTCT	ATTACCCGTG	CTGCACCAAC	300
	ATACGAAGAA	CTGTCTAACT	CCCAGGAAGT	GCTGGAAACA	GGTATCAAAG	350
40	TAATGGACCT	GATCTGCCCG	TTCGCGAAGG	GTGGTAAAGT	CGGTCTGTTC	400
	GGTGGTGCGG	GTGTGGGTAA	AACCGTAAAC	ATGATGGAAC	TGATCCGTAA	450
	CATCGCGATC	GAGCACTCCG	GTTACTCTGT	ATTGCGAGGG	GTCGGTGAGC	500
	GTACCCGTGA	AGGTAACGAC	TTCTATCATG	AAATGACAGA	CTCCAACGTT	550
	CTGGACAAAG	TATCACTCGT	GTACGGCCAG	ATGAACGAGC	CACCGGGAAA	600
45	CCGTCTGCGC	GTTGCTCTGA	CCGGTCTGAC	CATGGCGGAA	AAATTCCGTG	650
	ATGAAGGCCG	CGATGTACTG	CTGTTTCGTTG	ATAACATCTA	CCGTTATAAC	700
	CTGGCCGGTA	CTGAAGTATC	CGCGCTGTGA	GGCCGTATGC	CTTCAGCGGT	750
	AGGTTACCAG	CCGACACTGG	CGGAAGAAAT	GGGTGTGCTT	CAGGAACGTA	800
50	TCACATCGAC	CAAAACAGGC	TCTATCACGT	CTGTA		835

2) INFORMATION FOR SEQ ID NO: 330

(i) SEQUENCE CHARACTERISTICS:

- 55 (A) LENGTH: 824 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Pantoea agglomerans*
 5 (B) STRAIN: ATCC 27155

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 330

	GACGCGGTAC	CGCAAGTGTA	CAGCGCCCTC	GAGGTTATGA	ATGGTGATGC	50
10	GCGTCTGGTG	CTGGAAGTTC	AGCAGCAGCT	CGGCGGCGGC	GTAGTACGTA	100
	CCATCGCAAT	GGGTACGTCT	GACGGCCTGA	AGCGTGGTCT	GAGCGTCAAC	150
	GACCTGCAGA	AACCGATTCA	GGTACCCGTC	GGTAAAGCGA	CCCTGGGCCG	200
	TATCATGAAC	GTTCTCGGCG	AGCCAATCGA	TATGAAAGGC	GAGCTGAAAG	250
	AAGAAGATGG	CAGCGCAGTA	GAGATCGCCT	CTATTCACCG	CGCAGCCCCT	300
15	TCTTATGAAG	ATCAGTCTAA	CTCGCAGGAA	CTGCTGGAAA	CCGGCATCAA	350
	GGTTATCGAC	CTGATGTGTC	CGTTTGCTAA	AGGCGGTAAA	GTCGGTCTGT	400
	TCGGTGGTGC	GGGTGTAGGT	AAAACCGTCA	ACATGATGGA	ACTGATCCGT	450
	AACATCGCGG	CTGAACACTC	AGGTTACTCA	GTGTTTGCCG	GTGTGGGTGA	500
	GCGTACTCGT	GAGGGTAACG	ACTTCTACCA	CGAAATGACT	GACTCTAACG	550
20	TTATCGATAA	AGTTGCACTG	GTCTATGGCC	AGATGAACGA	GCCGCCGGGT	600
	AACCGTCTGC	GCGTAGCACT	GACCGGTCTG	ACCATGGCGG	AAAAATTCCG	650
	TGATGAAGGT	CGCGACGTTC	TGCTGTTCAT	CGATAACATC	TACCGTTATA	700
	CCCTGGCCCG	TACAGAAGTT	TCTGCACTGC	TGGGTCGTAT	GCCATCTGCG	750
	GTAGGTTACC	AGCCAACGCT	GGCAGAAGAG	ATGGGTGTGT	TGCAGGAGCG	800
25	TATTACCTCC	ACCAAGACCG	GTTC			824

2) INFORMATION FOR SEQ ID NO: 331

30

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 808 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 35 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 40 (A) ORGANISM: *Pantoea dispersa*
 (B) STRAIN: ATCC 14589

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 331

45	TATACAGCGC	TCTCGAGGTA	AAAAATGGTG	ATGCTCGTCT	GGTGCTGGAA	50
	GTACAGCAGC	AGCTGGGCGG	TGGCGTGGTG	CGTACCATCG	CCATGGGTTC	100
	TTCTGACGGC	CTGAAGCGCG	GTCTGGAAGT	CACCGACCTG	AAAAAACCTA	150
	TCCAGGTTCC	GGTTGGTAAA	GCAACACTCG	GCCGTATCAT	GAACGTGCTG	200
	GGTGAGCCAA	TCGACATGAA	AGGCGACCTG	AAAGAAGAAG	ACGGCAGCGC	250
50	TGTAGAGGTT	TCCTCTATTC	ATCGCGCAGC	GCCTTCTTAT	GAAGATCAGT	300
	CAAACCTCGA	GGAACCTGCTG	GAAACCGGCA	TCAAGGTTAT	CGACCTGATG	350
	TGTCCGTTCC	CGAAGGGCGG	TAAAGTCGGT	CTGTTCCGGT	GTGCGGGTGT	400
	AGGTAAACC	GTAAACATGA	TGGAGCTGAT	CCGTAACATC	GCGGCTGAGC	450
	ACTCAGGTTA	TTCGGTCTTT	GCCGGCGTGG	GTGAGCGTAC	TCGTGAGGGT	500
55	AACGACTTCT	ACCACGAAAT	GACGGACTCC	AACGTTATCG	ATAAAGTAGC	550
	GCTGGTGTAT	GGCCAGATGA	ACGAGCCGCC	GGGTAACCGT	CTGCGCGTAG	600
	CACTGACCGG	TCTGACCATG	GCGGAAAAAT	TCCGTGATGA	AGGCCGTGAC	650
	GTTCTGCTGT	TCATCGACAA	CATCTACCGT	TACACCCTGG	CCGGTACAGA	700
	GGTTTCTGCA	CTGCTGGGTC	GTATGCCATC	GGCGGTAGGT	TATCAGCCAA	750
60	CGCTGGCTGA	AGAGATGGGT	GTGCTGCAGG	AGCGTATTAC	CTCCACCAAG	800

5 2) INFORMATION FOR SEQ ID NO: 332

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 805 bases
(B) TYPE: Nucleic acid
10 (C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

15 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Pasteurella multocida*
(B) STRAIN: NCTC 10322

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 332

20 GATGCAGTAC CAAAAGTATA TGATGCCTTA AATGTTGAAA CAGGTTTAGT 50
ACTTGAAGTT CAACAACAAT TAGGTGGTGG TGTAGTTCGC TGTATCGCAA 100
TGGGATCATC TGATGGATTA AAACGCGGTT TAAGCGTAAC AAATACGAAT 150
AACCCAATTT CTGTTCCAGT GGGAAACGAAA ACATTGGGTC GTATCATGAA 200
25 CGTATTGGGT GAACCAATCG ATGAGCAAGG TGAAATCGGT GCAGAAGAGA 250
ATTGGTCTAT TCACCGTGC GACCAAGTT ATGAAGAACA ATCTAACAGT 300
ACTGAACTTT TAGAAACGGG AATTAAAGTT ATCGACTTAG TTTGTCCGTT 350
TGCAGAAAGGG GGTAAAGTAG GTTTATTCCG TGGTGCAGGT GTCGGTAAAA 400
CCGTCAATAT GATGGAATTA ATCCGTAACA TCGCAATTGA GCACTCAGGT 450
30 TACTCTGTCT TTGCGGGGGT AGGTGAGCGT ACGCGTGAAG GTAACGACTT 500
CTATCATGAG ATGAAAGACT CTAACGTATT AGATAAAGTG TCTCTTGTTT 550
ATGGTCAAAT GAACGAGCCA CCAGGTAACC GTTTACGTGT GGCATTAACA 600
GGCTTAAC TAAGCGGAAA ATTCCGTGAT GAAGGTCGTG ATGTCTTATT 650
CTTCGTTGAT AATATTTATC GTTATACTCT TGCTGGTACA GAAGTTTCTG 700
35 CATTATTAGG TCGTATGCCA TCTGCGGTAG GTTATCAACC AACCTTGCA 750
GAAGAAATGG GTGTTCTGCA AGAGCGTATT ACCTCAACCA AACAGGTTT 800
TATTA 805

10 2) INFORMATION FOR SEQ ID NO: 333

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 828 bases
15 (B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

50 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Pragia fontium*
(B) STRAIN: ATCC 49100

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 333

TTTCCTCAAG ACGCCGTACC AAAAGTGTAC GACGCGCTTG AAGTTCAGAA 50
CGATGCCAAG CTGGTGCTGG AAGTTCAACA ACAGCTCGGT GGTGGTGTGC 100
TTCGTTGTAT CGCAATGGGT ACTTCCGATG GCTTAAGCCG CGGTTTAAAA 150
50 GTGCTTGATT TAGAACATCC TATCGAAGTA CCGGTTGGTA CTGCGACGCT 200

	GGGCCGTATT	ATGAACGTGC	TCGGTCAGCC	AATCGATATG	AAAGGCGATA	250
	TTGGTGAAGA	AGAGCGTTGG	GCTATTCACC	GTGAAGCACC	AAGTTATGAA	300
	GATTTATCTG	GCGCCAATGA	ACTGCTGGAA	ACGGGTATCA	AGGTTATCGA	350
	CCTGATTTGT	CCGTTTGCTA	AAGGTGGTAA	AGTTGGTCTG	TTTGGTGGTG	400
5	CGGGTGTAGG	TAAAACCGTA	AACATGATGG	AGCTGATTCG	TAACATTGCG	450
	ACTGAGCACT	CAGGTTACTC	CGTATTCGCC	GGTGTAGGGG	AACGTACCCG	500
	TGAAGGTAAT	GACTTCTACC	ACGAAATGAC	CGAATCAAAC	GTACTGGATA	550
	AAGTATCTCT	GGTTTATGGC	CAGATGAACG	AGCCACCAGG	AAACCGTCTG	600
	CGCGTGGCGT	TAACGGGTTT	GACCATGGCT	GAAAAATTCC	GTGATGAAGG	650
10	TCGTGACGTT	CTGTTATTTA	TCGATAACAT	TTATCGCTAT	ACCTTAGCCG	700
	GTACCGAAGT	ATCAGCACTG	TTGGGGCGTA	TGCCATCAGC	GGTAGGTTAT	750
	CAGCCAACGT	TAGCAGAAGA	GATGGGTGTG	TTGCAGGAAC	GTATTACTTC	800
	AACCAAAACC	GGTTCAATCA	CTTCTGTA			828

15

2) INFORMATION FOR SEQ ID NO: 334

- (i) SEQUENCE CHARACTERISTICS:
- 20 (A) LENGTH: 807 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

- 25 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Proteus mirabilis*
- (B) STRAIN: ATCC 25933

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 334

	GTCCCTAAAG	TATACGACGC	TCTTGAGGTT	ATGAATGGTA	AAGAAAAACT	50
	GGTGCTGGAA	GTTCAAGCAAC	AGTTAGGCGG	TGGTATCGTT	CGTTGTATCG	100
35	CAATGGGTAC	ATCAGACGGT	TTAAGCCGTG	GCTTAAAGGT	TGAAGATTTA	150
	GGCCACCCAA	TTGAAGTACC	AGTAGGTAAA	GCGACTTTAG	GACGTATCAT	200
	GAACGTTCTG	GGTACACCTA	TTGATATGAA	AGGTGAGATT	GAAACCGAAG	250
	AGCGTTGGTC	AATCCACCGT	GAAGACCAA	CTTACGAAGA	GTTATCAAAC	300
	TCTCAAGAAC	TGCTTGAAAC	CGGTATCAAA	GTTATGGACT	TAATCTGTCC	350
40	ATTTGCTAAA	GGTGGTAAAG	TCGGTCTGTT	CGGTGGTGCG	GGTGTGGTA	400
	AAACAGTTAA	CATGATGGAA	TTGATCCGTA	ATATCGCGAT	CGAGCACTCA	450
	GTTTACTCTG	TATTTGCTGG	TGTTGGTGAG	CGTACTCGTG	AGGGTAACGA	500
	CTTCTATCAT	GAAATGACAG	ATTCTAACGT	TCTTGACAAA	GTATCGTTAG	550
	TTTACGGTCA	GATGAATGAG	CCACCAGGAA	ACCGTCTGCG	TGTTGCACTG	600
45	ACTGGTCTGA	CTATGGCTGA	GAAATTCCGT	GATGAAGGCC	GTGACGTACT	650
	GTTATTCGTC	GATAACATCT	ATCGTTACAC	CTTAGCCGGT	ACAGAAGTAT	700
	CAGCACTGTT	AGGTCGTATG	CCATCAGCGG	TAGGTTACCA	ACCAACATTG	750
	GCTGAAGAGA	TGGGTGTTCT	GCAAGAGCGT	ATCACTTCAA	CCAAAACAGG	800
	TTCTATC					807

50

2) INFORMATION FOR SEQ ID NO: 335

- 55 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 811 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Proteus vulgaris*
 5 (B) STRAIN: ATCC 13315

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 335

	CCCTAAAGTA	TACGACGCTC	TTGAGGTTAT	GAATGGTAAA	GAGAAACTGG	50
10	TGCTAGAAGT	TCAGCAACAG	TTAGGCGGTG	GTATCGTTCG	TTGTATCGCA	100
	ATGGGTACAT	CAGACGGTTT	AAGCCGTGGC	TTAAAAGTTG	AAAACCTAGG	150
	CCACCCAATT	GAAGTACCAG	TAGGTAAAGC	AACACTGGGA	CGTATCATGA	200
	ACGTTCTGGG	TACACCTATC	GATATGAAAG	GTGATATTGC	AACTGAAGAA	250
	CGTTGGTCTA	TTCACCGCGA	AGCGCCAACC	TATGAAGAGT	TATCAAGCTC	300
15	TCAAGAACTA	CTAGAAACCG	GTATCAAAGT	AATGGACTTA	ATCTGTCCGT	350
	TTGCTAAAGG	TGGTAAAGTA	GGTCTCTTCG	GTGGTGCGGG	TGTTGGTAAA	400
	ACAGTTAACA	TGATGGAATT	GATCCGTAAC	ATCGCGATTG	AGCACTCAGG	450
	TTATTCTGTA	TTTGCAGGTG	TTGGTGAGCG	TACTCGTGAG	GGTAACGACT	500
	TCTATCATGA	AATGACAGAT	TCTAACGTTC	TTGACAAAGT	ATCGTTAGTT	550
20	TATGGTCAGA	TGAATGAGCC	ACCAGGAAAC	CGTCTACGTG	TAGCACTGAC	600
	GGGTTTAAAC	ATGGCGGAAA	AATTCCGTGA	TGAAGGCCGT	GACGTACTGT	650
	TATTCGTCGA	TAACATCTAT	CGTTACACCT	TAGCCGGTAC	CGAAGTATCA	700
	GCACTGTTAG	GCCGTATGCC	ATCAGCAGTA	GGTTACCAAC	CAACATTGGC	750
	TGAAGAGATG	GGTGTCTGTC	AAGAACGTAT	CACTTCAACC	AAAACAGGTT	800
25	CAATCACCTC	T				811

2) INFORMATION FOR SEQ ID NO: 336

30

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 806 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 35 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 40 (A) ORGANISM: *Providencia alcalifaciens*
 (B) STRAIN: ATCC 9886

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 336

45	TCAAGATAAC	GTACCAAAAG	TGTACGATGC	TCTTGAGGTT	ATTAACGGTA	50
	AAGAAAAACT	GGTGTTGGAA	GTTCAACAAC	AGTTAGGTGG	TGGTGTGTGC	100
	CGTTGTATCG	CAATGGGTAC	ATCAGATGGT	CTGAGCCGTG	GTTTAGAAGT	150
	TGTAAACTTA	GAGCACCCAA	TCGAAGTACC	AGTCGGTAAA	GCAACTCTGG	200
	GACGTATCAT	GAACGTTCTG	GGTGAACCAA	TCGACATGAA	AGGTGATATC	250
50	GGCGAAGAAG	AGCGCTGGTC	TATTCACCGT	GCTGCACCAA	GCTACGAAGA	300
	ATTAGCTAAC	TCAACTGAAC	TGCTGGAAAC	CGGTATCAAA	GTAATGGACT	350
	TAATCTGTCC	ATTGCGGAAA	GGTGGTAAAG	TAGGTCTGTT	CGGTGGTGCG	400
	GGTGTTGGTA	AAACCGTAAA	CATGATGGAA	CTGATCCGTA	ACATCGCGAT	450
	TGAGCACTCA	GGTTACTCAG	TGTTGCTGCTG	TGTTGGTGAG	CGTACCCGTG	500
55	AAGGTAACGA	CTTCTATCAT	GAAATGACAG	ACTCAAACGT	TCTGGATAAA	550
	GTATCACTGG	TTTATGGCCA	GATGAACGAG	CCACCAGGAA	ACCGTCTGCG	600
	TGTTGCGCTG	ACTGGTCTGA	CTATGGCTGA	AAAATTCCGT	GACGAAGGTC	650
	GTGACGTAAT	GCTGTTCTGT	GACAACATTT	ATCGTTATAC	ACTGGCAGGT	700
	ACTGAAGTAT	CAGCACTGTT	AGGTCGTATG	CCATCAGCGG	TAGGTTACCA	750
60	ACCAACGCTG	GCGGAAGAGA	TGGGTGTTCT	TCAAGAACGT	ATTACCTCAA	800

CTCAAA

5 2) INFORMATION FOR SEQ ID NO: 337

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 830 bases
 (B) TYPE: Nucleic acid
 10 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

15 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Providencia rettgeri*
 (B) STRAIN: ATCC 9250

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 337

20 TTCCCTCAAG ATGACGTACC AAAAGTGTAC GACGCTCTTG AGGTTGTTAA 50
 CGGTAAAGAA ACACCTGGTGC TGGAAGTTCA GCAACAGTTA GGCGGTGGTG 100
 TTGTCCGTTG TATCGCAATG GGTACATCAG ATGGCCTGAG CCGTGGTTTA 150
 GAAGTTGTAA ACTTAGAGCA CCCAATTGAA GTACCAGTAG GTAAAGCAAC 200
 25 TTTAGGACGT ATCATGAACG TTCTGGGTCA GCCTATTGAT ATGAAAGGTG 250
 ATATCGGCGA AGAAGAGCGC TGGTCAATTC ACCGTGCTGC ACCTAGCTAC 300
 GAAGAGTTAG CTAACCTAAC AGAGCTGCTG GAAACCGGTA TCAAAGTAAT 350
 GGACTTAATC TGTCCATTTC CGAAAGGTGG TAAAGTTGGT CTGTTTCGGTG 400
 GTGCGGGTGT TGGTAAACA GTAAACATGA TGGAAGTATG CCGTAACATC 450
 30 GCGATTGAGC ACTCAGGTTA CTCAGTATTC GCTGGTGTG GTGAGCGTAC 500
 TCGTGAAGGG AACGACTTCT ATCATGAAAT GACTGACTCA AACGTTCTGG 550
 ATAAAGTATC ACTGGTTTAT GGCCAGATGA ATGAGCCACC AGGAAACCGT 600
 CTGCGCGTTG CGTTGACTGG TCTGACTATG GCTGAAAAAT TCCGTGACGA 650
 AGGTCGTGAC GTACTACTGT TCGTTGACAA CATCTATCGT TATACTACTG 700
 35 CAGGTACTGA AGTATCAGCA CTGTTAGGTC GTATGCCTTC AGCGGTAGGT 750
 TATCAGCCAA CGCTGGCGGA AGAGATGGGT GTTCTGCAAG AACGTATTAC 800
 CTCAACTCAA ACGGGTTCTA TCACTTCCGT 830

10 2) INFORMATION FOR SEQ ID NO: 338

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 812 bases
 15 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

50 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Providencia rustigianii*
 (B) STRAIN: ATCC 33673

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 338

AGCGTACCAA AAGTGTACGA TGCTCTTGAG GTTATTAACG GTAAAGAAAA 50
 ACTGGTGTG GAAGTTCAGC AGCAGTTAGG CGGTGGTGTT GTCCGTTGTA 100
 TCGCAATGGG TACATCAGAT GGTCTGAGCC GTGGTTTAGA AGTTGTAAAC 150
 50 TTAGAACACC CAATTGAAGT ACCAGTAGGT AAAGCAACTC TGGGACGTAT 200

	CATGAACGTT	CTGGGTGACC	CTATTGATAT	GAAAGGTGAT	ATCGGCGAAG	250
	AAGAGCGCTG	GTCTATTCAC	CGTTCAGCGC	CAAGCTATGA	AGAATTAGCT	300
	AACTCAACAG	AACTGCTAGA	AACCGGTATC	AAAGTAATGG	ACTTAATCTG	350
	TCCATTCGCG	AAAGGTGGTA	AAGTTGGTCT	GTTTCGGTGGT	GCGGGTGTTC	400
5	GTAAAACAGT	AAACATGATG	GAAGTATGCC	GTAACATCGC	GATTGAGCAC	450
	TCAGGTTACT	CAGTATTCGC	TGGTGTGGT	GAGCGTACCC	GTGAAGGTAA	500
	CGACTTCTAT	CATGAAATGA	CTGATTCTAA	CGTTCTGGAT	AAAGTATCAC	550
	TGGTTTATGG	CCAGATGAAC	GAGCCACCAG	GAAACCGTCT	GCGTGTTCGC	600
	CTGACTGGTC	TGACTATGGC	TGAAAAATTC	CGTGACGAAG	GTCGTGACGT	650
10	ACTGCTGTTC	GTTGACAACA	TTTATCGTTA	TACACTGGCA	GGTACTGAAG	700
	TATCAGCACT	GTTAGGTCGT	ATGCCTTCAG	CGGTAGGTTA	TCAGCCAACA	750
	TTGGCAGAAG	AGATGGGTGT	TCTACAAGAA	CGTATCACTT	CTACCAAAAC	800
	CGTTTCTATC	AC				812

15

2) INFORMATION FOR SEQ ID NO: 339

- (i) SEQUENCE CHARACTERISTICS:
- 20 (A) LENGTH: 819 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

- 25 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Providencia stuartii*
- (B) STRAIN: ATCC 33672

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 339

	TCAAGATGCA	GTACCAAAAG	TGTACGATGC	GCTTGAGGTT	GTTAACGGTA	50
	AAGAAAAACT	GGTGCTGGAA	GTTTCAGCAAC	AGTTAGGCGG	TGGTGTTC	100
35	CGTTGTATCG	CAATGGGTAC	ATCAGATGGC	CTAAGCCGTG	GTTTAGAAGT	150
	TAAAAATTTA	GAACACCCAA	TTGAAGTACC	AGTAGGTAAA	GCAACACTCG	200
	GACGTATCAT	GAACGTTCTG	GGTGACCCTA	TTGATATGAA	AGGTGATATC	250
	GGCGAAGAAG	AGCGTTGGTC	TATTCACCGC	GCTGCACCAA	GCTACGAAGA	300
	GCTATCGAGC	TCAACTGAAC	TGCTAGAGAC	AGGTATCAAA	GTCATGGACT	350
40	TGATCTGTCC	ATTCGCGAAA	GGTGTTAAAG	TTGGTCTGTT	CGGTGGTGCG	400
	GGTGTTGGTA	AAACGGTAAA	CATGATGGAA	CTTATCCGTA	ACATCGCGAT	450
	TGAGCACTCA	GGTTACTCAG	TATTCGCAGG	TGTTGGTGAG	CGTACCCGTG	500
	AAGGTAACGA	CTTCTATCAT	GAAATGACAG	ATTCAAACGT	TCTTGACAAA	550
	GTATCACTGG	TTTATGGTCA	GATGAATGAG	CCACCAGGAA	ACCGTCTACG	600
45	CGTAGCATTG	ACTGGTTTGA	CTATGGCTGA	GAAATTCCGT	GACGAAGGCC	650
	GTGATGTTCT	GTTGTTCGTG	GATAACATCT	ATCGTTATAC	ACTGGCAGGT	700
	ACAGAAGTAT	CGGCTCTGTT	AGGTCGTATG	CCATCAGCAG	TAGGTTATCA	750
	GCCAACATTG	GCAGAAGAGA	TGGGTGTTCT	TCAAGAACGT	ATCACTTCTA	800
50	CTAAGACAGG	TTCTATCAC				819

2) INFORMATION FOR SEQ ID NO: 340

- 35 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 907 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- 50 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Psychrobacter phenylpyruvicus*
 5 (B) STRAIN: ATCC 23333

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 340

10	AACCGCACTG	ACGTGCCTCA	AATTTATGAC	GCGTTAGTTG	TAGATGGTAC	50
	CGAAACCACC	CTAGAAGTTC	AGCAGCAGCT	GGGCGATGGT	GTGGTACGTA	100
	CTATTGCAAT	GGGATCTACT	GAAGGTCTTA	AGCGTGGTTT	ACCAGTAACA	150
	AACACTGGTG	CCCCAATTAC	AGTTCCAGTA	GGTGATGCGA	CTTTAGGTCTG	200
	TATTATGGAC	GTTTTAGGTC	GTCCAATTGA	CGAACAAGGT	CCAGTTAATT	250
	CTGAAGACCA	TTGGTCAATC	CACCGTCAAG	CGCCATCATA	TGATGAGCAA	300
15	GCTAACAGTA	CTGACCTATT	AGAGACAGGT	ATTAAAGTAA	TTGACTTACT	350
	TTGTCCGTTT	GCTAAAGGGG	GTAAAGTTGG	TCTGTTCGGT	GGTGCCCGTG	400
	TTGGTAAAAC	CGTAAACATG	ATGGAATTGA	TTAATAACAT	CGCTCTTAAG	450
	CACTCAGGTT	TATCAGTATT	CGCTGGTGTG	GGTGAGCGTA	CTCGTGAAGG	500
	TAACGACTTC	TACCACGAGA	TGCAAGAAGC	GGGTGTTGTT	GACGTTGAAA	550
20	ACTTCACCAA	CTCAAAAGTT	GCGATGGTTT	ATGGTCAGAT	GAATGAGCCA	600
	CCAGGTAACC	GTTTACGTGT	TGCGTTAACC	GGTCTGACTA	TGGCTGAGTA	650
	CTTCCGTGAT	CAAAAAGATG	AAAACGGTAA	AGGTAAAGAC	GTTCTATTAT	700
	TCGTTGATAA	CATCTACCGC	TACACGCTAG	CCGGTACTGA	AGTATCAGCA	750
	CTTCTAGGTC	GTATGCCATC	AGCAGTAGGT	TATCAGCCAA	CACTAGCGGA	800
25	AGAGATGGGT	GTACTACAAG	AGCGTATTAC	TTCAACTCAG	ACTGGTTCTA	850
	TTACTTC					907

30 2) INFORMATION FOR SEQ ID NO: 341

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 832 bases
 (B) TYPE: Nucleic acid
 35 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

40 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Rahnella aquatilis*
 (B) STRAIN: DSM 4594

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 341

45	GTTCCCTCAG	GATGCAGTAC	CGAACGTGTA	CAATGCTCTT	GAGGTAGAAA	50
	ACGGTACCTC	CAAACCTGGT	CTGGAAGTTC	AGCAACAGTT	AGGCGGCGGC	100
	GTTGTTCGTT	GTATCGCAAT	GGGTACCTCA	GACGGCCTGC	GTCGCGGTCT	150
	GAAAGTGAAC	AACCTGGAAC	ACCCAATTGA	AGTACCGGTA	GGTAAAGCGA	200
50	CTCTGGGTCG	TATCATGAAC	GTATTGGGTG	AACCAATCGA	CATGAAAGGT	250
	GAAATCGGCG	AAGAAGAACG	TCGTGCTATT	CACCGTGCTG	CGCCTTCTTA	300
	TGAAGAGCTG	GCAAACCTCC	AGGAATTGCT	GGAACCGGT	ATCAAAGTTA	350
	TGGACCTGAT	GTGTCCGTTT	GCTAAGGGCG	GTAAAGTTGG	TCTGTTCGGT	400
	GGTGCGGGTG	TAGGTAAAAC	TGTGAACATG	ATGGAGCTGA	TCCGTAACAT	450
55	TGCGATCGAG	CACTCCGGTT	ATTCTGTGTT	TGCAGGCGTG	GGTGAACGTA	500
	CTCGTGAGGG	TAACGACTTC	TACCACGAAA	TGACTGATTG	CAACGTTATC	550
	GACAAAGTTT	CCCTGGTGTA	TGGCCAGATG	AATGAGCCAC	CAGGTAACCG	600
	TCTGCGCGTT	GCACTGACCG	GCCTGACCAT	GGCGGAAAAA	TTCCGTGATG	650
	AAGGTCGTGA	CGTACTGCTG	TTCGTTGACA	ACATTTACCG	TTACACCCCTG	700
60	GCCGGTACCG	AAGTGTCCGC	ACTTCTGGGC	CGTATGCCAT	CGGCGGTAGG	750

TTATCAGCCA ACGCTGGCGG AAGAGATGGG CGCTCTGCAA GAACGTATCA' 800
CCTCGACCAA AAGTGGTTCT ATCACCTCCG TA 832

5

2) INFORMATION FOR SEQ ID NO: 342

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 824 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

15

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Salmonella choleraesuis* subsp. *arizonae*
(B) STRAIN: ATCC 13314

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 342

TTCCCTCAGG ATGCCGTACC ACGCGTGATG GATGCTCTTG AGGTGCAGAA 50
TGGTAATGAG AAGCTGGTGC TGGAAGTTCA GCAGCAGCTT GCGGCGGGTA 100
TCGTGCGTAC CATCGCGATG GGGTCTTCTG ACGGTCTGCG TCGCGGTCTT 150
25 GATGTAAAAG ATCTCGAACA CCCGATCGAA GTCCCGGTAG GTAAAGCCAC 200
GCTGGGTCGT ATCATGAACG TCCTGGGCGA ACCGGTCGAT ATGAAAGGCG 250
AGATCGGCGA AGAAGAGCGT TGGGCTATTC ACCGCGCGGC GCCGTCTTAC 300
GAAGAGTTGT CAAACTCTCA GGAAGTCTG GAAACCGGTA TAAAAGTTAT 350
CGACCTGATG TGTCCGTTCT CGAAGGGCGG TAAAGTCGGT CTGTTCCGGTG 400
30 GCGCGGGTGT AGGTAAAACC GTAAACATGA TGGAGCTTAT CCGTAACATC 450
GCGATCGAGC ACTCCGGTTA CTCTGTGTTT GCGGGCGTAG GTGAACGTAC 500
TCGTGAGGGT AACGACTTCT ACCACGAAAT GACCGACTCT AACGTTATCG 550
ATAAAGTATC CCTGGTGTAT GGCCAGATGA ACGAGCCACC GGGAAACCGT 600
CTGCGCGTTG CATTGACCGG CCTGACCATG GCGGAAAAAT TCCGTGATGA 650
35 AGGTCGTGAC GTTCTGCTGT TCGTCGACAA CATCTACCGT TATACCCTCG 700
CCGGTACGGA AGTATCCGCA CTGCTGGGTC GTATGCCTTC CGCGGTAGGT 750
TAYCASC CGA CTCTGGCGGA AGAGATGGG GTTCTGCAGG AACGTATCAC 800
CTCCACCAA ACCGGTTCTA TCAC 824

40

2) INFORMATION FOR SEQ ID NO: 343

(i) SEQUENCE CHARACTERISTICS:

- 45 (A) LENGTH: 820 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

50

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Salmonella choleraesuis* subsp. *choleraesuis*
serotype *Choleraesuis*
55 (B) STRAIN: ATCC 7001

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 343

60 GATGCCGTAC CACGCGTGTA CGATGCCCTT GAGGTGCAGA ATGGTAATGA 50
GAAGCTGGTG CTGGAAGTTC AGCAGCAGCT TGGCGGCGGT ATCGTGCGTA 100

	CCATCGCGAT	GGGGTCTTCT	GACGGTCTGC	GTCGCGGTCT	GGATGTAAAA	150
	GATCTCGAAC	ACCCGATCGA	AGTCCCGGTA	GGTAAAGCCA	CGCTGGGTCTG	200
	TATCATGAAC	GTCCTGGGCG	AACCGGTCGA	CATGAAAGGC	GAGATCGGCG	250
	AAGAAGAGCG	TTGGGCGATT	CACCGCGCAG	CACCTTCCTA	CGAAGAGTTG	300
5	TCAAACCTCTC	AGGAACTGCT	GGAAACCGGT	ATCAAAGTTA	TCGACCTGAT	350
	GTGTCCGTTT	GCGAAGGGCG	GTAAAGTCGG	TCTGTTCCGGT	GGTGGCGGTG	400
	TAGGTAAAAC	CGTAAACATG	ATGGAGCTTA	TTCGTAACAT	CGCGATCGAG	450
	CACTCCGGTT	ACTCAGTGTT	TGCGGGCGTA	GGGGAACGTA	CTCGTGAGGG	500
	TAACGACTTC	TACCACGAAA	TGACCGACTC	CAACGTTATC	GATAAAGTAT	550
10	CCCTGGTGTA	TGGCCAGATG	AACGAGCCGC	CGGGAAACCG	TCTGCGCGTT	600
	GCACTGACCG	GCCTGACCAT	GGCGGAGAAA	TTCCGTGACG	AAGGTCGTGA	650
	TGTACTGCTG	TTCGTCGATA	ACATCTATCG	TTACACCCTG	GCCGGTACGG	700
	AAGTATCCGC	ACTGCTGGGC	CGTATGCCTT	CCGCAGTAGG	TTACCAGCCG	750
	ACTCTGGCGG	AAGAGATGGG	CGTTCTGCAG	GAACGTATCA	CCTCCACCAA	800
15	AACCGGTTCT	ATCACCTCCG				820

2) INFORMATION FOR SEQ ID NO: 344

20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 831 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

25

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

30

- (A) ORGANISM: *Salmonella choleraesuis* subsp. *diarizonae*
- (B) STRAIN: ATCC 43973

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 344

35	TTCCCTCAGG	ATGCCGTACC	ACGCGTGTAC	GATGCTCTTG	AGGTGCAGAA	50
	TGGTAATGAG	AAGCTGGTGC	TGGAAGTTCA	GCAGCAGCTT	GGCGGCGGTA	100
	TCGTGCGTAC	CATCGCGATG	GGGTCTTCTG	ACGGTCTGCG	TCGCGGTCTT	150
	GATGTAAAAG	ATCTCGAACA	CCCGATCGAA	GTCCCGGTAG	GTAAAGCAAC	200
	GCTGGGTCGT	ATCATGAACG	TCCTGGGTGA	ACCGGTCGAT	ATGAAAGGCG	250
40	AGATCGGCCG	AGAAGAGCGT	TGGGCGATTC	ACCGCGCGGC	GCCGTCCTAC	300
	GAAGAGTTGT	CAAACCTCTCA	GGAACCTGCTG	GAAACCGGTA	TCAAAGTTAT	350
	CGACCTGATG	TGTCCGTTTCG	CGAAGGGCGG	TAAAGTCGGT	CTGTTCGGTG	400
	GCGCGGGTGT	AGGTAAAACC	GTAAACATGA	TGGAGCTTAT	CCGTAACATC	450
	GCGATCGAGC	ACTCCGGTTA	CTCTGTGTTT	GCGGGCGTAG	GTGAACGTAC	500
45	TCGTGAGGGT	AACGACTTCT	ACCACGAAAT	GACCGACTCT	AACGTTATCG	550
	ATAAAGTATC	CCTGGTGTAT	GGCCAGATGA	ACGAGCCACC	GGGAAACCGT	600
	CTGCGCGTTG	CATTGACCGG	CCTGACCATG	GCGGAAAAAT	TCCGTGATGA	650
	AGGTCGTGAC	GTTCTGCTGT	TCGTGACAAA	CATCTACCGT	TATACCCTCG	700
	CCGGTACGGA	AGTATCCGCA	CTGCTGGGTC	GTATGCCTTC	CGCGGTAGGT	750
50	TATCAGCCGA	CTCTGGCTGA	AGAAATGGGC	GTTCTGCAGG	AACGTATCAC	800
	CTCCACCAAA	ACCGGTTCTA	TCACCTCCGT	A		831

55 2) INFORMATION FOR SEQ ID NO: 345

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 831 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double

60

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

5 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Salmonella choleraesuis* subsp. *houtenae*

(B) STRAIN: ATCC 43974

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 345

10

 TTCCCTCAGG ATGCCGTACC ACGCGTGTAC GATGCTCTTG AGGTGCAGAA 50
 TGGTAATGAG AAGCTGGTGC TGGAAGTTCA GCAGCAGCTT GGCGGCGGTA 100
 TCGTACGTAC CATCGCGATG GGGTCTTCTG ACGGTCTGCG TCGCGGTCTG 150
 GATGTAAAAG ATCTCGAACA CCCGATCGAA GTCCCGGTAG GTAAAGCTAC 200
 15 GCTGGGTCGT ATCATGAACG TCCTGGGCGA ACCGGTCGAT ATGAAAGGCG 250
 AGATCGGCGA AGAAGAGCGT TGGGCGATTG ACCGCGCTGC GCCGTCCTAC 300
 GAAGAGTTGT CAAACTCTCA GGAAGTGTG GAAACCGGTA TCAAAGTTAT 350
 CGACCTGATG TGTCCGTTCT CGAAGGGCGG TAAAGTCGGT CTGTTCGGTG 400
 GCGCGGGTGT AGGTAAAACC GTAAACATGA TGGAGCTTAT CCGTAACATC 450
 20 GCGATCGAGC ACTCCGGTTA CTCCGTGTTT GCGGGCGTAG GTGAACGTAC 500
 TCGTGAGGGT AACGACTTCT ACCACGAAAT GACCGACTCC AACGTTATCG 550
 ATAAAGTATC CCTGGTGTAT GGTCAGATGA ACGAGCCGCC GGGAAACCGT 600
 CTGCGCGTTG CATTGACCGG CCTGACCATG GCGGAAAAAT TCCGTGACGA 650
 AGGTCGTGAC GTTCTGCTGT TCGTCGATAA CATCTATCGT TACACCCTGG 700
 25 CCGGTACGGA AGTATCCGCA CTGCTGGGTC GTATGCCTTC CGCGGTAGGT 750
 TATCAGCCGA CGCTGGCGGA AGAGATGGGC GTTCTGCAGG AACGTATCAC 800
 CTCCACCAAG ACCGGTTCTA TCACCTCCGT A 831

30

2) INFORMATION FOR SEQ ID NO: 346

(i) SEQUENCE CHARACTERISTICS:

35 (A) LENGTH: 829 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

40

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Salmonella choleraesuis* subsp. *indica*

(B) STRAIN: ATCC 43974

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 346

TTCCCTCAGG ATGCCGTACC ACGCGTGTAC GATGCCCTTG AGGTGCAGAA 50
 TGGTAATGAG AAGCTCGTGC TGGAAGTTCA GCAGCAGCTT GGCGGCGGTA 100
 TCGTGCGTAC CATCGCGATG GGGTCTTCTG ACGGTCTGCG TCGCGGTCTG 150
 50 GATGTAAAAG ATCTCGAACA CCCGATCGAA GTCCCGGTAG GTAAAGCCAC 200
 GCTGGGTCGT ATCATGAACG TCCTGGGCGA ACCGGTCGAT ATGAAAGGCG 250
 AGATCGGCGA AGAAGAGCGT TGGGCGATTG ACCGCGCGGC GCCGTCCTAT 300
 GAAGAGTTGT CAAACTCTCA GGAAGTGTG GAAACCGGTA TCAAAGTTAT 350
 CGACCTGATG TGTCCGTTCT CGAAGGGCGG TAAAGTCGGT CTGTTCGGTG 400
 55 GTGCGGGCGT AGGTAAAACC GTAAACATGA TGGAGCTTAT CCGTAACATC 450
 GCGATCGAGC ACTCCGGTTA CTCTGTGTTT GCGGGCGTAG GTGAACGTAC 500
 TCGTGAGGGT AACGACTTCT ACCACGAAAT GACCGACTCC AACGTTATCG 550
 ACAAAGTATC CCTGGTGTAT GGCCAGATGA ACGAGCCGCC GGGAAACCGT 600
 CTGCGCGTTG CACTGACCGG CCTGACCATG GCGGAGAAGT TCCGTGACGA 650
 60 AGGTCGTGAC GTACTGCTGT TCGTCGATAA CATCTATCGT TATACCCTGG 700

CCGGTACGGA AGTTTCCGCA CTGCTGGGTC GTATGCCTTC CGCGGTAGGT 750
 TATCAGCCAA CTCTGGCGGA AGAGATGGGC GTTCTGCAGG AACGTATCAC 800
 CTCCACCAAA ACCGGTTCTA TCACCTCCG 829

5

2) INFORMATION FOR SEQ ID NO: 347

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 817 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

15 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Salmonella choleraesuis* subsp. *choleraesuis*
 serotype Paratyphi A
 20 (B) STRAIN: ATCC 9150

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 347

GCCGTACCAC GCGTGTACGA TGCCCTTGAG GTGCAGAATG GTAATGAGAA 50
 25 GCTGGTGTCTG GAAGTTCAGC AGCAGCTTGG CGGCGGTATC GTGCGTACCA 100
 TCGCGATGGG GTCTTCTGAC GGTCTGCGTC GCGGTCTGGA TGTAAGAGAT 150
 CTCGAACACC CGATCGAAGT CCCGGTAGGT AAAGCTACGC TGGGTCGTAT 200
 CATGAACGTC CTGGGCGAAC CGGTCGACAT GAAAGGCGAG ATCGGCGAAG 250
 AAGAGCGTTG GGCATTTCAC CGCGCAGCGC CTTCTTACGA AGAGTTGTCA 300
 30 AACTCTCAGG AACTGCTGGA AACCGGTATC AAAGTTATCG ACCTGATGTG 350
 TCCGTTTCGG AAGGGCGGTA AAGTCGGTCT GTTCGGTGGT GCGGGTGTAG 400
 GTAAACCGT AAACATGATG GAGCTTATCC GTAACATCGC GATCGAGCAC 450
 TCCGTTTACT CTGTGTTTGC GGGCGTAGGT GAACGTAATC GTGAGGGTAA 500
 CGACTTCTAC CATGAAATGA CCGACTCCAA CGTTATCGAT AAAGTATCCC 550
 35 TGGTGTATGG CCAGATGAAC GAGCCGCCGG GAAACCGTCT GCGCGTTGCA 600
 CTGACCGGCC TGACCATGGC GGAGAAATTC CGTGACGAAG GTCGTGACGT 650
 ACTGCTGTTC GTCGATAACA TCTATCGTTA CACCCTGGCC GGTACGGAAG 700
 TATCCGCACT GCTGGGTCGT ATGCCTTCCG CGGTAGGTTA CCAGCCGACT 750
 CTGGCGGAAG AGATGGGCGT TCTGCAGGAA CGTATCACCT CCACCAAGAC 800
 40 CGGTTCTATC ACCTCCG 817

2) INFORMATION FOR SEQ ID NO: 348

45

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 806 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 50 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 55 (A) ORGANISM: *Salmonella choleraesuis* subsp. *choleraesuis*
 serotype Paratyphi B
 (B) STRAIN: ATCC 8759

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 348

60

	GCCGTACCAC	GCGTGTACGA	TGCCCTTGAG	GTGCAGAATG	GTAATGAGAA	50
	GCTGGTGCTG	GAAGTTCAGC	AGCAGCTTGG	CGGCGGTATT	GTGCGTACCA	100
	TCGCGATGGG	GTCTTCTGAC	GGTCTGCGTC	GCGGTCTGGA	TGTAAAAGAT	150
	CTCGAACACC	CGATCGAAGT	CCCGGTAGGT	AAAGCCACGC	TGGGTCGTAT	200
5	CATGAACGTC	CTGGGCGAAC	CGGTCGACAT	GAAAGGCGAG	ATCGGCGAAG	250
	AAGAGCGTTG	GGCGATTAC	CGCGCAGCGC	CTTCCTACGA	AGAGTTGTCA	300
	AACTCTCAGG	AACTGCTGGA	AACCGGTATC	AAAGTTATCG	ACCTGATGTG	350
	TCCGTTCCGG	AAGGGCGGTA	AAGTCGGTCT	GTTCCGGTGGT	GCGGGTGTGG	400
	GTAACACCGT	AAACATGATG	GAGCTTATCC	GTAACATCGC	GATCGAGCAC	450
10	TCCGGTTACT	CTGTGTTTGC	GGGCGTAGGT	GAACGTACTC	GTGAGGGTAA	500
	CGACTTCTAC	CACGAAATGA	CCGACTCCAA	CGTTATCGAT	AAAGTATCCC	550
	TGGTGTATGG	CCAGATGAAC	GAGCCGCCGG	GAAACCGTCT	GCGCGTTGCA	600
	TTGACCGGTC	TGACCATGGC	GGAGAAATTC	CGTGACGAAG	GTCGTGACGT	650
	ACTGCTGTTC	GTCGATAACA	TCTATCGTTA	CACCCTGGCC	GGTACGGAAG	700
15	TATCCGCACT	GCTGGGCCGT	ATGCCTTCCG	CAGTAGGTTA	CCAGCCGACT	750
	CTGGCGGAAG	AGATGGGCGT	TCTGCAGGAA	CGTATCACCT	CCACCAAAC	800
	CGGTTT					806

20

2) INFORMATION FOR SEQ ID NO: 349

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 831 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

30

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Salmonella choleraesuis* subsp. *salamae*
 (B) STRAIN: ATCC 43972

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 349

	TTCCCTCAGG	ATGCCGTACC	ACGCGTGTAC	GATGCCCTTG	AGGTGCAGAA	50
	TGGTAATGAG	AAGCTGGTGC	TGGAAGTTCA	GCAGCAGCTT	GGCGGCCGTA	100
	TCGTGCGTAC	CATCGCGATG	GGGTCTTCTG	ACGGTCTGCG	TCGKGGTCTG	150
40	GATGTAAAAG	ATCTCGAACA	CCCGATCGAA	GTCCCGGTAG	GTAAAGCAAC	200
	GCTGGGCCGT	ATCATGAACG	TACTGGGCGA	ACCGGTCGAC	ATGAAAGGCG	250
	AGATTGGTGA	AGAAGAGCGT	TGGGCTATTC	ACCGTGCTGC	GCCGTCCTAC	300
	GAAGAGTTGT	CAAACCTCTCA	GGAACCTGCTG	GAAACCGGTA	TCAAAGTTAT	350
	CGACCTGATG	TGTCCGTTCG	CGAAGGGCGG	TAAAGTCGGT	CTGTTCCGGTG	400
45	GCGCGGGTGT	AGGTAAAACC	GTAAACATGA	TGGAGCTCAT	CCGTAACATC	450
	GCGATCGAGC	ACTCCGGTTA	CTCCGTGTTT	GCGGGCGTAG	GTGAACGTAC	500
	TCGTGAGGGT	AACGACTTCT	ACCACGAAAT	GACCGACTCC	AACGTTATCG	550
	ATAAAGTATC	CCTGGTGTAT	GGCCAGATGA	ACGAGCCGCC	GGGAAACCGT	600
	CTGCGCGTTG	CACTGACCGG	CCTGACCATG	GCGGAAAAAT	TCCGTGACGA	650
50	AGGTCGTGAC	GTAAGTCTGT	TCGTGATAA	CATCTATCGT	TATACCCTGG	700
	CCGGTACGGA	AGTATCCGCA	CTGCTGGGTC	GTATGCCTTC	CGCGGTAGGT	750
	TATCAGCCGA	CGCTGGCGGA	AGAGATGGGC	GTTCTGCAGG	AACGTATCAC	800
	CTCCACTAAA	ACCGGTTCTA	TCACCTCCGT	A		831

55

2) INFORMATION FOR SEQ ID NO: 350

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 823 bases

60

- (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

5 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Salmonella choleraesuis* subsp. *choleraesuis*
 serotype Typhi
 10 (B) STRAIN: ATCC 10749

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 350

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15 TTCCCTCAGG ATGCCGTACC ACGCGTGTAC GATGCCCTTG AGGTGCAGAA      50
   TGGTAATGAG AAGCTGGTGC TGGAAATTCA GCAGCAGCTT GGCGGCGGTA      100
   TCGTGCGTAC CATCGCGATG GGGTCTTCTG ACGGTCTGCG TCGCGGTCTG      150
   GATGTAAAAG ATCTCGAACA CCCGATCGAA GTCCCGGTAG GTAAAGCTAC      200
   GCTGGGTCGT ATCATGAACG TCCTGGGCGA ACCGGTCGAC ATGAAAGGCG      250
   AGATCGGCGA AGAAGAGCGT TGGGCGATTC ACCGCGCAGC GCCTTCCTAC      300
20 GAAGAGTTAT CAAACTCTCA GGAAGTCTG GAAACCGGTA TCAAAGTTAT      350
   CGACCTGATG TGTCCGTTCT CGAAGGGCGG TAAAGTCGGT CTGTTCGGTG      400
   GTGCGGGTGT AGGTAAAACC GTAAACATGA TGGAGCTTAT CCGTAACATC      450
   GCGATCGAGC ACTCCGGTTA CTCTGTGTTT GCGGGCGTAG GTGAACGTAC      500
   TCGTGAGGGT AACGACTTCT ACCATGAAAT GACCGACTCC AACGTTATCG      550
25 ATAAAGTATC CCTGGTGTAT GGCCAGATGA ACGAGCCGCC GGGAAACCGT      600
   CTGCGCGTTG CACTGACCGG CCTGACCATG GCGGAGAAAT TCCGTGACGA      650
   AGGTCGTGAC GTACTGCTGT TCGTCGATAA CATCTATCGT TACACCCTGG      700
   CCGGTACGGA AGTATCCGCA CTGCTGGGTC GTATGCCTTC CGCGGTAGGT      750
   TACCAGCCGA CTCTGGCGGA AGAGATGGGC GTTCTGCAGG AACGTATCAC      800
30 CTCCACCAAG ACCGGTTCTA TCA                                     823

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2) INFORMATION FOR SEQ ID NO: 351

35

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 831 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 40 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 45 (A) ORGANISM: *Salmonella choleraesuis* subsp. *choleraesuis*
 serotype Typhimurium
 (B) STRAIN: ATCC 14028

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 351

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   TTCCCTCAGG ATGCCGTACC ACGCGTGTAC GATGCCCTTG AGGTGCAGAA      50
   TGGTAATGAG AAGCTGGTGC TGGAAATTCA GCAGCAGCTT GGCGGCGGTA      100
   TTGTGCGTAC CATCGCGATG GGGTCTTCTG ACGGTCTGCG TCGCGGTCTG      150
   GATGTAAAAG ATCTCGAACA CCCGATCGAA GTCCCGGTAG GTAAAGCTAC      200
55 GCTGGGTCGT ATCATGAACG TCCTGGGCGA ACCGGTCGAC ATGAAAGGCG      250
   AGATCGGCGA AGAAGAGCGT TGGGCGATTC ACCGCGCAGC GCCTTCCTAC      300
   GAAGAGTTGT CAAACTCTCA GGAAGTCTG GAAACCGGTA TCAAAGTTAT      350
   CGACCTGATG TGTCCGTTCT CGAAGGGCGG TAAAGTCGGT CTGTTCGGTG      400
   GTGCGGGTGT AGGTAAAACC GTAAACATGA TGGAGCTTAT CCGTAACATC      450
60 GCGATCGAGC ACTCCGGTTA CTCAGTGTTC GCGGGCGTAG GGAACGTAC      500

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	TCGTGAGGGT	AACGACTTCT	ACCACGAAAT	GACCGACTCC	AAAGTTATCG	511
	ATAAAGTATC	CCTGGTGTAT	GGCCAGATGA	ACGAGCCGCC	GGGAAACCGT	600
	CTGCGCGTTG	CATTGACCGG	TCTGACCATG	GCGGAGAAAT	TCCGTGACGA	650
	AGGTCGTGAC	GTA CTGCTGT	TCGTGATAA	CATCTATCGT	TACACCCTGG	700
5	CCGGTACGGA	AGTATCCGCA	CTGCTGGGCC	GTATGCCTTC	CGCAGTAGGT	750
	TACCAGCCGA	CTCTGGCGGA	AGAGATGGGC	GTTCTGCAGG	AACGTATCAC	800
	CTCCACCAAA	ACCGGTTCTA	TCACCTCCGT	A		831

10

2) INFORMATION FOR SEQ ID NO: 352

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 810 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Salmonella choleraesuis* subsp. *choleraesuis*
 serotype Virchow
 (B) STRAIN: ATCC 51955

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 352

	GCCGTACCAC	GCGTGTACGA	TGCCCTTGAG	GTGCAGAATG	GTAATGAGAA	50
	GCTGGTGCTG	GAAGTTCAGC	AGCAGCTTGG	CGGCGGTATC	GTGCGTACCA	100
30	TCGCGATGGG	GTCTTCTGAC	GGTCTGCGTC	GCGGTCTGGA	TGTAAAAGAT	150
	CTCGAACACC	CGATCGAAGT	CCCGGTAGGT	AAAGCCACGC	TGGGTCGTAT	200
	CATGAACGTC	CTGGGCGAAC	CGGTCGACAT	GAAAGGCGAG	ATCGGCCAAG	250
	AAGAGCGTTG	GGCGATTAC	CGCGCAGCAC	CTTCCTACGA	AGAGTTGTCA	300
	AACTCTCAGG	AACTGCTGGA	AACCGGTATC	AAAGTTATCG	ACCTGATGTG	350
35	TCCGTTCCGG	AAGGGCGGTA	AAGTCGGTCT	GTTCCGGTGGT	GCGGGTGTAG	400
	GTAACACCGT	AAACATGATG	GAGCTTATTC	GTAACATCGC	GATCGAGCAC	450
	TCCGGTTACT	CTGTGTTTGC	GGGCGTAGGG	GAACGTACTC	GTGAGGGTAA	500
	CGACTTCTAC	CACGAAATGA	CCGACTCCAA	CGTTATCGAT	AAAGTCTCCC	550
	TGGTGTATGG	CCAGATGAAC	GAGCCGCCGG	GAAACCGTCT	GCGCGTTGCA	600
40	TTGACCGGTC	TGACCATGGC	GGAGAAATTC	CGTGACGAAG	GTCGTGACGT	650
	ACTGCTGTTC	GTCGATAACA	TCTATCGTTA	CACCCTGGCC	GGTACGGAAG	700
	TATCCGCACT	GCTGGGCCGT	ATGCCTTCCG	CAGTAGGTTA	CCAGCCGACT	750
	CTGGCGGAAG	AGATGGGCGT	TCTGCAGGAA	CGTATCACCT	CCACCAAAAC	800
	CGGTTCTATC					810

45

2) INFORMATION FOR SEQ ID NO: 353

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 820 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

55

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Serratia ficaria*
 (B) STRAIN: ATCC 33105

60

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 353

5	GATGCCGTAC	CAAAAGTGTA	CGATGCCCTT	GAGGTAGAAA	ACGGTACCGA	50
	GAAACTGGTG	CTGGAAGTTC	AGCAGCAGCT	GGGCGGTGGC	GTCGTTTCGCT	100
	GTATCGCAAT	GGGGACCTCT	GACGGTCTGC	GTCGCGGTCT	GAAAGTGAAC	150
	AACCTGGAAC	ACCCGATTGA	AGTGCCGGTG	GGTAAAGCTA	CCCTGGGCCG	200
	TATCATGAAC	GTATTGGGCG	AACCAATCGA	CATGAAAGGC	GAGATCGGCG	250
	AAGAAGAGCG	TTGGGCGATT	CACCGTCTCG	CGCCAAGCTA	CGAAGAGCTG	300
10	TCCAACCTCCC	AGGACCTGCT	GGAAACCGGT	ATCAAGGTAA	TGGACCTGAT	350
	TTGTCCGTTT	GCCAAGGGCG	GTAAAGTCCG	TCTGTTTCGGT	GGTGCGGGCG	400
	TGGGCAAAAC	CGTAAACATG	ATGGAGCTGA	TCCGTAACAT	CGCGATCGAG	450
	CACTCCGGTT	ATTCCGTGTT	TGCGGGCGTG	GGCGAGCGTA	CTCGTGAGGG	500
	TAACGACTTC	TACCACGAAA	TGAACGACTC	CAACGTTCTG	GACAAAGTAT	550
15	CCCTGGTTTA	CGGCCAGATG	AACGAGCCGC	CGGGTAACCG	TCTGCGCGTT	600
	GCATTGACCG	GCCTGACCAT	GGCGGAGAAA	TTCCGTGACG	AAGGCCGCGA	650
	CGTTCTGCTG	TTCGTTGACA	ACATTTACCG	TTACACCCTG	GCCGGTACCG	700
	AAGTGTCCGC	ACTTCTGGGC	CGTATGCCAT	CCGCGGTAGG	TTATCAGCCA	750
	ACGCTGGCGG	AAGAGATGGG	CGTTCTGCAA	GAACGTATCA	CCTCGACCAA	800
20	GACCGGTTCC	ATCACCTCCG				820

2) INFORMATION FOR SEQ ID NO: 354

25

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 816 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

30

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Serratia fonticola*
 (B) STRAIN: ATCC 29844

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 354

40	GATGCCGTAC	CGAAAGTGTA	CAACGCTCTT	GAGGTTGCAA	ACGGCACC GA	50
	GAAATTGGTG	CTGGAAGTTC	AGCAACAGCT	GGGTGGCGGC	GTGGTTTCGCT	100
	GTATCGCAAT	GGGGACCTCA	GACGGTCTGC	GTCGTGGTCT	GGCCGTAAACC	150
	GACCTGCAGC	ACCCAATTGA	AGTACCGGTA	GGTAAAGCTA	CCCTGGGCCG	200
	TATCATGAAC	GTATTGGGTG	AACCAATCGA	CATGAAGGGC	GACATCGGCG	250
45	AAGAAGAACG	TTGGGCTATT	CACCGCCCTG	CGCCAAGCTA	CGAAGAGCTG	300
	TCCAGCTCCC	AGGATCTGCT	GGAAACCGGT	ATCAAGGTAA	TGGACCTGAT	350
	CTGCCC GTTC	GCCAAGGGTG	GTAAAGTTGG	TCTGTTTCGGT	GGTGCTGGTG	400
	TAGGTAAAAC	CGTAAACATG	ATGGAGCTGA	TCCGTAACAT	CGCGATCGAG	450
	CACTCCGGTT	ATTCTGTGTT	TGCGGGCGTG	GGTGAACGTA	CTCGTGAGGG	500
50	TAACGACTTC	TACCACGAAA	TGACCGATTC	CAACGTACTG	GACAAAGTTT	550
	CCCTGGTTTA	CGGCCAGATG	AACGAGCCAC	CAGGTAACCG	TCTGCGCGTT	600
	GCGCTGACCG	GCCTGACCAT	GGCTGAGAAG	TTCCGTGACG	AAGGTCGTGA	650
	CGTACTGCTG	TTCGTCGATA	ACATCTACCG	TTATACCCTG	GCCGGTACCG	700
	AAGTGTCCGC	ACTTCTGGGC	CGTATGCCAT	CGGCGGTAGG	TTATCAGCCA	750
55	ACGCTGGCGG	AAGAGATGGG	TGTTCTGCAA	GAACGTATCA	CCTCTACCAA	800
	GACTGGTTCA	ATCACC				816

60 2) INFORMATION FOR SEQ ID NO: 355

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 822 bases
 (B) TYPE: Nucleic acid
 5 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

10 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Serratia grimesii*
 (B) STRAIN: ATCC 14460

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 355

15 GATGCCGTAC CAAAAGTGTA CAACGCTCTT GAGGTAGAAA ACGGTGCCAA 50
 TAAGCTGGTG CTGGAAGTTC AGCAACAGTT GGGCGGTGGC GTGGTTCGCT 100
 GTATCGCAAT GGGGACCTCT GATGGTCTGC GTCGCGGTCT GAAAGTCACA 150
 GACCTGGACC ACCCAATTGA AGTACCGGTA GGTAAGCTA CTCTGGGCCG 200
 20 TATCATGAAC GTATTGGGTG AACCAATCGA CATGAAGGGC GATATCGGCG 250
 AAGAAGAACG TTGGGCGATT CACCGTCCGG CGCCAAGCTA CGAAGATTTG 300
 GCCAACTCCC AGGATCTGCT GGAAACCGGT ATCAAGGTAA TGGACCTGAT 350
 CTGCCCCTTC GCCAAGGGTG GTAAAGTCGG TCTGTTCGGT GGTGCGGGTG 400
 TTGGTAAAAC CGTAAACATG ATGGAGCTGA TCCGTAAAT CGCGATCGAG 450
 25 CACTCCGGTT ATTCTGTGTT TCGGGCGGTG GGTGAGCGTA CTCGTGAGGG 500
 TAACGACTTC TACCACGAAA TGAACGACTC CAACGTACTG GACAAAGTAT 550
 CCCTGGTTTA CGGCCAGATG AACGAGCCAC CGGGTAACCG TCTGCGCGTT 600
 GCTCTGACCG GTCTGACCAT GGCTGAGAAA TTCCGTGACG AAGGCCGTGA 650
 CGTTCTGCTG TTCGTTGATA ACATCTACCG TTATACCCTG GCCGGTACCG 700
 30 AAGTGTCCGC ACTTCTGGGC CGTATGCCAT CGGCGGTAGG TTATCAGCCA 750
 ACGCTGGCGG AAGAGATGGG TGTCTGCAA GAACGTATCA CCTCTACCAA 800
 GACTGGTTCA ATCACCTCCG TA 822

35

2) INFORMATION FOR SEQ ID NO: 356

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 819 bases
 40 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

45

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Serratia liquefaciens*
 (B) STRAIN: ATCC 27592

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 356

ATGCCGTACC AAAAGTGTA AATGCTCTTG AGGTAGAAAA CCGTACCGAG 50
 AAGCTGGTGC TGGAAGTTCA GCAGCAGTTG GGCGGTGGCG TAGTTCGCTG 100
 TATCGCGATG GGGACCTCAG ATGGTCTGCG CCGCGGTCTG AAAGTGAACG 150
 55 ATCTGGAACA CCAATTGAA GTACCGGTAG GTAAAGCTAC CCTGGGCCGT 200
 ATCATGAACG TATTGGGTGA ACCAATCGAC ATGAAAGGCG ACATCGGCGA 250
 AGAAGAACGT TGGGCGATTC ACCGTCCAGC GCCAAGCTAC GAAGATTTGT 300
 CAAACTCCCA GGATCTGCTG GAAACCGGTA TCAAGGTTAT GGACCTGATT 350
 TGTCCGTTTC CTAAGGGCGG TAAAGTTGGT CTGTTCCGGT GTGCTGGTGT 400
 60 TGGTAAACC GTAAACATGA TGGAGCTGAT CCGTAACATC GCGATCGAGC 450

	ACTCCGGTTA	TTCCCGTGT	GCAGGCGTGG	GTGAGCGTAC	TCGTGAGGGT	500
	AACGACTTCT	ACCACGAAAT	GAACGACTCC	AACGTACTGG	ACAAAGTATC	550
	CCTGGTTTAC	GGCCAGATGA	ACGAGCCACC	GGGTAACCGT	CTGCGCGTTG	600
	CTCTGACCGG	TCTGACCATG	GCGGAGAAAT	TCCGTGACGA	AGGCCGCGAC	650
5	GTTCTGCTGT	TCGTTGATAA	CATTTACCGT	TATACCCTGG	CCGGTACCGA	700
	AGTGTCCGCA	CTTCTGGGCC	GTATGCCATC	TGCGGTAGGT	TATCAGCCAA	750
	CGCTGGCGGA	AGAGATGGGC	GTTCTGCAAG	AACGTATCAC	CTCTACCAAG	800
	ACCGGTTCTA	TCACTTCCG				819

10

2) INFORMATION FOR SEQ ID NO: 357

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 805 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

20 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Serratia marcescens*

(B) STRAIN: ATCC 13880

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 357

	TCAGGATGCC	GTACCGAAAG	TGTACGACGC	CCTTGAGGTA	GAAAACGGCA	50
	CCGAAAAACT	GGTGTTGGAA	GTTTCAGCAAC	AGCTGGGCGG	TGGCGTGTTT	100
30	CGCTGTATCG	CAATGGGGAC	CTCCGACGGT	CTGCGTCGCG	GTCTGAAAGT	150
	GAACAACCTG	GACCACCCGA	TTGAAGTGCC	GGTGGGTAAA	GCTACCCTGG	200
	GTCGTATCAT	GAACGTATTG	GGTCAACCGA	TCGACATGAA	AGGCGACATC	250
	GGCGAAGAAG	AGCGTTGGGC	GATTCACCGC	GCGGCGCCAA	GCTACGAAGA	300
	GCTGTCAAGC	TCTCAGGAAC	TGCTGGAAAC	CGGTATCAAG	GTAATGGACC	350
35	TGATTTGTCC	GTTCCGCAAG	GGCGGTAAAG	TCGGTCTGTT	CGGCGGTGCG	400
	GGCGTAGGTA	AAACCGTAAA	CATGATGGAG	CTGATCCGTA	ACATCGCGAT	450
	CGAGCACTCC	GGTTATTCCG	TGTTTGCGGG	CGTGGGCGAG	CGTACTCGTG	500
	AGGGTAACGA	CTTCTACCAC	GAAATGACCG	ACTCCAACGT	TCTGGACAAA	550
	GTATCCCTGG	TTTACGGCCA	GATGAACGAG	CCACCAGGTA	ACCGTCTGCG	600
40	CGTTGCGCTG	ACCGGTCTGA	CCATGGCGGA	GAAATTCCGT	GACGAAGGCC	650
	GTGACGTTCT	GCTGTTTCGTT	GACAACATCT	ACCGTTACAC	CCTGGCCGGT	700
	ACCGAAGTGT	GCGCACTTCT	GGGCCGTATG	CCATCCGCGG	TAGGTTATCA	750
	GCCAACGCTG	GCGGAAGAGA	TGGGCGTTCT	GCAAGAACGT	ATCACCTCGA	800
	CCAAG					805

45

2) INFORMATION FOR SEQ ID NO: 358

50 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 822 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

55

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Serratia odorifera*

60 (B) STRAIN: ATCC 33077

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 358

5	GATGCCGTAC	CAAAAGTGTA	CGATGCCCTT	GAGGTAGAAA	ACGGTACCGA	50
	AACTCTGGTG	CTGGAAGTTC	AGCAGCAGCT	GGGCGGTGGC	GTGGTTCGTT	100
	GTATCGCTAT	GGGCACCTCC	GACGGTTTGC	GTCGCGGCCT	GAAAGTGAAC	150
	GATCTGCAAC	ACCCAATCGA	AGTCCCAGTT	GGCAAGGCAA	CGCTGGGTCTG	200
	TATCATGAAC	GTATTGGGTC	AACCAATCGA	CATGAAAGGC	GACATCGGCG	250
	AAGAAGAGCG	TTGGGCGATT	CACCGCGCGG	CGCCAAGCTA	CGAAGAAGCTG	300
10	TCCAATCCC	AGGATCTGCT	GGAAACCGGT	ATCAAGGTTA	TGGACCTGAT	350
	CTGCCCGTTT	GCCAAGGGTG	GTAAAGTCGG	TCTGTTTCGGT	GGTGCGGGTG	400
	TTGGTAAAAC	CGTAAACATG	ATGGAGCTGA	TCCGTAACAT	CGCGATCGAG	450
	CACTCCGGTT	ATTCAGTGTT	TGCGGGCGTG	GGTGAGCGTA	CTCGTGAGGG	500
	TAACGACTTC	TACCACGAAA	TGACCGACTC	CAACGTACTG	GACAAGGTTT	550
15	CCCTGGTTTA	CGGCCAGATG	AACGAGCCAC	CGGGTAACCG	TCTGCGCGTT	600
	GCGCTGACCG	GTCTGACCAT	GGCCGAGAAA	TTCCGTGACG	AAGGTCGTGA	650
	CGTTCTGCTG	TTCGTTGACA	ACATTTACCG	TTACACCCTG	GCCGGTACCG	700
	AAGTGTCTGC	ACTTCTGGGC	CGTATGCCAT	CGGCGGTAGG	TTATCAGCCA	750
	ACGCTGGCGG	AAGAGATGGG	CGTTCTGCAA	GAACGTATCA	CCTCGACCAA	800
20	GACCGGTTCT	ATCACCTCCG	TA			822

2) INFORMATION FOR SEQ ID NO: 359

25

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 805 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

30

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Serratia plymuthica*
 (B) STRAIN: ATCC 183

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 359

40	GTGTACAACG	CTCTTGAGGT	AGAAAACGGT	GCCAATAAGC	TGGTGCTGGA	50
	AGTTCAGCAA	CAGCTGGGCG	GTGGCGTGGT	TCGCTGTATC	GCGATGGGGA	100
	CCTCTGATGG	TCTGCGTCGC	GGTCTGAAAG	TGATCGACCT	GGATCACCCG	150
	ATTGAAGTAC	CGGTAGGTAA	AGCTACCCCTG	GGCCGTATCA	TGAACGTATT	200
	GGGTGAACCA	ATCGACATGA	AAGGCGACAT	CGGCGAAGAA	GAACGTTGGG	250
45	CAATTCACCG	TCCAGCGCCA	AGCTACGAAG	ATTTGGCCAA	CTCCCAGGAT	300
	CTGCTGGAAG	CCGGTATCAA	GGTTATGGAC	CTGATCTGTC	CGTTCGCTAA	350
	GGGCGGTAAA	GTGGGTCTGT	TCGGCGGTGC	GGGCGTGGGT	AAAACCGTAA	400
	ACATGATGGA	GCTGATCCGT	AACATCGCGA	TCGAACACTC	CGGTTATTCC	450
	GTGTTTGCGG	GCGTGGGTGA	GCGTACTCGT	GAGGGTAACG	ACTTCTACCA	500
50	CGAAATGAAC	GAATCCAACG	TACTGGACAA	AGTATCCCTG	GTTTACGGCC	550
	AGATGAACGA	GCCACCGGGT	AACCGTCTGC	GCGTTGCTCT	GACCGGTCTG	600
	ACCATGGCGG	AGAAATTCCG	TGACGAAGGC	CGCGACGTTT	TGCTGTTCGT	650
	TGATAACATC	TACCGTTATA	CCCTGGCCCG	TACCGAAGTG	TCCGCACTTC	700
	TGGGCCGTAT	GCCATCTGCG	GTAGGTTATC	AGCCAACGCT	GGCGGAAGAG	750
55	ATGGGCGTTC	TGCAAGAACG	TATCACCTCT	ACCAAGACCG	GTTCTATCAC	800
	CTCCG					805

60 2) INFORMATION FOR SEQ ID NO: 360

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 831 bases
 (B) TYPE: Nucleic acid
 5 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

10 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Serratia rubidaea*
 (B) STRAIN: ATCC 27593

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 360

15 TTCCCTCAGG ATGCCGTACC AAAAGTGTAC GATGCCCTTG AGGTAGAGAA 50
 CGGTAACGAA AAAGTGGTGC TGGAAGTTCA GCAGCAGCTG GGCGGCGGCG 100
 TTGTACGCTG TATCGCCATG GGTACTTCCG ACGGTCTGCG TCGCGGTCTG 150
 AAAGTTAACG ACCTCGAGCA CCAATCGAA GTGCCAGTTG GTAAAGCAAC 200
 20 GCTGGGTCTG ATCATGAACG TATTGGGTCA GCCAATCGAC ATGAAAGGCG 250
 ACATCGGCGA AGAAGAGCGT TGGGCGATTC ACCGCGCGGC GCCAAGCTAC 300
 GAAGAGCTGT CCAGCTCCCA AGAGCTGCTG GAAACCGGTA TCAAGGTAAT 350
 GGACCTGATC TGCCCGTTCG CCAAGGGTGG TAAAGTTGGT CTGTTCTGGT 400
 GTGCGGGCGT AGGTAAACC GTAAACATGA TGGAGCTGAT CCGTAACATC 450
 25 GCGATCGAGC ACTCCGGTTA CTCTGTGTTT GCGGGCGTGG GTGAGCGTAC 500
 TCGTGAGGGT AACGACTTCT ACCACGAAAT GACCGACTCC AACGTACTGG 550
 ACAAAGTATC CCTGGTTTAC GGCCAGATGA ACGAGCCGCC GGGTAACCGT 600
 CTGCGCGTTG CACTGACCGG CCTGACCATG GCGGAAAAAT TCCGTGATGA 650
 AGGCCGCGAC GTTCTGCTGT TCGTGGATAA CATCTACCGT TACACCCTGG 700
 30 CCGGTACCGA AGTGTCCGCA CTGCTCGGCC GTATGCCATC TGCGGTAGGT 750
 TATCAGCCAA CGCTGGCGGA AGAGATGGGC GTTCTGCAAG AACGTATCAC 800
 CTCGACCAAG ACCGGTTCAA TCACCTCCGT A 831

35

2) INFORMATION FOR SEQ ID NO: 361

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 406 bases
 40 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

45

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Pseudomonas putida*
 (B) STRAIN: LCD C D7172

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 361

CCGTAAACAT GATGGAAGT ATCCGTAAAC TCGCCATCGA GCACAGCGGT 50
 TATTCCTGT TCGCCGGTGT GGGTGAAGCT ACTCGTGAGG GTAACGACTT 100
 CTACCACGAG ATGAAGGACT CCAACGTTCT CGACAAGGTA GCGCTGGTCT 150
 55 ACGGTCAGAT GAACGAGCCA CCAGGAAACC GTCTGCGCGT AGCGCTGACC 200
 GGCCTGACCA TGGCCGAGAA GTTCCGTGAC GAAGGTAACG ACGTTCTGCT 250
 GTTCGTCGAC AACATCTATC GTTACACCCT GGCCGGTACC GAAGTATCCG 300
 CACTGCTGGG CCGTATGCCT TCGGCGGTAG GTTACCAGCC GACCCTGGCT 350
 GAAGAGATGG GCGTTCTGCA AGAACGTATC ACTTCGACCA AGGAAGGTTC 400
 60 GATCAC 406

2) INFORMATION FOR SEQ ID NO: 362

5

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 831 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

10

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Shigella boydii*
 (B) STRAIN: ATCC 9207

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 362

20	TTCCCTCAGG	ATGCCGTACC	GCGCGTGTAC	GATGCTCTTG	AGGTGCAAAA	50
	TGGTAATGAG	CGTCTGGTGC	TGGAAGTTCA	GCAGCAGCTC	GGCGGCGGTA	100
	TCGTGCGTAC	CATCGCAATG	GGTTCCTCCG	ACGGTCTGCG	TCGCGGTCTG	150
	GATGTAAAAG	ACCTCGAACA	CCCGATCGAA	GTCCCGGTAG	GTAAAGCGAC	200
	TCTGGGCCGT	ATCATGAACG	TACTGGGTGA	ACCGGTCGAC	ATGAAAGGCG	250
25	AGATCGGTGA	AGAAGAGCGT	TGGGCGATTC	ACCGCGCAGC	ACCTTCCTAC	300
	GAAGAGCTGT	CAAACCTCTCA	GGAACCTGCTG	GAAACCGGTA	TCAAAGTTAT	350
	CGACCTGATG	TGTCCGTTCG	CTAAGGGCGG	TAAAGTTGGT	CTGTTCGGTG	400
	GTGCGGGTGT	AGGTAAAACC	GTAAACATGA	TGGAGCTCAT	TCGTAACATC	450
	GCGATCGAGC	ACTCCGGTTA	CTCTGTGTTT	GCGGGCGTAG	GTGAACGTAC	500
30	TCGTGAGGGT	AACGACTTCT	ACCACGAAAT	GACCGACTCC	AACGTTATCG	550
	ACAAAGTATC	CCTGGTGTAT	GGCCAGATGA	ACGAGCCGCC	GGGAAACCGT	600
	CTGCGCGTTG	CTCTGACCGG	TCTGACCATG	GCTGAGAAAT	TCCGTGACGA	650
	AGGTCGTGAC	GTTCTGCTGT	TCGTTGACAA	CATCTATCGT	TACACCCTGG	700
	CCGGTACGGA	AGTATCCGCA	CTGCTGGGCC	GTATGCCTTC	AGCGGTAGGT	750
35	TATCAGCCGA	CCCTGGCGGA	AGAGATGGGC	GTTCTGCAGG	AACGTATCAC	800
	CTCCACCAAA	ACTGGTTCTA	TCACCTCCGT	A		831

40 2) INFORMATION FOR SEQ ID NO: 363

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 802 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

45

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Shigella dysenteriae*
 (B) STRAIN: ATCC 11835

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 363

55

55	GCCGTACCGC	GCGTGTACGA	TGCTCTTGCG	GTGCAAAATG	GTAATGAGCG	50
	TCTGGTGCTG	GAAGTTCAGC	AGCAGCTCGG	CGGCGGTATC	GTGCGTACCA	100
	TCGCAATGGG	TTCCTCCGAC	GGTCTGCGTC	GCGGTCTGGA	TGTAAAAGAC	150
	CTCGAACACC	CGATCGAAGT	CCCGGTAGGT	AAAGCGACTC	TGGGCCGTAT	200
60	CATGAACGTA	CTGGGTGAAC	CGGTCGACAT	GAAAGGCGAG	ATCGGTGAAG	250

	AAGAGCGTTG	GGCTATTCAC	CGCGCAGCAC	CTTCCTACGA	AGAGCTGTCA	300
	AACTCTCAGG	AACTGCTGGA	AACCGGTATC	AAAGTTATCG	ACCTGATGTG	350
	TCCGTTGCT	AAGGGCGGTA	AAGTTGGTCT	GTTTCGGTGGT	GCGGGTGTAG	400
	GTAAAACCGT	AAACATGATG	GAGCTCATTC	GTAACATCGC	GATCGAGCAC	450
5	TCCGGTTACT	CTGTGTTTGC	GGGCGTAGGT	GAACGTACTC	GTGAGGGTAA	500
	CGACTTCTAC	CACGAAATGA	CCGACTCCAA	CGTTATCGAC	AAAGTATCCC	550
	TGGTGTATGG	CCAGATGAAC	GAGCCGCCGG	GAAACCGTCT	GCGCGTTGCT	600
	CTGACCGGTC	TGACCATGGC	TGAGAAATTC	CGTGACGAAG	GTCGTGACGT	650
	TCTGCTGTTT	GTTGACAACA	TCTATCGTTA	CACCTGGGCC	GGTACGGAAG	700
10	TATCCGCACT	GCTGGGCCGT	ATGCCTTCAG	CGGTAGGTTA	TCAGCCGACC	750
	CTGGCGGAAG	AGATGGGCGT	TCTGCAGGAA	CGTATCACCT	CCACCAAAC	800
	CG					802

15

2) INFORMATION FOR SEQ ID NO: 364

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 819 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

25

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Shigella flexneri*
- (B) STRAIN: ATCC 12022

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 364

	ATGCCGTACC	GCGCGTGTAC	GATGCTCTTG	AGGTGCAAAA	TGGTAATGAG	50
	CGTCTGGTGC	TGGAAGTTCA	GCAGCAGCTC	GGCGGCGGTA	TCGTGCGTAC	100
	CATCGCAATG	GGTTCCTCCG	ACGGTCTGCG	TCGCGGTCTG	GATGTAAAAG	150
35	ACCTCGAACA	CCCGATCGAA	GTCCCGGTAG	GTAAAGCGAC	TCTGGGCCGT	200
	ATCATGAACG	TACTGGGTGA	ACCGGTCGAC	ATGAAAGGCG	AGATCGGTGA	250
	AGAAGAGCGT	TGGGCGATTC	ACCGCGCAGC	ACCTTCCTAC	GAAGAGCTGT	300
	CAAACCTCTA	GGAACCTGCT	GAAACCGGTA	TCAAAGTTAT	CGACCTGATG	350
	TGTCCGTTTC	CTAAGGGCGG	TAAAGTTGGT	CTGTTCCGGT	GTGCGGGTGT	400
40	AGGTAAAACC	GTAAACATGA	TGGAGCTCAT	TCGTAACATC	GCGATCGAGC	450
	ACTCCGGTTA	CTCTGTGTTT	GCGGGCGTAG	GTGAACGTAC	TCGTGAGGGT	500
	AACGACTTCT	ACCACGAAAT	GACCGACTCC	AACGTTATCG	ACAAAGTATC	550
	CCTGGTGTAT	GGCCAGATGA	ACGAGCCGCC	GGGAAACCGT	CTGCGCGTTG	600
	CTCTGACCGG	TCTGACCATG	GCTGAGAAAT	TCCGTGACGA	AGGTCGTGAC	650
45	GTTCTGCTGT	TCGTTGACAA	CATCTATCGT	TACACCCTGG	CCGGTACGGA	700
	AGTATCCGCA	CTGCTGGGCC	GTATGCCTTC	AGCGGTAGGT	TATCAGCCGA	750
	CCCTGGCGGA	AGAGATGGGC	GTTCTGCAGG	AACGTATCAC	CTCCACCAA	800
	ACTGGTTCTA	TCACCTCCG				819

50

2) INFORMATION FOR SEQ ID NO: 365

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 802 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Shigella sonnei*
 (B) STRAIN: ATCC 29930

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 365

	GTACCGCGCG	TGTACGATGC	TCTTGAGGTG	CAAAATGGTA	ATGAGCGTCT	50
	GGTGCTGGAA	GTTTACGAGC	AGCTCGGCGG	CGGTATCGTG	CGTACCATCG	100
10	CAATGGGTTT	CTCCGACGGT	CTGCGTCGCG	GTCTGGATGT	AAAAGACCTC	150
	GAACACCCGA	TCGAAGTCCC	GGTAGGTAAA	GCGACTCTGG	GCCGTATCAT	200
	GAACGTA	CTG				
	AGCGTTGGGC	GATTCACCGC	GCAGCACCTT	CCTACGAAGA	GCTGTCAAAC	300
	TCTCAGGAAC	TGCTGGA	CGGTATCAA	GTTATCGACC	TGATGTGTCC	350
15	GTTTCGCTAAG	GGCGGTAAAG	TTGGTCTGTT	CGGTGGTGCG	GGTGTAGGTA	400
	AAACCGTAAA	CATGATGGAG	CTCATTCGTA	ACATCGCGAT	CGAGCACTCC	450
	GGTTACTCTG	TGTTTGCGGG	CGTAGGTGAA	CGTACTCGTG	AGGGTAACGA	500
	CTTCTACCAC	GAAATGACCG	ACTCCAACGT	TATCGACAAA	GTATCCCTGG	550
	TGTATGGCCA	GATGAACGAG	CCGCCGGGAA	ACCGTCTGCG	CGTTGCTCTG	600
20	ACCGGTCTGA	CCATGGCTGA	GAAATTCCGT	GACGAAGGTC	GTGACGTTCT	650
	GCTGTTCGTT	GACAACATCT	ATCGTTACAC	CCTGGCCGGT	ACGGAAGTAT	700
	CCGCACTGCT	GGGCCGTATG	CCTTCAGCGG	TAGGTTATCA	GCCGACCCTG	750
	GCGGAAGAGA	TGGGCGTTCT	GCAGGAACGT	ATCACCTCCA	CCAAA	800
	TT					802

25

2) INFORMATION FOR SEQ ID NO: 366

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 785 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus aureus*

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 366

	TAACGCCTTG	GTTATTGATG	TGCCTAAAGA	AGAAGGTACA	ATACAACTAA	50
	CATTAGAAAGT	TGCGCTGCAA	TTAGGTGACG	ACGTTGTTTCG	TACAATTGCG	100
45	ATGGATTCAA	CTGATGGTGT	CCAAAGAGGC	ATGGATGTAA	AAGATACAGG	150
	CAAAGAAATT	AGTGACCTG	TTGGTGATGA	AACATTAGGT	CGTGTATTTA	200
	ATGTACTAGG	TGAAACAATT	GACCTTAAAG	AAGAAATTAG	TGATTCTGTT	250
	CGCCGCGATC	CTATCCATCG	TCAAGCACCA	GCATTGATG	AACTTTCAAC	300
	AGAAGTTCAA	ATTTTAGAAA	CAGGTATTAA	AGTAGTAGAT	TTACTAGCAC	350
50	CTTATATTAA	AGGTGGTAAA	ATCGGATTGT	TCGGTGGTGC	CGGTGTAGGT	400
	AAAACAGTAT	TAATCCAAGA	ATTAATTAAC	AACATCGCTC	AAGAGCACGG	450
	TGGTATTTCT	GTATTCGCCG	GTGTAGGTGA	ACGTACTCGT	GAAGGTAACG	500
	ATTTATACTT	CGAAATGAGT	GATAGTGGTG	TAATTAAGAA	AACAGCCATG	550
	GTATTCGGGC	AAATGAATGA	GCCACCTGGT	GCACGTATGC	GTGTTGCATT	600
55	ATCTGGTTTA	ACAATGGCTG	AATATTCCG	TGACGAACAA	GGTCAAGACG	650
	TATTATTATT	CATCGATAAC	ATTTTCAGAT	TTACACAAGC	TGGTTCTGAG	700
	GTATCTGCAT	TATTAGGTCG	TATGCCTTCT	GCAGTAGGTT	ACCAACCAAC	750
	ACTTGCTACT	GAAATGGGAC	AATTACAAGA	ACGTA		785

60

2) INFORMATION FOR SEQ ID NO: 367

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 843 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

10 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus auricularis*
 (B) STRAIN: ATCC 33753

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 367

GAACATAACG AAGTGCCTAA TATTAATAAC GCCTTAGTAC TCGATGTTGA 50
 AAGAGAAGAC GGAACAGTGT CTTTAACTTT AGAAGTAGCT TTACAATTAG 100
 20 GCGATGACGT TGTTCGTACC ATTGCAATGG ATTCAACTGA TGGTGTTAAA 150
 CGTGGTAACG AAGTCAAAGA TACTGGTAAT AGCATTAGCG TACCAGTCGG 200
 AGACGAAACT TTAGGACGTG TCTTCAACGT TCTAGGTGAA ACAATTGATT 250
 TAGAAGATAA ACTTGATGAT TCTGCGCGAC GTGACCCTAT ACATAGAGAA 300
 GCGCCAGCGT TTGATCAATT ATCAACTCAA GTTGAAATTT TAGAAACAGG 350
 25 AATTAAAGTT GTTGACTTAT TAGCACCTTA TATTAAAGGT GGTAAAGTTG 400
 GACTCTTCGG TGGTGCCGGT GTTGGTAAAA CCGTTTAAAT CCAAGAATTA 450
 ATCAACAACA TCGCTCAAGA ACACGGTGGT ATTTCACTCT TTGCCGGTGT 500
 AGGTGAACGT ACACGTGAAG GTAACGACTT GTACTATGAA ATGAGCGACA 550
 GTGGTGTAAT CAAGAAAACA GCCATGGTCT TCGGACAAAT GAACGAACCA 600
 30 CCTGGCGCAC GTATGCGTGT TGCTTTATCT GGTTTAACAA TGGCTGAATA 650
 TTTCCGTGAT GAACAAGGAC AAGACGTATT GTTATTCATC GACAATATTT 700
 TCCGTTTCAC ACAAGCCGGT TCAGAAGTTT CTGCCTTACT AGGTCGTTTA 750
 CCATCAGCCG TTGGTTATCA ACCTACATTA GCAACAGAAA TGGGACAATT 800
 ACAAGAACGT ATTACTTCAA CAACAAAAGG ATCAGTTACT TCA 843

35

2) INFORMATION FOR SEQ ID NO: 368

40 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 849 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

45

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus capitis* subsp. *capitis*
 50 (B) STRAIN: ATCC 27840

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 368

GCTTTGAACA TAATGAAGTT CCTGATATTA ACAATGCCTT ACACATCGAA 50
 55 GTTCCTAAAG AAGATAGCAC ACTTCATTTA ACTTTAGAAG TTGCACTTCA 100
 ATTAGGTGAC GATGTAGTAC GTACAATCGC AATGGACTCA ACTGACGGCG 150
 TTCAAAGAGG TATGGAAGTT AAAGATACAG GTAAAGATAT TAGCGTACCT 200
 GTTGGTGATG CAACTTTAGG AAGAGTATTT AACGTATTAG GAGAAACAAT 250
 CGATTTAGAT GAAAAGATTG ATGATTCACT ACGTCGTGAT CCTATTTCATA 300
 60 GACAGGCACC TGGCTTCGAT GAATTATCTA CTAAAGTAGA AATCTTAGAA 350

	ACAGGTATCA	AAGTAGTAGA	CTTATTAGCA	CCTTACATTA	AAGGTGGTAA	400
	AATTGGATTA	TTCGGTGGTG	CCGGTGTG	TAAGACAGTT	TTAATCCAAG	450
	AACTTATCAA	TAATATCGCT	CAAGAGCATG	GTGGTATTTT	AGTATTCGCC	500
	GGTGTGGTG	AACGTACACG	TGAAGGTAAC	GACCTTACT	ATGAAATGAG	550
5	CGATAGTGGT	GTAATTAAGA	AAACAGCGAT	GGTATTCGGT	CAGATGAACG	600
	AGCCACCTGG	TGCTCGTATG	CGTGTTGCAT	TATCAGGTTT	AACAATGGCA	650
	GAATATTTCC	GTGATGAAGA	AGGCCAAGAC	GTATTATTAT	TCATTGATAA	700
	TATCTTCAGA	TTCACACAAG	CTGGTTCTGA	AGTTTCAGCA	TTACTTGGAC	750
	GTATGCCTTC	AGCCGTTGGT	TATCAACCAA	CACCTTGCTAC	TGAAATGGGT	800
10	CAATTACAAG	AACGTATTAG	TTCAACTAAT	AAAGGTTCTG	TTACTTCAA	849

2) INFORMATION FOR SEQ ID NO: 369

15

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 830 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

25

- (A) ORGANISM: *Staphylococcus cohnii*
- (B) STRAIN: DSM 20260

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 369

30	GAAGTTCCAG	AAATTAATAA	TGCCTTAGTT	CTCGATATAG	AAAGAGAAGA	50
	AGGTACTGTT	GAATTAACGT	TAGAAGTTGC	ATTACAACCT	GGTGATGACG	100
	TAGTACGAAC	AATCGCAATG	GATTCAACTG	ATGGTGTTAA	ACGTGGTACA	150
	GAAGTTAGAG	ATAGCGGAAA	TAGTATCAGC	GTACCAGTTG	GTAATGAAAC	200
	ATTAGGTAGA	GTATTTAATG	TATTAGGTGA	TACGATAGAT	TTAGATGAAG	250
35	ACATAGATGA	CTCAGTGCGT	CGTGACCCAA	TTCATAGAGA	AGCACCTGCA	300
	TTTGATCAGT	TATCTACTAA	AGTTGAAATT	TTAGAAACAG	GTATCAAAGT	350
	CATTGATTTA	TTAGCACCAT	ATATCAAAGG	TGGTAAAGTT	GGATTATTTCG	400
	GTGGTGCCCG	TGTTGGTAA	ACTGTATTAA	TTCAAGAATT	AATCAATAAT	450
	ATCGCTCAAG	AGCATGGTGG	TATATCCGTA	TTTGCTGGTG	TAGGTGAGCG	500
40	TACGCGTGAA	GGTAATGACC	TATACTTTGA	AATGAGTGAT	AGTGGTGTTA	550
	TTAAAAAGAC	AGCTATGGTA	TTTGGACAAA	TGAACGAACC	ACCTGGTGCG	600
	CGTATGCGAG	TAGCACTTTC	TGGTTTAAAC	ATGGCTGAAT	ATTTCCGGGA	650
	TGAACAAGGA	CAAGATGTTC	TATTATTCAT	AGATAACATC	TTTAGATTTA	700
	CTCAAGCTGG	TTCAGAAGTT	TCTGCGTTAT	TAGGTCGTAT	GCCTTCAGCT	750
45	GTTGGTTACC	AACCAACGTT	AGCAACTGAA	ATGGGACAAT	TACAAGAACG	800
	TATTACTTCT	ACAACATAAG	GTTTCAGTAAC			830

50 2) INFORMATION FOR SEQ ID NO: 370

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 787 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

55

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

60

(A) ORGANISM: *Staphylococcus epidermidis*
 (B) STRAIN: ATCC 14990

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 370

5
 AATAATGCAT TACACATCGA AGTTCCTAAA GAAGATGGAG CGCTTCAATT 50
 AACATTAGAA GTTGCACTTC AACTAGGTGA CGATGTAGTT CGTACAATTG 100
 CAATGGACTC AACTGACGGC GTTCAAAGAG GAATGGAAGT TAAAGATACA 150
 GGTAGAGACA TAAGTGTACC TGTCGGTGAC GTAACCTAG GAAGAGTGTT 200
 10 TAACGTAGTA GGAGAACTA TTGACTTAGA TGAAAAAATT GATGATTCAG 250
 TACGACGTGA CCCTATCCAT AGACAAGCTC CAGGATTCGA CGAATTATCA 300

 ACAAAAGTAG AAATCTTAGA AACTGGTATT AAAGTAGTAG ACTTATTAGC 350
 ACCTTACATA AAAGGTGGTA AAATTGGATT ATTTGGTGGT GCCGGTGTAG 400
 GTAAAACCGT ACTAATCCAA GAACTTATTA ATAACATCGC TCAAGAACAC 450
 15 GGTGGTATCT CAGTATTCGC TGGTGTGGT GAACGTACAC GTGAAGGTAA 500
 TGATCTTTAC TATGAAATGA GTGACAGTGG TGTTATCAAG AAAACTGCAA 550
 TGGTCTTTGG TCAAATGAAT GAGCCACCTG GTGCACGTAT GCGTGTAGCA 600
 TTATCCGGAT TAACAATGGC CGAATATTTT CGAGATGAAG AAGGCCAAGA 650
 TGTGTTATTA TTCATTGATA ACATTTTCAG ATTCACTCAA GCTGGTTCAG 700
 20 AAGTTTCTGC GTTATTAGGT CGTATGCCAT CAGCTGTTGG TTATCAACCT 750
 ACACTTGCTA CAGAAATGGG TCAATTACAA GAACGTA 787

25 2) INFORMATION FOR SEQ ID NO: 371

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 830 bases
 (B) TYPE: Nucleic acid
 30 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

35 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Staphylococcus haemolyticus*
 (B) STRAIN: ATCC 29970

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 371

40
 GAAGTACCTG AAATTAATAA CGCCTTAATC ATCGAAGTTC CCAAAGAAGA 50
 TGGTACTTTT GAATTAACGC TTGAAGTTGC ATTACAACCTA GGTGATGACG 100
 TTGTTTCGTAC AATTGCTATG GATTCAACAG ATGGTGTTCA ACGTGGTATG 150
 GAAGTTCAGA ACACTGGAAA AGACATTTCA GTACCAGTTG GCGAAGTAAC 200
 45 TTTAGGACGT GTATTTAACG TATTAGGTGA CACAATTGAT TTAGAAGATA 250
 AATTAGATGG TTCAGTAAGA CGTGATCCAA TTCATAGACA ATCACCTAAC 300
 TTTGACGAAT TATCTACTGA AGTAGAAATT CTTGAAACTG GAATCAAAGT 350
 TGTAGACTTA TTAGCACCAT ACATCAAAGG TGGTAAATC GGTCTATTTG 400
 GTGGTGCCGG TGTTGGTAAA ACCGTTTAA TCCAAGAATT GATTAATAAT 450
 50 ATCGCACAAG AACATGGTGG TATCTCAGTA TTTGCTGGTG TAGGTGAACG 500
 TACACGTGAA GGTAACGACC TATATTATGA AATGAGAGAT AGTGGTGTTA 550
 TTAAGAAAAC AGCAATGGTA TTTGGTCAAA TGAACGAGCC ACCTGGTGCA 600
 CGTATGCGTG TGGCACTTTC TGCATTGACA ATGGCTGAGT ATTTCCGTGA 650
 TGAACAAGGA CAAGACGTTC TGTTATTCAT CGATAACATT TTCAGATTTA 700
 55 CTCAAGCAGG TTCAGAAGTA TCAGCATTAT TGGGACGTAT GCCTTCAGCT 750
 GTAGGTTATC AACCTACTTT AGCTACAGAA ATGGGTCAAT TACAAGAACG 800
 TATTACATCA ACGAATAAAG GTTCAGTAAC 830

60

2) INFORMATION FOR SEQ ID NO: 372

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 846 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

10

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus hominis* subsp. *hominis*
 (B) STRAIN: ATCC 27844

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 372

TCGAACATAA TGAAGTCCCT GAAATTAATA ATGCCCTAAT TATTGAAGTA 50
 CCCAAAAATG ATGGCACATT TAAATTAACA TTAGAAGTTG CATTGCAACT 100
 AGGTGATGAT GTTGTTTCGTA CTATTGCAAT GGATTCAACT GATGGTGTTT 150
 20 AACGTGGTAT GCAAGTTGTG AATACTGGTA AAGATATTAG TGTTCTTGTA 200
 GGTGAAGAAA CACTTGGACG TGTGTTTAAC GTTTTAGGAG AAACAATAGA 250
 TTTAAACGAA AAAATAGATA GTTCTGTTAG ACGTGATCCA ATTCATCGTC 300
 GTCAACCTAA TTTTGATGAA TTATCTACTG AAGTAGAAAT TCTTGAAACA 350
 GGTATTAAAG TTGTAGACTT ATTAGCACCT TATATTAAAG GTGGTAAGAT 400
 25 TGGTTTATTC GGTGGTGCCG GCGTAGGTAA AACTGTATTA ATTCAAGAAT 450
 TAATCAATAA TATCGCTCAA GAACATGGTG GTATTTCTGT ATTCGCTGGT 500
 GTAGGTGAAC GTACTCGTGA AGGTAACGAT TTATACTATG AAATGAGCGA 550
 TAGTGGCGTT ATCAATAAAA CAGCCATGGT ATTTGGGCAA ATGAATGAGC 600
 CGCCAGGTGC GCGTATGCGT GTTGCTTTAT CAGCATTGAC AATGGCTGAA 650
 30 TATTTCCGTG ATGAACAAGG TCAAGATGTA CTTTTATTCA TTGACAATAT 700
 TTTCCGCTTT ACTCAAGCTG GTTCTGAAGT TTCAGCATT TTAGGACGTA 750
 TGCCTTCAGC TGTAGGTTAT CAACCTACAT TAGCAACTGA AATGGGTCAA 800
 TTACAAGAAC GTATTACATC TACTAATAAA GGTTCAGTCA CTTCAA 846

35

2) INFORMATION FOR SEQ ID NO: 373

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 846 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

45

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus hominis*
 (B) STRAIN: CSG 175

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 373

TCGAACATAA TGAAGTCCCT GAAATTAATA ATGCCCTAAT TATTGAAGTA 50
 CCCAAAAATG ATGGCACATT CAAATTAACA TTAGAAGTTG CATTGCAACT 100
 55 AGGTGATGAT GTTGTTTCGTA CTATTGCAAT GGATTCAACT GATGGTGTTT 150
 AACGTGGTAT GCAAGTTGTG AATACTGGTA AAGATATTAG TGTTCTTGTA 200
 GGTGAAGAAA CACTTGGACG TGTGTTTAAC GTTTTAGGAG AAACAATAGA 250
 TTTAAACGAA AAAATAGATA GTTCTGTTAG ACGTGATCCA ATTCATCGTC 300
 GTCAACCTAA TTTTGATGAA TTATCTACTG AAGTAGAAAT TCTTGAAACA 350
 60 GGTATTAAAG TTGTAGACTT ATTAGCACCT TATATTAAAG GTGGTAAGAT 400

	TGGTTTATTC	GGTGGTGCCG	GCGTAGGTAA	AACTGTATTA	ATTCAAGAAT	450
	TAATCAATAA	TATCGCTCAA	GAACATGGTG	GTATTTCTGT	ATTGCTGGT	500
	GTAGGTGAAC	GTAATCGTGA	AGGTAACGAT	TTATACTATG	AAATGAGCGA	550
	TAGTGGCGTT	ATCAATAAAA	CAGCCATGGT	ATTTGGGCAA	ATGAATGAGC	600
5	CGCCAGGTGC	GCGTATGCGT	GTTGCTTTAT	CAGCATTGAC	AATGGCTGAA	650
	TATTTCCGTG	ATGAACAAGG	TCAAGATGTA	CTTTTATTCA	TTGACAATAT	700
	TTTCCGCTTT	ACTCAAGCTG	GTTCTGAAGT	TTCAGCATT	TTAGGACGTA	750
	TGCCTTCAGC	TGTAGGTTAT	CAACCTACAT	TAGCAACTGA	AATGGGTCAA	800
	TTACAAGAAC	GTATTACATC	TACTAATAAA	GGTTCAGTCA	CTTCAA	846

10

2) INFORMATION FOR SEQ ID NO: 374

15 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 835 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus lugdunensis*
 (B) STRAIN: ATCC 43809

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 374

	ATAATGAAGT	GCCTGAAATA	AATAATGCGC	TCATTGTTGA	AATTCCTAAA	50
30	AGTGATACAA	CAATCAGTTT	AACACTTGAA	GTTGCTTTGC	AATTAGGTGA	100
	CGATGTTGTA	CGTACTATTG	CAATGGATTC	AACTGATGGC	GTTCAACGTG	150
	GTATGGAAGT	TCAAAACACA	GGTAAAGACA	TCAGTGTACC	TGTTGGAGAT	200
	GAAACATTAG	GAAGAGTATT	TAACGTTTTA	GGAGAATCTA	TTGATTTAGA	250
	AGAAAAGCTA	GATGACTCTG	TGCGTAGAGA	TCCAATTCAT	AGACTAGCAC	300
35	CTAAATTTGA	TGAATTATCT	ACAGAAGTAG	AAATTCTTGA	AACTGGTATT	350
	AAAGTTGTTG	ATTTATTAGC	ACCATATATT	AAAGGTGGTA	AAGTTGGATT	400
	GTTTGGTGGT	GCCGGAGTAG	GTAAAACGGT	ATTAATTCAA	GAATTAATCA	450
	ACAATATTGC	TCAAGAACAT	GGTGGTATTT	CTGTGTTTGC	CGGAGTAGGT	500
	GAACGTACAC	GTGAAGGTAA	TGACTTATAT	TATGAAATGA	GCGATAGTGG	550
40	CGTAATTAAG	AAAACAGCGA	TGGTATTTGG	CCAAATGAAT	GAACCACCTG	600
	GTGCACGTAT	GAGAGTTGCG	TTATCTGCCCT	TAACAATGGC	TGAATATTTT	650
	CGTGACGAGC	AAGGACAAGA	CGTATTGCTG	TTTATCGATA	ATATATTCCG	700
	TTTTACACAA	GCAGGTTTCA	AAGTATCTGC	ATTACTTGGA	CGTATGCCAT	750
	CTGCCGTTGG	TTATCAACCA	ACATTGGCTA	CAGAAATGGG	ACAATTGCAA	800
45	GAAAGAATTA	CATCTACAAA	TAAAGGTTCT	GTAAC		835

2) INFORMATION FOR SEQ ID NO: 375

50

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 842 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

55

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus saprophyticus*

60

(B) STRAIN: ATCC 15305

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 375

5	GAGCACAATG	AAGTTCCAGA	AATTAACAAT	GCCTTAGTGC	TAGACGTTGA	50
	AAGAGATGAA	GGTACAGTAT	CTCTTACATT	AGAAGTGGCA	TTACAACCTG	100
	GCGATGATGT	CGTACGTACA	ATTGCAATGG	ATTCTACTGA	TGGTGTTAAA	150
	CGTGGTACAG	AAGTTTCGAGA	TAGCGGAGAT	AGCATCAGTG	TTCCAGTTGG	200
	TGATGCTACG	TTAGGACGTG	TGTTTAATGT	TCTTGGTGAT	ACAATTGACT	250
10	TAGACGAGAA	GCTTGATACT	TCTGTCAAAC	GTGATCCAAT	TCATAGAGAA	300
	GCACCTGCAT	TCGATCAATT	ATCAACAAAA	GTTGAAATCT	TAGAAACAGG	350
	TATTAAAGTA	ATTGATTTAC	TTGCACCATA	TATTAAAGGT	GGTAAAATCG	400
	GTTTATTCGG	TGGCGCTGGT	GTAGGTAAAA	CAGTATTAAT	TCAAGAATTA	450
	ATTAATAATA	TAGCTCAAGA	ACATGGTGGT	ATTTCAGTAT	TTGCCGGCGT	500
15	AGGTGAACGT	ACGCGTGAAG	GTAATGACTT	ATACTACGAA	ATGAGTGATA	550
	GTGGTGTTAT	TAAGAAAACA	GCTATGGTCT	TCGGACAAAT	GAATGAGCCA	600
	CCTGGTGCGC	GTATGCGTGT	TGCTTTATCA	GGCTTAACAA	TGGCTGAACA	650
	CTTCCGTGAT	GTACAAGGAC	AAGATGTTTT	ACTATTTATT	GATAACATAT	700
	TCAGATTTAC	GCAAGCTGGT	TCAGAAAGTAT	CAGCACTATT	AGGTCGTATG	750
20	CCATCAGCCG	TTGGTTATCA	ACCTACCCTT	GCTACTGAAA	TGGGTCAATT	800
	ACAAGAACGT	ATTACATCAA	CAACTAAAGG	ATCTGTAACG	TC	842

25 2) INFORMATION FOR SEQ ID NO: 376

(i) SEQUENCE CHARACTERISTICS:

	(A)	LENGTH: 842 bases
	(B)	TYPE: Nucleic acid
30	(C)	STRANDEDNESS: Double
	(D)	TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

35 (vi) ORIGINAL SOURCE:

	(A)	ORGANISM: <i>Staphylococcus simulans</i>
	(B)	STRAIN: ATCC 27848

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 376

40	TGATGAACCTG	CCTAAGATTA	ATAACGCATT	AGTGCTAGAT	GTACCTAAGA	50
	AAGATGGCAC	GACTGAATCT	CTTACATTAG	AAGTAGCACT	TGAATTAGGC	100
	GACGACGTAG	TTAGAACTAT	CGCCATGGAC	TCTACAGACG	GAATTAAACG	150
	TGGTGACGAC	GTTAAAGACA	CTGGTCGTCC	AATCAGTGTA	CCTGTCGGTG	200
45	AAGATACGTT	AGGAAGAGTA	TTTAACGTTT	TAGGTGATCC	AATCGATAAT	250
	GATGGACCGA	TTTCTGAATC	AGTTCCACGT	GAACCAATTC	ATAGACAACC	300
	ACCTAAATTT	GATGAATTAT	CAACAAAAGT	TGAACTACTT	GAAACTGGTA	350
	TCAAAGTAGT	AGACTTATTA	GCACCATATA	TCAAAGGTGG	TAAAGTTGGT	400
	TTATTCCGTG	GTGCCGGAGT	AGGTAAAACT	GTATTAATCC	AAGAATTAAT	450
50	TAATAACATC	GCTCAAGAAC	ACGGCGGTAT	TTCAGTATTC	GCAGGTGTTG	500
	GTGAACGTAC	ACGTGAAGGT	AACGACTTGT	ACTTCGAAAT	GAGCGACAGT	550
	GGTGTTATCA	AGAAAACAGC	GATGGTATTC	GGACAAATGA	ACGAACCACC	600
	TGGTGACAGT	ATGCGTGTAG	CTTTATCAGG	TTTAACAATG	GCTGAATACT	650
	TCCGTGATGT	TAAAGGACAA	GACGTTCTTT	TATTCATCGA	TAACATTTTC	700
55	CGCTTCACAC	AAGCAGGTTC	TGAGGTATCA	GCATTGCTTG	GCCGTATGCC	750
	ATCAGCCGTT	GGTTACCAAC	CAACATTGGC	AACAGAAAATG	GGTCAATTAC	800
	AAGAACGTAT	CACTTCTACA	ATGAAAGGTT	CTATCACATC	TA	842

60

2) INFORMATION FOR SEQ ID NO: 377

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 841 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

10

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus warneri*
(B) STRAIN: ATCC 27836

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 377

CATAACGAAG TCCCTGATAT TAATAATGCC CTTATTATTG AAGTTCCAAA 50
AGAAGATGGA ACGTTAAACT TAACATTAGA AGTTGCACTA CAATTAGGTG 100
ATGATGTTGT ACGTACAATT GCAATGGATT CAACTGATGG TGTTCAAAGA 150
20 GGCATGGATG TTAAAGACAC AGGTAAAGAT ATTAGTGTAC CTGTAGGCCGA 200
TGAAACGCTT GGAAGAGTGT TTAATGTACT AGGTGAAACA ATTGACTTGG 250
AAGAGAAAAT TGATGATTCC GTACGTCGTG ATCCAATCCA TAGACAATCA 300
CCAGGTTTCG ATGAATTATC TACTGAAGTA GAAATCTTAG AAACAGGTAT 350
TAAAGTAGTA GACTTATTAG CACCTTACAT TAAAGGTGGT AAAGTTGGAC 400
25 TATTCGGTGG TGCCGGAGTA GGTAACCCG TTTTAATCCA AGAATTAATT 450
AACAATATTG CACAAGAAC A TGGTGGTATT TCAGTATTCG CGGGTGTAGG 500
TGAACGTA CTGTAAGGTA ATGATTTATA CTATGAAATG AGTGATAGTG 550
GTGTAATTAA GAAAACAGCG ATGGTATTTG GACAAATGAA TGAACCACCT 600
GGCGCACGTA TGCCTGTAGC TTTATCTGGT TTAACATATG CTGAATACTT 650
30 CCGTGATGAA CAAGGACAAG ACGTACTTTT ATTCATCGAT AATATTTTCA 700
GATTTACACA AGCTGGTTCT GAAGTTTCTG CATTACTTGG TCGTATGCCT 750
TCAGCCGTTG GTTACCAACC AACATTAGCA ACTGAAATGG GTCAATTACA 800
AGAACGAATT ACATCTACAA ATAAAGGTTT TGTAACATCT A 841

35

2) INFORMATION FOR SEQ ID NO: 378

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 846 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

45 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus acidominimus*
(B) STRAIN: ATCC 51726

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 378

TTTAACACGA ATGAACCGCT TCCTGAGATA AATAATGCAC TTGTTGTTTA 50
CAAAGACAGT GAGAAAAAAC ATAAATCGT TCTTGAAGTA GCTCTTGAAC 100
55 TTGGTGAAGG CCTCGTTCGT ACCATTGCTA TGGAATCAAC TGATGGTTTG 150
ACACGTGGTC TAGAAGTTCT TGATACAGGC CGTGCAATCA GTGTACCAGT 200
TGGTAAAGAA ACGCTTGGAC GTGTCTTCAA CGTTCTTGGT GATGCTATCG 250
ATCTTGAAGA ACCATTTGGA GAAGATGCAG AACGTCACCC CATTGATAAG 300
AGTGCCCCAA CTTTTGATGA ATTATCAACG TCAACAGAAA TCCTTGAAAC 350
60 AGGGATTAAA GTTATCGACC TACTTGCCCC TACTTAAAA GGAGGGAAGG 400

	TTGGACTTTT	CGGTGGTGCC	GGAGTTGGTA	AGACCGTTCT	TATCCAAGAG	450
	TTGATTCATA	ACATTGCTCA	AGAGCATGGT	GGTATTCAG	TATTTACCGG	500
	AGTTGGTGAA	CGTACACGTG	AAGGTAATGA	CCTCTATTGG	GAAATGAAAG	550
	AATCAGGCGT	TATTGAAAAA	ACAGCTATGG	TATTTGGTCA	GATGAATGAG	600
5	CCACCTGGTG	CACGTATGCG	TGTAGCCCTT	ACTGGTTTGA	CAATCGCTGA	650
	ATATTTCCGT	GATGTTGAAG	GACAGGACGT	GCTTCTCTTT	ATTGATAACA	700
	TTTTTCGTTT	CACACAAGCA	GGTTCTGAAG	TTTCAGCTCT	TCTTGGACGT	750
	ATGCCATCAG	CCGTTGGTTA	TCAACCAACC	TTGGCAACTG	AAATGGGTCA	800
	ATTGCAAGAA	CGTATCACGT	CAACTAAAAA	AGGTTCTGTT	ACATCA	846

10

2) INFORMATION FOR SEQ ID NO: 379

15 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 846 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus agalactiae*
- (B) STRAIN: ATCC 12403

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 379

	TTGCAAGTGG	CGACAACTT	CCTGAGATTA	ATAATGCATT	GATTGTCTAT	50
30	AAAAATGGCG	ATAAGTCACA	AAAAGTAGTA	CTTGAAGTTA	CTCTTGAAGT	100
	TGGTGACGGC	CTCGTTCGTA	CAATCGCTAT	GGAATCAACT	GATGGGCTTA	150
	CACGTGGTTT	GGAAGTATTA	GATACTGGTC	GCGCAATTAG	TGTGCCCGTT	200
	GGTAAGGATA	CTTTGGGTCG	TGTCTTCAAC	GTTCTTGGAG	ATGCTATTGA	250
	CCTTGAAGAG	CCTTTTGCAG	AAGATGCAGA	ACGTCAACCA	ATCCATAAAA	300
35	AAGCACCATC	GTTTGATGAA	TTATCAACAT	CATCAGAAAT	CTTAGAAACA	350
	GGTATTAAAG	TTATTGACTT	ATTAGCACCT	TACTTAAAAG	GTGGTAAAGT	400
	TGGACTTTTC	GGTGGTGCAG	GTGTTGGTAA	AACCGTTCTT	ATTCAAGAAT	450
	TAATCCACAA	CATCGCCCAA	GAACATGGTG	GTATTTTCAGT	ATTTACTGGT	500
	GTAGGAGAAC	GTA CTCTGTA	AGGGAATGAC	CTTTATTGGG	AAATGAAAGA	550
40	ATCTGGCGTT	ATTGAAAAAA	CGGCTATGGT	CTTTGGTCAA	ATGAATGAAC	600
	CACCAGGAGC	ACGTATGCGT	GTGGCACTTA	CTGGTCTTAC	AATAGCTGAG	650
	TACTTCCGTG	ATGTAGAAGG	ACAAGATGTG	CTTCTCTTCA	TTGATAATAT	700
	CTTCCGTTTC	ACACAAGCTG	GGTCAGAAGT	GTCAGCGCTT	TTAGGTCGTA	750
	TGCCTTCAGC	CGTTGGTTAT	CAACCAACAC	TTGCTACAGA	AATGGGACAA	800
45	TTACAAGAGC	GTATCACTTC	AACTAAAAAA	GGTTCTGTTA	CCTCAA	846

2) INFORMATION FOR SEQ ID NO: 380

50

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 846 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

55

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus agalactiae*

60

(B) STRAIN: ATCC 13813

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 380

5	TTGCAAGTGG	CGACAAACTT	CCTGAGATTA	ATAATGCATT	GATTGTCTAT	50
	AAAAATGGCG	ATAAGTCACA	AAAAGTAGTA	CTTGAAGTTG	CTCTTGAAC	100
	TGGTGACGGC	CTCGTTCGTA	CAATCGCTAT	GGAATCAACT	GATGGGCTTA	150
	CACGTGGTTT	GGAAGTATTA	GATACTGGTC	GCGCAATTAG	TGTGCCGGTT	200
	GGTAAGGATA	CTTTGGGTCG	TGTCTTCAAC	GTTCTTGGAG	ATGCTATTGA	250
10	TCTTGAAGAG	CCTTTTGCAG	AAGATGCAGA	ACGTCAACCA	ATCCATAAAA	300
	AAGCACCATC	GTTTGATGAA	TTATCAACAT	CATCAGAAAT	CTTAGAAACT	350
	GGTATTAAAG	TTATTGACTT	ATTAGCACCT	TACTTAAAAG	GTGGTAAAGT	400
	TGGACTTTTC	GGTGGTGCGG	GTGTTGGTAA	AACCGTTCTT	ATTCAAGAAT	450
	TAATCCACAA	CATCGCCCAA	GAACATGGTG	GTATTTTCAGT	ATTTACTGGT	500
15	GTAGGAGAAC	GTAATCGTGA	AGGGAATGAC	CTTTATTGGG	AAATGAAAGA	550
	ATCTGGCGTT	ATTGAAAAAA	CGGCTATGGT	CTTTGGTCAA	ATGAATGAAC	600
	CACCAGGAGC	ACGTATGCGT	GTGGCACTTA	CTGGTCTTAC	AATAGCTGAG	650
	TACTTCCGTG	ATGTAGAAGG	ACAAGATGTG	CTTCTCTTCA	TTGATAATAT	700
	CTTCCGTTTC	ACACAAGCTG	GGTCAGAAGT	GTCAGCGCTT	TTAGGTCGTA	750
20	TGCCTTCAGC	CGTTGGTTAT	CAACCAACAC	TTGCTACAGA	AATGGGACAA	800
	TTACAAGAGC	GTATCACTTC	AACTAAAAAA	GGTTCTGTTA	CCTCAA	846

25 2) INFORMATION FOR SEQ ID NO: 381

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 845 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

35 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus agalactiae*
 (B) STRAIN: ATCC 12973

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 381

40	TTGCAAGTGG	CGACAAACTT	CCTGAGATTA	ATAATGCATT	GATTGTCTAT	50
	AAAAATGGCG	ATAAGTCACA	AAAAGTAGTA	CTTGAAGTTG	CTCTTGAAC	100
	TGGTGACGGC	CTCGTTCGTA	CAATCGCTAT	GGAATCAACT	GATGGGCTTA	150
	CACGTGGTTT	GGAAGTATTA	GATACTGGTC	GTGCAATTAG	TGTGCCGGTT	200
45	GGTAAGGATA	CTTTGGGTCG	TGTCTTCAAC	GTTCTTGGAG	ATGCTATTGA	250
	CCTTGAAGAG	CCTTTTGCAG	AAGATGCAGA	ACGTCAACCA	ATCCATAAAA	300
	AAGCACCATC	ATTTGATGAA	TTATCAACAT	CATCAGAAAT	CTTAGAAACA	350
	GGTATTAAAG	TTATTGACTT	ATTAGCACCT	TACTTAAAAG	GTGGTAAAGT	400
	TGGACTTTTC	GGTGGTGCGG	GTGTTGGTAA	AACCGTTCTT	ATTCAAGAAT	450
50	TAATCCACAA	CATCGCCCAA	GAACATGGTG	GTATTTTCAGT	ATTTACTGGT	500
	GTAGGAGAAC	GTAATCGTGA	AGGGAATGAC	CTTTATTGGG	AAATGAAAGA	550
	ATCTGGCGTT	ATTGAAAAAA	CGGCTATGGT	CTTTGGTCAA	ATGAATGAAC	600
	CACCAGGAGC	ACGTATGCGT	GTGGCACTTA	CTGGTCTTAC	AATAGCTGAG	650
	TACTTCCGTG	ATGTAGAAGG	ACAAGATGTG	CTTCTCTTCA	TTGATAATAT	700
55	CTTCCGTTTC	ACACAAGCTG	GGTCAGAAGT	GTCAGCGCTT	TTAGGTCGTA	750
	TGCCTTCAGC	CGTTGGTTAT	CAACCAACAC	TTGCTACAGA	AATGGGACAA	800
	TTACAAGAGC	GTATCACTTC	AACTAAAAAA	GGTTCTGTTA	CCTCA	845

60

2) INFORMATION FOR SEQ ID NO: 382

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 845 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

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(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus agalactiae*
 (B) STRAIN: ATCC 27591

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 382

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TTGCAAGTGG CGACAAACTT CCTGAGATTA ATAATGCATT GATTGTCTAT      50
AAAAATGGCG ATAAGTCACA AAAAGTAGTA CTTGAAGTTG CTCTTGAAGT      100
TGGTGACGGC CTCGTTTCGTA CAATCGCTAT GGAATCAACT GATGGGCTTA      150
20 CACGTGGTTT GGAAGTATTA GATACTGGTC GCGCAATTAG TGTGCCGGTT      200
GGTAAGGATA CTTTGGGTCG TGTCTTCAAC GTTCTTGGAG ATGCTATTGA      250
CCTTGAAGAG CCTTTTGCAG AAGATGCAGA ACGTCAACCA ATCCATAAAA      300
AAGCACCATC GTTTGATGAA TTATCAACAT CATCAGAAAT CTTAGAAACT      350
GGTATTAAAG TTATTGACTT ATTAGCACCT TACTTAAAAG GTGGTAAAGT      400
25 TGGACTTTTC GGTGGTGCAG GTGTTGGTAA AACCGTTCTT ATTCAAGAAT      450
TAATCCACAA CATCGCCCAA GAACATGGTG GTATTTTCAGT ATTTACTGGT      500
GTAGGAGAAC GTACTCGTGA AGGGAATGAC CTTTATTGGG AAATGAAAGA      550
ATCTGGCGTT ATTGAAAAAA CGGCTATGGT CTTTGGTCAA ATGAATGAAC      600
CACCAGGAGC ACGTATGCGT GTGGCACTTA CTGGTCTTAC AATAGCTGAG      650
30 TACTTCCGTG ATGTAGAAGG ACAAGATGTG CTTCTCTTCA TTGATAATAT      700
CTTCCGTTTC ACACAAGCTG GGTGAGAAGT GTCAGCGCTT TTAGGTCGTA      750
TGCCTTCAGC CGTTGGTTAT CAACCAACAC TTGCTACAGA AATGGGACAA      800
TTACAAGAGC GTATCACTTC AACTAAAAAA GGTTCGTGTA CATCA          845

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35

2) INFORMATION FOR SEQ ID NO: 383

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 845 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

45

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus agalactiae*
 (B) STRAIN: CDC ss1073

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 383

```

TTGCAAGTGG CGACAAACTT CCTGAGATTA ATAATGCATT GATTGTCTAT      50
AAAAATGGCG ATAAGTCACA AAAAGTAGTA CTTGAAGTTG CTCTTGAAGT      100
55 TGGTGACGGC CTCGTTTCGTA CAATCGCTAT GGAATCAACT GATGGGCTTA      150
CACGTGGTTT GGAAGTATTA GATACTGGTC GCGCAATTAG TGTGCCGGTT      200
GGTAAGGATA CTTTGGGTCG TGTCTTCAAC GTTCTTGGAG ATGCTATTGA      250
CCTTGAAGAG CCTTTTGCAG AAGATGCAGA ACGTCAACCA ATCCATAAAA      300
AAGCACCATC GTTTGATGAA TTATCAACAT CATCAGAAAT CTTAGAAACT      350
60 GGTATTAAAG TTATTGACTT ATTAGCACCT TACTTAAAAG GTGGTAAAGT      400

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	TGGA	CTTTTC	GGTGGTGCAG	GTGTTGGTAA	AACCGTTCTT	ATTCAAGAAT	450
	TAATCCACAA	CATCGCCCAA	GAACATGGTG	GTATTTTCAGT	ATTTACTGGT		500
	GTAGGAGAAC	GTACTCGTGA	AGGGAATGAC	CTTTATTGGG	AAATGAAAGA		550
	ATCTGGCGTT	ATTGAAAAAA	CGGCTATGGT	CTTTGGTCAA	ATGAATGAAC		600
5	CACCAGGAGC	ACGTATGCGT	GTGGCACTTA	CTGGTCTTAC	AATAGCTGAG		650
	TACTTCCGTG	ATGTAGAAGG	ACAAGATGTG	CTTCTCTTCA	TTGATAATAT		700
	CTTCCGTTTC	ACACAAGCTG	GGTCAGAAGT	GTCAGCGCTT	TTAGGTCGTA		750
	TGCCTTCAGC	CGTTGGTTAT	CAACCAACAC	TTGCTACAGA	AATGGGACAA		800
	TTACAAGAGC	GTATCACTTC	AACTAAAAAA	GGTTCTGTTA	CATCA		845

10

2) INFORMATION FOR SEQ ID NO: 384

15 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 845 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus dysgalactiae*

25 (B) STRAIN: ATCC 43078

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 384

	TTGCTAGTGG	GGACAAACTT	CCAGAGATTA	ATAATGCATT	GATTGTTTAT	50	
30	AAAGATAGTG	ATAAAAAGCA	AAAAATCGTC	CTTGAAGTTG	CTCTGGAAGT	100	
	TGGTGACGGT	ATGGTGCGAA	CAATCGCTAT	GGAATCAACT	GATGGGCTTA	150	
	CACGTGGGTT	AGAAGTTCTT	GACACTGGTC	GTGCGATTAG	TGTACCAGTA	200	
	GGTAAAGAAA	CTTTGGGACG	CGTCTTTAAT	GTACTTGGAG	AAACCATTGA	250	
	CTTGGAAGAA	CCATTTGCAG	AAGACGTTGA	CCGTCAGCCA	ATCCATAAAA	300	
35	AAGCACCATC	GTTTGATGAA	TTATCAACAT	CATCAGAAAT	TCTTGAAACT	350	
	GGTATCAAGG	TAATTGACCT	TCTTGCCCCT	TACCTTAAAG	GTGGTAAAGT	400	
	TGGA	CTTTTC	GGGGGTGCCG	GAGTTGGTAA	GACTGTCCTT	ATCCAAGAAT	450
	TAATCCACAA	TATCGCCCAA	GAACACGGAG	GTATTTTCAGT	ATTTACCGGT	500	
	GTTGGTGAGC	GAACACGTGA	AGGAAATGAC	CTTTACTGGG	AAATGAAAGA	550	
40	ATCAGGCGTT	ATTGAGAAAA	CTGCCATGGT	TTTTGGTCAG	ATGAATGAGC	600	
	CGCCTGGGGC	ACGTATGCGT	GTAGCCCTTA	CTGGTTTAAC	CATTGCTGAG	650	
	TATTTCCGTG	ATGTAGAAGG	CCAAGATGTT	TTGCTCTTTA	TTGATAATAT	700	
	CTTCCGTTTC	ACTCAGGCAG	GTTCAGAAGT	ATCAGCCCTC	TTAGGCCGTA	750	
	TGCCTTCTGC	TGTTGGTTAC	CAACCGACCC	TTGCTACTGA	AATGGGACAA	800	
45	TTGCAAGAAC	GTATTACGTC	AACTCAAAAA	GGATCTGTTA	CTTCT	845	

2) INFORMATION FOR SEQ ID NO: 385

50

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 846 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- 55 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

60 (A) ORGANISM: *Streptococcus equi* subsp. *equi*

(B) STRAIN: ATCC 9528

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 385

5	TTGCGAGTGG	GGACAAACTA	CCAGAGATTA	ATAATGCGTT	GATAGTTTAT	50
	AAAGATGGCG	ATAAAAAGCA	AAAAATCGTT	CTCGAGGTTG	CCCTAGAGCT	100
	TGGAGACGGT	ATGGTACGTA	CAATTGCTAT	GGAATCAACC	GATGGGCTTA	150
	CACGTGGATT	AGAGGTTCTT	GATACTGGTC	GTGCCATTAG	TGTACCAGTT	200
	GGTAAAGAGA	CTCTAGGTCG	TGTTTTCAAC	GTTCTTGGTG	AAACCATCGA	250
10	CCTAGAAGCA	CCATTTGCAG	ATGATGTTAA	TCTGTAACCG	ATCCATAAAA	300
	AAGCACCAGC	CTTTGATGAA	TTGTCAACAT	CATCAGAAAT	TCTTGAAACA	350
	GGTATCAAGG	TTATTGACCT	GCTTGCCCCT	TACTTAAAGG	GTGGTAAGGT	400
	CGGTCTTTTC	GGTGGTGCCG	GAGTTGGTAA	AACCGTTCTT	ATCCAAGAAT	450
	TAATCCACAA	TATCGCTCAA	GAGCATGGTG	GGATCTCGGT	ATTTACCGGT	500
15	GTTGGTGAGC	GTACGCGTGA	AGGAAATGAC	CTTTACTGGG	AAATGAAGGA	550
	ATCAGGCGTT	ATTGAAAAAA	CAGCCATGGT	TTTTGGTCAG	ATGAATGAAC	600
	CACCAGGAGC	CCGTATGCGT	GTTGCCTTGA	CCGGCTTGAC	AATTGCTGAA	650
	TATTTCCGCG	ATGTTGAAGG	CCAAGACGTC	CTGCTCTTCA	TTGACAATAT	700
	TTTCCGCTTT	ACTCAAGCAG	GCTCAGAGGT	ATCAGCCCTT	CTAGGTCGTA	750
20	TGCCTTCAGC	CGTTGGTTAC	CAGCCAACAC	TTGCCACTGA	AATGGGACAA	800
	TTGCAAGAGC	GTATCACCTC	AACGAAAAAA	GGCTCTGTTA	CCTCTA	846

25 2) INFORMATION FOR SEQ ID NO: 386

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 846 bases
 (B) TYPE: Nucleic acid
 30 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

35 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus anginosus*
 (B) STRAIN: ATCC 27335

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 386

40	TTGCAGCTGG	TGATAAATTA	CCTGAGATAA	ATAATGCACT	TGTAGTCTAT	50
	AAAAATGACG	AAAATAAATC	AAAAATCGTC	CTTGAAGTAG	CTCTTGAGCT	100
	TGGTGATGGA	GTGGTTCGAA	CTATTGCCAT	GGAATCCACT	GATGGGTTGA	150
	CTCGTGGCAT	GGAAGTTCTA	GATACTGGTC	GACCAATTTT	TGTTCCAGTT	200
45	GGGAAAGAAA	CACCTGGTCG	CGTCTTTAAC	GTTTTAGGCG	ATACCATTGA	250
	TTTGATACT	CCATTGCGCG	AAGATGCAGA	ACGTCAACCA	ATCCATAAAA	300
	AAGCTCCAAC	TTTTGATGAG	TTATCTACTT	CATCAGAAAT	CTTAGAAACA	350
	GGAATAAAGG	TTATTGACCT	TTTAGCCCCC	TACCTCAAAG	GTGGGAAAGT	400
	CGGCCTCTTC	GGTGGTGCTG	GCGTTGGGAA	AACTGTCTTG	ATTCAAGAGT	450
50	TGATTCATAA	TATCGCCCAA	GAACACGGCG	GGATTTCAAGT	CTTTACTGGT	500
	GTTGGGGAAC	GAATCGTGA	AGGGAATGAC	CTGTACTGGG	AAATGAAAGA	550
	ATCTGGTGTT	ATCGAAAAGA	CGGCTATGGT	CTTTGGGCAA	ATGAATGAAC	600
	CGCCTGGAGC	ACGTATGCGT	GTAGCTTTGA	CTGGGTAAAC	GATTGCAGAG	650
	TATTTCCGTG	ATGTGGAAGG	TCAAGATGTT	CTTTTGTTTA	TTGATAATAT	700
55	TTTCCGTTTC	ACTCAAGCTG	GTTCTGAAGT	GTCAGCCCTT	CTTGGTCGTA	750
	TGCCATCAGC	TGTTGGTTAC	CAACCAACCT	TGGCTACTGA	AATGGGGCAA	800
	TTACAAGAAC	GTATTACATC	AACGAAAAAA	GGTTCTGTTA	CCTCAA	846

60

2) INFORMATION FOR SEQ ID NO: 387

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 843 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

10

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus salivarius*
 (B) STRAIN: ATCC 7073

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 387

GCAGCTGGTG ATAAACTTCC TGAGATTAAAC AATGCATTGG TCGTTTATAC 50
 TGATGAACAA AAGTCTAAAC GTATCGTGCT CGAAGTAGCT CTTGAACTTG 100
 GAGAAGGTGT GGTTCGTACC ATTGCCATGG AATCTACTGA TGGATTGACT 150
 20 CGTGGACTAG AAGTTCTGGA CACTGGTCGT CCAATCAGCG TTCCTGTTGG 200
 TAAAGATACC CTTGGACGTG TCTTTAACGT TCTTGGTGAT ACCATTGACT 250
 TGGAAGCACC TTTTGCAGAC GATGCAGAGC GTGAACCAAT TCACAAAAAA 300
 GCACCAACTT TCGATGAATT GTCAACATCT ACTGAAATCC TTGAAACAGG 350
 GATTAAAGTT ATCGACTTGC TAGCCCCTTA CCTTAAGGGT GGTAAAGTCG 400
 25 GACTCTTCGG TGGTGCCGGT GTTGGTAAAA CCGTTCTTAT TCAAGAGTTG 450
 ATTCACAACA TTGCCCAAGA GCACGGTGGT ATTTCCGTGT TTACAGGTGT 500
 TGGTGAACGT ACACGTGAAG GTAATGACCT TTAAGTGGAA ATGAAAGAAT 550
 CTGGCGTTAT CGAGAAAACA GCCATGGTCT TCGGTCAAAT GAACGAACCA 600
 CCTGGAGCAC GTATGCGTGT TGCCCTTACT GGTTTGACAA TTGCGGAATA 650
 30 CTTCCGTGAT GTCGAGGGTC AAGACGTTCT TCTCTTCATC GATAACATCT 700
 TCCGTTTAC TCAAGCAGGT TCTGAGGTTT CTGCCCTTCT TGGTCGTATG 750
 CCATCAGCCG TTGGTTACCA ACCTACACTT GCTACTGAAA TGGGTCAATT 800
 GCAAGAACGT ATCACATCAA CTAAAAAAGG TTCTGTTACA TCT 843

35

2) INFORMATION FOR SEQ ID NO: 388

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 841 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

45

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus suis*
 (B) STRAIN: ATCC 43765

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 388

TTGCAGCAGA AGATAAACTT CCTGAGATTA ACAACGCACT CGTTGTATAT 50
 AAAAATGATG ATTCCAAACA AAAAGTCGTG CTTGAAGTGG CTTTGGAAGT 100
 55 TGGTGATGGC GTTGTACGGA CCATTGCCAT GGAATCAACG GATGGATTGA 150
 CACGTGGGAT GGAAGTTCTC GATACAGGTC GTCCCATCTC TGTTCAGTC 200
 GGTAAAGAAA CGCTGGGTCG TGTCTTCAAT GTGTTGGGAG ATACCATTGA 250
 CCTTGAAGAG TCTTTTCCGG CAGATTTTGA ACGTGAGCCT ATCCATAAGA 300
 AAGCGCCGGC TTTTGACGAA TTATCTACTT CAAGCGAAAT TTTGGAAACA 350
 60 GGGATTAAGG TTATCGACCT CCTAGCACCT TATCTAAAAG GTGGTAAGGT 400

TGGTCTCTTC GGTGGTGCTG GTGTTGGTAA AACCGTTCCTT ATCCAAGAAT 450
 TGATTACAA TATTGCCCAA GAACACGGTG GTATCTCTGT ATTTACCGGA 500
 GTTGGCGAGC GTACCCGTGA AGGGAACGAT CTTTACTGGG AAATGAAAGA 550
 ATCAGGTGTT ATTGAAAAAA CGGCCATGGT ATTTGGTCAG ATGAATGAGC 600
 5 CACCAGGAGC CCGTATGCGT GTTGCTCTTA CTGGTTTGAC TATTGCGGAA 650
 TACTTCCGTG ATGTGGAAGG GCAGGATGTT CTTCTGTTCA TCGATAATAT 700
 CTTCCGTTT ACACAGGCTG GTTCAGAAAGT GTCTGCCCTC TTGGGTCGTA 750
 TGCCATCAGC CGTTGGTTAT CAGCCAACAC TTGCGACGGA GATGGGACAA 800
 TTGCAGGAGC GTATTACCTC AACCAAGAAG GGTCTGTGTA C 841

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2) INFORMATION FOR SEQ ID NO: 389

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 844 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
 20 (ii) MOLECULE TYPE: Genomic DNA
 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus uberis*
 25 (B) STRAIN: ATCC 19436

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 389

GCAAACGGTG AAAAATTACC AGAGATTAAT AATGCATTGA TAGTTTATAA 50
 30 AGGTAGCGAT AAAAACAACAA AGATTGTTCT TGAAGTTGCT TTGGAACCTG 100
 GGGACGGAAT GGTTCGTACA ATCGCTATGG AATCAACTGA TGGGCTTACA 150
 CGTGGAATTAG AAGTTTTAGA TACTGGCCGT GCCATTAGTG TACCAGTCGG 200
 AAAAGAACT TTGGGTCGTG TTTTCAATGT GCTTGGTGAA ACCATTGATT 250
 TGGATGAACC ATTTGCCGCT GATGCTGCAA GAGAACCCAT CCATAAAAAA 300
 35 GCCCCAGCAT TTGATGAACT ATCAACGTCT TCAGAAATTC TTGAAACCGG 350
 AATAAAAGTT ATTGACTTAT TAGCCCCTTA TCTCAAAGGT GGTAAAGTTG 400
 GTTTATTTGG TGGTGCCGGA GTAGGTAAAA CGGTTTTAAT TCAAGAATTA 450
 ATTCATAATA TTGCACAAGA ACATGGTGGT ATTTCAGTAT TTACCGGTGT 500
 TGGTGAAAGA ACTCGTGAAG GTAATGACCT TTATTGGGAA ATGAAAGAAT 550
 40 CTGGCGTTAT TGAAAAACA GCCATTGGTAT TTGGACAAAT GAACGAACCA 600
 CCAGGAGCAC GTATGCGCGT TGCTTTAACA GGTTTAACCA TTGCTGAATA 650
 TTTCCGGGAT GTTGAAGGTC AAGATGTTTT GCTCTTTATT GACAACATTT 700
 TCCGTTTCAC GCAAGCTGGT TCAGAAAGTT CAGCCCTATT GGGTCGTATG 750
 CCTTCAGCGG TAGGATACCA ACCAACACTT GCTACCGAAA TGGGACAATT 800
 45 GCAAGAAAGA ATTACCTCAA CTAACAAGGG ATCTGTTACT TCTA 844

2) INFORMATION FOR SEQ ID NO: 390

50 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 896 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 55 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

60 (A) ORGANISM: *Tatumella ptyseos*

(B) STRAIN: ATCC 33301

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 390

5	TTCCCTCAGG	ACGCTGTACC	ACAGGTGTAC	AACGCTCTTG	AGGTTGAAAA	50
	TGGTGATACC	CGTCTGGTGC	TGGAAGTTCA	GCAGCAGCTG	GGCGGTGGTG	100
	TCGTTTCGTAC	GATTGCAATG	GGAACCTCTG	ACGGCCTGAA	ACGTGGCCTT	150
	AAGGTGACCG	ATCTGCAAAA	ACCGATTTCAG	GTACCGGTCTG	GTAAAGCGAC	200
	GCTGGGCCGT	ATCATGAACG	TACTGGGTCA	GCCAATCGAT	ATGAAAGGCG	250
10	ACCTGAAGAA	CGAAGATGGT	AGCAATGTTG	AGGTGAAGTC	TATTCACCGT	300
	GCAGCGCCAA	GCTACGAAGA	ACTGGCTAAC	TCTACTGAGC	TGCTGGAAAC	350
	GGGTATCAAG	GTTATCGACC	TGATCTGTCC	GTTTGCAAAA	GGCGGTAAAG	400
	TGGGTCTGTT	CGGTGCTGCG	GGGTAGGTA	AGACCGTCAA	CATGATGGAA	450
	CTGATCCGTA	ACATCGCTAT	CGAGCACTCT	GGTACTCTG	TATTTGCAGG	500
15	GGTGGGTGAG	CGTACCCGTG	AAGGTAACGA	CTTCTACCAC	GAAATGACCG	550
	AGTCTAACGT	TCTGGATAAA	GTTGCTCTGG	TTTATGGCCA	GATGAACGAG	600
	CCACCAGGAA	ACCGTCTGCG	CGTTGCGCTG	ACCGGTCTGA	CTATGGCTGA	650
	AAAATTCCGT	GACGAAGGCC	GTGACGTACT	GCTGTTTCGT	GATAACATCT	700
	ATCGTTATAC	CCTGGCCGGT	ACTGAAGTTT	CAGCACTGCT	GGGTCGTATG	750
20	CCTTCTGCGG	TAGGTTATCA	GCCAACTG	GCCGAAGAAA	TGGGTGTTCT	800
	TCAGGAACGT	ATCACGTCAA	CCAAACCGG	TTCAATCACT	TCCGTA	896

25 2) INFORMATION FOR SEQ ID NO: 391

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 829 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

35 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Trabulsiella guamensis*
 (B) STRAIN: ATCC 49490

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 391

40	TTCCCTCAGG	ATGCCGTACC	GCGCGTGTAC	GATGCTCTTG	AGGTTATGAA	50
	TGGTAGTGAG	CGTCTGGTGC	TGGAAGTTCA	GCAGCAGCTC	GGTGGTGGTA	100
	TCGTACGTAC	TATCGCCATG	GGTTCTTCCG	ACGGTCTGCG	TCGTGGTCTG	150
	GATGTAAAAG	ATCTCGAGCA	TCCGATCGAA	GTCCCGGTAG	GTAAAGCAAC	200
45	GCTGGGTCTG	ATCATGAACG	TGCTGGGTCA	GCCGATCGAT	ATGAAAGGCG	250
	ACATCGGCGA	AGAAGAGCGT	TGGGCTATCC	ACCGCGCAGC	ACCGTCCTAC	300
	GAAGAGCTGT	CCAGCTCTCA	GGAAGTGTCT	GAAACCGGCA	TCAAAGTTAT	350
	CGACCTGATG	TGTCCGTTCT	CGAAGGGCGG	TAAAGTCGGT	CTGTTCGGTG	400
	GTGCGGGTGT	AGGTAAAACC	GTAAACATGA	TGGAGCTGAT	TCGTAACATC	450
50	GCGATCGAGC	ACTCCGGTTA	CTCTGTGTTT	GCGGGCGTGG	GTGAACGTAC	500
	TCGTGAGGGT	AACGACTTCT	ACCACGAAAT	GACCGACTCC	AACGTTCTGG	550
	ACAAAGTATC	CCTGGTGTAT	GGACAGATGA	ACGAGCCGCC	GGGAAACCGT	600
	CTGCGCGTTG	CACTGACCGG	TCTGACCATG	GCTGAGAAGT	TCCGTGACGA	650
	AGGTCGTGAC	GTTCTGCTGT	TCGTGATAAA	CATCTACCGT	TACACCCTGG	700
55	CGGGTACTGA	AGTATCTGCA	CTGCTGGGCC	GTATGCCTTC	AGCGGTAGGT	750
	TACCAGCCGA	CCCTGGCGGA	AGAGATGGGT	GTTCTTCAGG	AACGTATCAC	800
	CTCAACCAAA	ACCGGTTCTA	TCACCTCCG			829

60

2) INFORMATION FOR SEQ ID NO: 392

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 835 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

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(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Yersinia bercovieri*
 (B) STRAIN: ATCC 43970

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 392

CGAATTCCCC CAAGACGCTG TACCAAAAGT GTACAACGCC CTTGAGGTTG 50
 AAGGCACAGC TCAGAAGCTG GTGCTGGAAG TTCAGCAACA GCTGGGCGGT 100
 GGTGTTGTTC GTTGATCGC AATGGGCTCT TCCGATGGTC TGAGCCGCGG 150
 20 GTTGAAAGTC ATCAACCTGG AACACCCAAT TGAAGTGCCG GTGGGTAAAT 200
 CAACTCTGGG CCGTATCATG AACGTATTGG GTGACCCAAT CGACATGAAA 250
 GGTCTATCG GTGAAGAAGA GCGTTGGGCA ATCCACCGCG AAGCGCCTTC 300
 TTACGAAGAG CTTGCCAGCT CGCAAGATCT GTTAGAAACC GGTATCAAGG 350
 TAATGGATCT GATTTGTCCG TTCGCTAAGG GCGGTAAAGT CCGTCTGTTC 400
 25 GGTGGTGCGG GTGTGGGTAA AACAGTCAAC ATGATGGAGC TGATTCGTAA 450
 TATTGCGATT GAGCACTCAG GTTATTCTGT ATTTGCCGGT GTGGGTGAGC 500
 GTACTCGTGA GGGTAACGAC TTCTACCACG AGATGACTGA CTCCAACGTT 550
 CTGGACAAAG TATCCTTGGT TTATGGCCAG ATGAATGAGC CACCAGGTAA 600
 CCGTCTGCGC GTTGCACTGA CCGGCTTGAC CATGGCGGAG AAATTCGCTG 650
 30 ATGAAGGTCG TGATGTACTG TTATTCATCG ATAACATCTA TCGTTATAACC 700
 CTGGCCGGTA CAGAGGTATC TGCACTGCTA GGTCGTATGC CATCAGCGGT 750
 AGGCTATCAG CCAACGCTGG CAGAAGAGAT GGGTGTGTTG CAGGAACGTA 800
 TCACTTCCAC CAAGACGGGT TCAATCACCT CCGTA 835

35

2) INFORMATION FOR SEQ ID NO: 393

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 812 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

45

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Yersinia enterocolitica*
 (B) STRAIN: ATCC 9610

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 393

GCTGTACCAA AAGTGTACAA CGCCCTTGAG GTTGAAGGCG CAGCTGAGAA 50
 GCTGGTGCTG GAAGTTCAGC AACAGCTGGG CCGTGGTGTT GTTCGTTGTA 100
 55 TCGCAATGGG CTCTTCCGAT GGTCTGAGCC GTGGGTGAA AGTCATCAAC 150
 CTGGAACACC CAATTGAAGT GCCTGTGGGC AAGTCAACTC TGGGCCGTAT 200
 CATGAACGTA TTGGGTGACC CAATCGACAT GAAAGGTCCT ATCGGCGAAG 250
 AAGAGCGTTG GGCAATCCAT CGTGAAGCGC CTTCTTACGA AGATCTTGCC 300
 AGCTCGCAAG ACTTGTTAGA AACCGGTATC AAGGTAATGG ACTTGATTTG 350
 60 TCCGTTGCTG AAGGGCGGTA AAGTCGGTCT GTTCGGTGGT GCGGGTGTAG 400

	GTAAAACGGT	AAACATGATG	GAGCTTATTC	GTAACATTGC	GATTGAGCAC	450
	TCAGGTTATT	CCGTATTTGC	TGGCGTGGGT	GAGCGTACTC	GTGAGGGTAA	500
	CGACTTCTAC	CACGAGATGA	CTGACTCCAA	CGTTCTGGAC	AAAGTATCCT	550
	TGGTTTATGG	CCAAATGAAT	GAGCCACCAG	GTAACCGTCT	GCGCGTTGCA	600
5	CTGACCGGCT	TGACCATGGC	GGAGAAATTC	CGTGATGAAG	GTCGTGACGT	650
	ATTGCTGTTC	ATCGATAACA	TCTATCGCTA	TACCTTAGCC	GGTACGGAAG	700
	TTTCCGCACT	GCTGGGTCGT	ATGCCATCTG	CCGTAGGTTA	CCAGCCAACG	750
	CTGGCAGAAG	AGATGGGTGT	GTTGCAGGAA	CGTATTACTT	CCACCAAGAC	800
	GGGTTCAATC	AC				812

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2) INFORMATION FOR SEQ ID NO: 394

15 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 802 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

25 (A) ORGANISM: *Yersinia frederiksenii*
 (B) STRAIN: ATCC 33641

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 394

	AAAGTGACA	ACGCCCTTGA	GGTTGAAGGT	ACTGCTGAGA	AGTTAGTACT	50
30	GGAAGTTCAG	CAACAGCTGG	GCGGTGGTGT	TGCTCGTTGT	ATCGCCATGG	100
	GCTCTTCCGA	TGGTTTGAGC	CGCGGGTTGA	AAGTTGTCAA	CCTGGAACAC	150
	CCAATTGAAG	TACCGGTTGG	TAAATCAACT	CTGGGCCGTA	TCATGAACGT	200
	ATTGGGTGAC	CCAATCGACA	TGAAAGGTCC	TATCGGTGAA	GAAGAGCGTT	250
	GGGCAATCCA	CCGCGAAGCG	CCTTCTTACG	AAGAGCTTGC	CAGCTCGCAA	300
35	GATCTGTTAG	AAACCGGTAT	CAAGGTAATG	GATCTGATTT	GCCCCGTTCCG	350
	TAAAGGCGGT	AAAGTCGGTC	TGTTCCGGTG	TGCGGGTGTA	GGTAAAACGG	400
	TAAACATGAT	GGAGCTGATC	CGTAATATCG	CGATCGAGCA	CTCAGGTTAT	450
	TCCGTATTTG	CGGGTGTTGG	TGAACGTACC	CGTGAGGGTA	ACGACTTCTA	500
	CCACGAGATG	ACTGACTCCA	ACGTTCTGGA	CAAAGTATCC	TTGGTTTATG	550
40	GCCAGATGAA	TGAGCCACCA	GGTAACCGTC	TTCGCGTTGC	ACTGACCGGT	600
	CTGACCATGG	CGGAGAAATT	CCGTGATGAA	GGTCGTGACG	TATTGCTGTT	650
	CATCGATAAC	ATCTATCGTT	ATACCTTGGC	CGGTACGGAA	GTATCCGCAC	700
	TGCTGGGTG	TATGCCATCT	GCGGTAGGCT	ATCAGCCAAC	GCTGGCAGAA	750
	GAGATGGGTG	TGTTGCAGGA	ACGTATTACT	TCCACCAAGA	CGGGTTCAAT	800
45	CA					802

2) INFORMATION FOR SEQ ID NO: 395

50

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 806 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

55

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

60 (A) ORGANISM: *Yersinia intermedia*

(B) STRAIN: ATCC 29909

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 395

5	GCTGTACCAA	GAGTGTACAA	CGCCCTTGAG	GTTGAAGGCA	CTGCTGAGAA	50
	GCTGGTGCTG	GAAGTTCAGC	AACAGCTAGG	CGGTGGTGTT	GTTTCGTTGTA	100
	TCGCAATGGG	CTCTTCCGAT	GGTCTGAGCC	GCGGGTTGAA	AGTCATCAAC	150
	CTGGAACACC	CAATTGAAGT	GCCGGTTGGT	AAATCAACTC	TGGGCCGTAT	200
	CATGAACGTA	TTGGGTGACC	CAATCGACAT	GAAAGGTCCT	ATCGGTGAAG	250
10	AAGAGCGTTG	GGCAATCCAC	CGCGAAGCGC	CTTCTTACGA	AGAGCTTGCC	300
	AGCTCACAAG	ATTTGTTAGA	AACCGGTATC	AAAGTAATGG	ACTTGATTTG	350
	CCCGTTTCGCT	AAGGGCGGTA	AAGTGGGTCT	GTTTCGGTGGT	GCGGGTGTAG	400
	GTA AACACAGT	AAACATGATG	GAGCTTATTC	GTAACATCGC	GATTGAGCAC	450
	TCAGGTTATT	CTGTATTTGC	TGGTGTGGGT	GAGCGTACTC	GTGAGGGTAA	500
15	CGACTTCTAC	CACGAGATGA	CTGACTCCAA	CGTTCTGGAC	AAAGTATCCT	550
	TGGTGTATGG	CCAGATGAAT	GAGCCACCAG	GTAACCGTCT	GCGCGTTGCA	600
	CTGACCGGCC	TGACCATGGC	GGAGAAATTC	CGTGATGAAG	GTCGTGACGT	650
	ACTGTTGTTC	ATCGATAACA	TCTATCGCTA	TACCTTGGCC	GGTACGGAAG	700
	TATCCGCACT	GCTGGGTCGT	ATGCCATCAG	CGGTAGGCTA	CCAGCCAACG	750
20	CTGGCAGAAG	AGATGGGTGT	GTTGCAGGAA	CGTATTACGT	CCACCAAGAC	800
	GGGTTT					806

25 2) INFORMATION FOR SEQ ID NO: 396

(i) SEQUENCE CHARACTERISTICS:

- | | | |
|----|-----|----------------------|
| | (A) | LENGTH: 806 bases |
| | (B) | TYPE: Nucleic acid |
| 30 | (C) | STRANDEDNESS: Double |
| | (D) | TOPOLOGY: Linear |

(ii) MOLECULE TYPE: Genomic DNA

35 (vi) ORIGINAL SOURCE:

- | | | |
|--|-----|--|
| | (A) | ORGANISM: <i>Yersinia pseudotuberculosis</i> |
| | (B) | STRAIN: ATCC 29833 |

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 396

40	GCTGTACCAA	AAGTGTACAA	CGCCCTTGAG	GTAGAAGGCA	CAACTGAAAA	50
	GTTAGTGCTG	GAAGTTCAGC	AACAGTTGGG	CGGTGGTGTT	GTTTCGTTGTA	100
	TCGCAATGGG	CTCTTCCGAT	GGTCTGAGCC	GTGGGTGAA	AGTAACCAAC	150
	CTGGAACACC	CGATCGAAGT	ACCGGTGGT	AAAGCGACCC	TTGGCCGTAT	200
45	CATGAACGTA	TTGGGTGAAC	CAATCGACAT	GAAAGGTCCT	ATCGGTGAAG	250
	AAGAGCGTTG	GGCAATCCAT	CGCGAAGCGC	CTTCTTATGA	AGAGCTTGCT	300
	AGCTCACAAG	ATCTGTTAGA	AACCGGTATC	AAGGTTATGG	ACCTGATTTG	350
	TCCGTTTGCT	AAGGGCGGTA	AAGTCGGTCT	GTTTCGGTGGT	GCGGGTGTAG	400
	GTA AACACAGT	AAACATGATG	GAGCTGATCC	GTAACATCGC	GATCGAGCAC	450
50	TCTGGGTATT	CTGTATTTGC	CGGTGTAGGT	GAGCGTACCC	GTGAGGGTAA	500
	TGACTTCTAC	CATGAAATGA	CTGACTCCAA	CGTTTTGGAC	AAAGTATCCT	550
	TGGTTTACGG	CCAGATGAAT	GAGCCACCAG	GTAACCGTCT	ACGCGTTGCA	600
	CTGACCGGCC	TGACCATGGC	GGAGAAATTC	CGTGATGAAG	GTCGTGACGT	650
	ACTGCTGTTC	ATCGATAATA	TCTATCGTTA	TACCCTAGCT	GGTACGGAAG	700
55	TATCCGCATT	GCTGGGTCGT	ATGCCATCAG	CGGTAGGTTA	TCAGCCAACA	750
	CTGGCTGAAG	AGATGGGTGT	GTTGCAGGAA	CGTATTACTT	CCACTAAGAC	800
	GGGTTT					806

60

2) INFORMATION FOR SEQ ID NO: 397

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 829 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

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(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Yersinia rohdei*
 (B) STRAIN: ATCC 43380

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 397

TTCCCCCAAG ACGCTGTACC AAAAGTGTAC AACGCCCTTG AGGTTGAAGG 50
 TGCAGCTGAG AAGCTTGTGC TGGAAGTTCA GCAGCAGCTG GCGGGTGGTG 100
 TTGTTGTTG TATCGCAATG GGCTCTTCCG ATGGTTTGAG CCGTGGGTTG 150
 20 AAAGTTATCA ACCTGGAACA CCAATTGAA GTGCCAGTTG GTAAATCAAC 200
 TCTGGGCGGT ATCATGAACG TATTGGGTGA CCAATCGAC ATGAAAGGCC 250
 CTATCGGTGA AGAAGAGCGT TGGGCAATCC ACCGTGAAGC GCCTTCTTAC 300
 GAAGAGCTTG CCAGCTCGCA AGATCTGTTA GAAACCGGTA TCAAGGTAAT 350
 GGATCTGATT TGTCCGTTCG CTAAGGGCGG TAAAGTCGGT CTGTTCGGTG 400
 25 GTGCGGGTGT TGGTAAACA GTAAACATGA TGGAGCTTAT TCGTAACATC 450
 GCGATTGAGC ACTCAGGTTA TTCTGTATTT GCCGGGGTAG GTGAACGTAC 500
 TCGTGAGGGT AACGACTTCT ACCACGAGAT GACTGACTCC AACGTTCTGG 550
 ACAAAGTATC CTTGGTTTAT GGCCAGATGA ATGAGCCACC AGGTAACCGT 600
 CTGCGCGTTG CACTGACCGG CTTGACCATG GCGGAAAAAT TCCGTGATGA 650
 30 AGGCCGTGAC GTATTGCTGT TCATCGATAA CATTTATCGT TATACCCTAG 700
 CCGGTACGGA AGTATCCGCA CTGCTGGGTC GTATGCCATC TGCGGTAGGC 750
 TATCAGCCAA CACTGGCAGA AGAGATGGGT GTGTTGCAGG AACGTATTAC 800
 TTCCACTAAG ACGGGTTCAA TCACCTCCG 829

35

2) INFORMATION FOR SEQ ID NO: 398

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 819 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

45 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Yokenella regensburgei*
 (B) STRAIN: ATCC 35313

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 398

ATGCCGTACC GCGCGTGTAC GATGCTCTTG AGGTACAAAA TGGTAACGAG 50
 AAAGTGGTGC TGGAAGCTCA GCAGCAGCTC GCGGGCGGTA TCGTGCGTAC 100
 55 TATCGCCATG GGTCTTCCG ACGGTCTGCG TCGTGGTCTG GAAGTTAAAG 150
 ACCTCGAGCA CCCGATCGAA GTCCCGGTAG GTAAAGCAAC CCTGGGCGGT 200
 ATCATGAACG TCCTGGGTCA GCCGATCGAC ATGAAAGGCG ACATCGGTGA 250
 AGAAGAGCGT TGGGCTATCC ACCGCGCAGC ACCTTCCTAT GAAGAGCTGT 300
 CCAGCTCTCA GGAAGTCTG GAAACCGGTA TCAAAGTAAT GGATCTGATC 350
 60 TGCCCGTTCG CTAAGGGTGG TAAAGTCGGT CTGTTCCGGT GTGCGGGTGT 400

	AGGTAAACT	GTAAACATGA	TGGAGCTTAT	CCGTAACATC	GCGATTGAGC	450
	ACTCCGGTTA	CTCTGTGTTT	GCAGGCGTGG	GTGAACGTAC	TCGTGAGGGT	500
	AACGACTTCT	ACCACGAAAT	GACCGACTCC	AACGTACTGG	ATAAAGTATC	550
	CCTGGTGTAC	GGCCAGATGA	ACGAGCCGCC	GGGAAACCGT	CTGCGCGTTG	600
5	CGCTGACCGG	CCTGACCATG	GCTGAGAAAT	TCCGTGACGA	AGGCCGTGAC	650
	GTTCTGCTGT	TCGTCGATAA	CATCTACCGT	TATACCCTGG	CCGGTACGGA	700
	AGTATCCGCA	CTGCTGGGTC	GTATGCCTTC	TGCGGTAGGT	TATCAGCCAA	750
	CTCTGGCGGA	AGAGATGGGT	GTTCTTCAGG	AACGTATCAC	CTCTACCAAA	800
	ACCGGTTCTA	TCACCTCCG				819
10						

2) INFORMATION FOR SEQ ID NO: 399

- 15 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1097 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Double
 - (D) TOPOLOGY: Linear

- 20 (ii) MOLECULE TYPE: Genomic DNA

- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Yarrowia lipolytica*
 - 25 (B) STRAIN: ATCC 38295

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 399

	AAGCTTAAGG	CTGAGCGAGA	GCGAGGTATC	ACCATTGATA	TCGCTCTCTG	50
30	GAAGTTCCAG	ACCCCTAAGT	ACTACGTCAC	CGTTATTGAT	GCTCCCGGTC	100
	ACCGAGATTT	CATCAAGAAC	ATGATTACCG	GTAATTCCCA	GGCTGACTGC	150
	GCCATCCTCA	TCATTGCTGG	TGGTGTGTTG	GAGTTCGAGG	CTGGTATCTC	200
	CAAGGATGGT	CAGACCCGAG	AGCACGCCCT	GCTCGCTTTC	ACCCCTCGGTG	250
	TTAAGCAGCT	CATTGTTGCT	ATCAACAAGA	TGGACTCCGT	CAAGTGGTCT	300
35	CAGGATCGAT	ACCTCGAGAT	TTGCAAGGAG	ACTGCCAACT	TCGTCAAGAA	350
	GGTCGGTTAC	AACCCCAAGG	CTGTCCCTT	CGTCCCCATT	TCCGGATGGA	400
	ACGGTGACAA	CATGATCGAG	CCCTCTACCA	ACTGTGACTG	GTACAAGGGA	450
	TGGACCAAGG	AGACCAAGGC	CGGCGAGATC	AAGGGTAAGA	CCCTCCTCGA	500
	GGCCATTGAT	GCCATTGAGC	CCCCCGTGCG	ACCCACGAC	AAGCCCCTCC	550
40	GACTTCCCCT	CCAGGATGTC	TACAAGATCG	GTGGTATCGG	CACAGTGCCC	600
	GTTGGCCGAG	TCGAGACCGG	TGTTATCAAG	GCCGGTATGG	KTGTTACCTT	650
	CGCTCCCGCC	AACGTGACCA	CTGAGGTCAA	GTCTGTCGAG	ATGCACCACG	700
	AGATCCTCCC	CGATGGAGGT	TTCGCCGGTG	ACAACGTCGG	TTTCAACGTC	750
	AAGAACGTTT	CCGTCAAGGA	TATCCGACGA	GGTAACGTTG	CTGGTGACTC	800
45	CAAGAACGAC	CCCCCAAGG	GCTGCGACTC	TTTCAACGCT	CAGGTCATTG	850
	TTCTTAACCA	CCCCGGTCAG	ATCGGTGCTG	GTTACGCTCC	CGTCCTTGAT	900
	TGCCACACTG	CCCACATTGC	TTGCAAGTTC	GACACCCTGA	TCGAGAAGAT	950
	CGACCGACGA	ACCGGTAAGA	AGATGGAGGA	CTCCCCAAG	TTCATCAAGT	1000
	CTGGTGATGC	TGCCATTGTC	AAGATGGTTC	CCTCCAAGCC	CATGTGTGTC	1050
50	GAGGCCTTCA	CTGAGTACCC	CCCTCTTGGT	CGATTGCGCC	TCCGAGA	1097

2) INFORMATION FOR SEQ ID NO: 400

- 55 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1233 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Double
 - 60 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 5 (A) ORGANISM: *Absidia corymbifera*
 (B) STRAIN: ATCC 46775

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 400

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10 CAAGCTTAAG GCTGAACGTG AGCGTGGTAT CACCATCGAT ATCGCTCTCT 50
   GGAAGTTCTGA GACTCCCAAG TACCACGTTA CCGTCATTGA TGCCCCTGGC 100
   CATCGTGATT TCATCAAGAA CATGATTACT GGTACTTCCC AAGCTGACTG 150
   CGGTATCTTG ATTATTGCTG CTGGTACTGG TGAATTCGAA GCTGGTATCT 200
   CCAAGGATGG TCAAACCCGT GAACACGCTT TGCTTGCTTT CACCCTTGGT 250
15 GTCCGTCAAT TGATTGTCGC TATCAACAAG ATGGATTCCA CCAAGTACTC 300
   TGAGGCCCGT TACAACGAAA TTGTCAAGGA AGTCTCCACC TTCATCAAGA 350
   AGATTGGTTT CAACCCCAAG TCCGTTCTT TCGTCCCTAT CTCTGGCTGG 400
   AACGGTGACA ACATGTTGGA GGARTCCACC AACATGCCTT GGTTCAAGGG 450
   ATGGAACAAG GAGACTAAGG CTGGTGCCAA GACYGGCAAG ACCCTTCTTG 500
20 AAGCCATTGA CAACATTGAT CCCCCTGTTC GTCCTTCCGA CAAGCCCCTT 550
   CGTCTTCCCC TTCAAGATGT CTACAAGATC GGTGGTATTG GTACAGTTCC 600
   TGTCGGTTCG GTTGAGACTG GTGTCATCAA GCCTGGTATG GTTGTCACCT 650
   TCGCTCCCGC TAACGTCACC ACTGAAGTCA AGTCCGTYGA AATGCACCAC 700
   GAGCAACTTG CTGAAGGTGT TCCCGGTGAC AACGTCGGTT TCAACGTCAA 750
25 GAACGTTTCC GTCAAGGATA TCCGCCGTGG TAACGTYTGC TCTGACTCCA 800
   AGAACGACCC CGCCAAGGAA TCCGCTTCCT TCACCGCTCA AGTTATTGTC 850
   TTGAACCACC CTGGTCARAT TGGTGCTGGT TACTCTCCTG TCTTGGATTG 900
   CCACACTGCT CACATTGCAT GCAAGTTCTY TKAGCTTCTT KAGAAGATCG 950
   ATYGTCGTTT CCGTAAGTAA ATANTTTGGT TTRGGATATG GGTATTGGGC 1000
30 TTAATCTYTG GATTTTGCCT CAATTGCTCC TTCCTTGATC TTTCTCGATT 1050
   ACTTTTTGAT CATTTGCTAA TCCAAACCCT TTCCATTTYA TTGAAAACAG 1100
   GTAAGAAGTT GGAAGACTCC CCAAAGTTCG TCAAGWSYGG TGAAGCTGCT 1150
   ATCGTCAAGA TGGTTCCTTC CAAGCCCATG TCGGTTGAAG CCTACACTGA 1200
   ATATCCTCCT CTTGGTCGTT TCGCTGTCCG TGA 1233
35

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2) INFORMATION FOR SEQ ID NO: 401

- 40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1151 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

45 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 50 (A) ORGANISM: *Alternaria alternata*
 (B) STRAIN: ATCC 62099

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 401

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55 CAAGTTGAAG GCCGAGCGTG AGCGTGGTAT CACCATCGAC ATTGCTCTCT 50
   GGAAGTTCTGA GACTCCCAAG GTTAGTACCC CTCTGCCTAC TACATCAAGT 100
   TCTTTACAAT GCTAACATGT TGTACTCAGT ACTATGTCAC CGTCATTGAC 150
   GCCCCCGGTC ACCGTGATTT CATCAAGAAC ATGATCACTG GTACCTCCCA 200
   GGCCGACTGC GCTATTCTCA TCATTGCCGC CGGTACTGGT GAGTTCGAGG 250
   CTGGTATCTC CAAGGATGGC CAGACTCGTG AGCACGCTCT CCTCGCTTAC 300
60 ACCCTCGGTG TCAAGCAGCT CATCGTTGCC ATCAACAAGA TGGACACCAC 350

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	CAAGTGGTCC	GAGGAGCGTT	ACCAGGAGAT	CATCAAGGAG	ACCTCCAACCT'	400
	TCATCAAGAA	GGTCGGCTAC	AACCCCAAGC	ACGTTCCCTT	CGTCCCCATC	450
	TCCGGTTTCA	ACGGTGACAA	CATGATTGAG	GCCTCATCCA	ACTGCCCCCTG	500
	GTACAAGGGT	TGGGAGAAGG	AGACCAAGGC	CAAGGCCACT	GGTAAGACCC	550
5	TCCTCGAGGC	CATCGACGCC	ATCGACCCTY	CCAGCCGTCC	CACCGACAAG	600
	CCCCTCCGTC	TTCCCCCTYCA	GGATGTTTAC	AAGATTGGTG	GTATTGGCAC	650
	GGTGCCCGTC	GGTCGTGTCG	AGACCGGTAT	CATCAAGGCC	GGTATGGTCCG	700
	TCACCTTCGC	CCCCGCTGGT	GTCACCACTG	AAGTCAAGTC	CGTCGAGATG	750
	CACCACGAGC	AGCTCACCGA	GGGTGTCCCC	GGTGACAACG	TCGGCTTCAA	800
10	CGTCAAGAAC	GTCTCCGTCA	AGGAGATCCG	TCGTGGTAAC	GTTGCCGGTG	850
	ACTCCAAGAA	CGACCCCCCC	AAGGGTGCCG	AGTCCTTCAA	CGCCCAGGTC	900
	ATCGTCCTCA	ACCACCCTGG	TCAGGTCGGT	GCTGGTTACG	CCCCAGTCCT	950
	CGACTGCCAC	ACCGCCACAC	TTGCTTGCAA	GTTCTCTGAG	CTCCTCGAGA	1000
	AGATTGACCG	CCGTACCGGA	AAGTCTGTTG	AGAACTCTCC	CAAGTTCATC	1050
15	AAGTCCGGTG	ACGCCGCCAT	CGTCAAGATG	GTTCCCTCCA	AGCCCATGTG	1100
	CGTTGAGGCT	TTCACTGACT	ACCCTCCTCT	CGGTCGTTTC	GCTGTCCGTG	1150
	A					1151

20

2) INFORMATION FOR SEQ ID NO: 402

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1283 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Aspergillus flavus*
 (B) STRAIN: ATCC 26947

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 402

	CAAGCTCAAG	TCCGAGCGTG	AGCGTGGTAT	CACCATCGAT	ATCGCCCTCT	50
	GGAAGTTCCA	GACCTCCAAG	TATGAGGTCA	CCGTCATTGG	TAAGCATTTG	100
	AGTTCCAACC	TACGTTGCCC	AACATTTACA	GTCATCTAAC	AAAGTTCAAT	150
40	AGATGCCCCC	GGTCACCGTG	ACTTCATCAA	GAACATGATC	ACTGGTACTT	200
	CCCAGGCTGA	CTGCGCTATC	CTCATCATTG	CCTCCGGTAC	TGGTGAATTC	250
	GAGGCTGGTA	TCTCCAAGGA	TGGTCAGACC	CGTGAGCACG	CTCTGCTCGC	300
	TTTCAACCCTC	GGTGTCCGTC	AGCTCATCGT	TGCCCTCAAC	AAGATGGACA	350
	CCTGCAAGTG	GTCTCAGGAT	CGTTACAACG	AAATCGTTAA	GGAGACTTCC	400
45	AACTTCATCA	AGAAGGTCGG	ATACAACCCC	AAGAGCGTTC	CTTTCGTCCC	450
	CATCTCCGGT	TTCAACGGTG	ACAACATGAT	TGAGGCCTCC	ACCAACTGCC	500
	CCTGGTACAA	GGGTTGGGAG	AAGGAGACCA	AGGCTGGCAA	GTCCACCGGT	550
	AAGACCCTTC	TCGAGGCCAT	CGATGCCATC	GAGCCCCCGG	TCCGTCCCAC	600
	CGACAAGCCT	CTCCGTCTTC	CCCTYCAGGA	TGTCTACAAG	ATCTCTGGTA	650
50	TCGGTACTGT	GCCCGTCGGT	CGTGTGCGAG	CTGGTGTCAT	CAAGCCTGGT	700
	ATGGTCGTTA	CTTTCGCTCC	TGCCAACGTG	ACCACTGAAG	TCAAGTCCGT	750
	TGAAATGCAC	CACCAGCAGC	TCCAGGCCGG	TAACCCCGGT	GACAACGTTG	800
	GTTTCAACGT	CAAGAACGTC	TCCGTCAAGG	AAGTCCGCCG	TGGTAACGTT	850
	GCCGGTGACT	CCAAGAACGA	CCCCCCTGCT	GGCTGCGATT	CCTTCAACGC	900
55	CCAGGTCATC	GTCCTTAACC	ACCCCGGTCA	GGTCGGCAAC	GGTTACGCTC	950
	CCGTCTGGA	CTGCCACACC	GCTCACATTG	CTTGCAAGTT	CGCTGAGCTC	1000
	CTTGAGAAGA	TTGACCGCCG	TACCGGTAAA	TCTGTTGAGG	ACAAGCCCAA	1050
	GTTTCATCAAG	TCTGGTGATG	CTGCCATCGT	CAAGATGATT	CCCTCCAAGC	1100
	CCATGTGTGT	GGAGTCTTTC	ACTGACTTCC	CCCCTCTTGG	TCGTTTCGCT	1150
60	GTCCGTGACG	TAAGTTTTTC	CCTCTTGACT	ATCTTCACAA	TTTTTCACAT	1200

ATTTTCACGC CTCGTCCCAC TCTTTTTCCT CCCTTCCTCT TTGGTTCCCC 1250
TTTTTGCCGTG CAAGTTCTCT ATAGCTAACA TGA 1283

5

2) INFORMATION FOR SEQ ID NO: 403

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 1103 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

15

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Aspergillus fumigatus*
(B) STRAIN: DAL95

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 403

TCCGAGCGTG AGCGTGGTAT CACCATCGAC ATTGCCCTCT GGAAGTTCCA 50
GACTCCCAAG TATGAGGTCA CTGTCATCGG TAAGCTCGAC TCGCCCCGAT 100
ATGTTTTGGT GCTGTAGCTA ACACGATCTG AAGATGCCCC CGGTCACCGT 150
25 GACTTCATCA AGAACATGAT CACTGGTACC TCCCAGGCTG ACTGCGCTAT 200
CCTCATCATT GCCTCCGGTA CTGGTGAGTT CGAGGCTGGT ATCTCCAAGG 250
ATGGCCAGAC CCGTGAGCAC GCTCTGCTGG CTTTCACCCT CGGTGTCAAG 300
CAGCTCATCG TCGCCCTCAA CAAGATGGAC ACCTGCAAGT GGTCCGAGGA 350
TCGTTACAAC GAAATTGTCA AGGAAACCTC CAACTTCATC AAGAAGGTCG 400
30 GCTACAACCC CAAGGCCGTT CCCTTCGTCC CCATCTCTGG CTTCAACGGT 450
GACAACATGC TTGAGCCCTC CTCCAACGTC CCCTGGTACA AGGGATGGGA 500
GAAGGAGACC AAGGCCGGCA AGGTCACTGG TAAGACCCTC ATCGAGGCCA 550
TCGACGCCAT TGAGCCCCCT GTCCGTCCCT CCAACAAGCC CCTCCGTCTT 600
CCCCTCCAGG ATGTCTACAA GATCTCTGGT ATCGGAACGG TCCCTGTCTGG 650
35 CCGTGTCTGAG ACCGGTATCA TCAAGCCCGG CATGGTCGTC ACCTTCGCCC 700
CCGCCAACGT CACCACTGAA GTCAAGTCCG TCGAGATGCA CCACCAGCAG 750
CTCCAGGAGG GTGTCCCCGG TGCAACGTC GGTTCACACG TCAAGAACGT 800
TTCCGTCGAG GAAGTCCGCC GTGGTAACGT CTGCGGTGAC TCCAAGAACG 850
ATCCCCCTCA GGGTGCTGCC TCCTTCAACG CCCAGGTCAT CGTCCTCAAC 900
40 CACCCCGGTC AGGTCGGCGC TGGTTACGCC CCCGTCCTCG ACTGCCACAC 950
TGCCACATT GCTTGCAAGT TCTCTGAGCT GCTTGAGAAG ATTGACCGCC 1000
GTACCGGCAA GTCTGTTGAG AACAAACCCA AGTTCATCAA GTCCGGTGAT 1050
GCCGCCATCG TGAAGATGGT TCCTTCCAAG CCCATGTGTG TCGAGTCCTT 1100
CAC 1103

45

2) INFORMATION FOR SEQ ID NO: 404

50 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1149 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

55

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 60 (A) ORGANISM: *Aspergillus fumigatus*
(B) STRAIN: WSA-172

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 404

5	AAGCTCAAGT	CCGAGCGTGA	GCGTGGTATC	ACCATCGACA	TTGCCCTCTG	50
	GAAGTTCCAG	ACTCCCAAGT	ATGAGGTCAC	TGTCATCGGT	AAGCTCGACT	100
	CGCCCCGATA	TGTTTTGGTG	CTGTAGCTAA	CACGATCTGA	AGATGCCCCC	150
	GGTCACCGTG	ACTTCATCAA	GAACATGATC	ACTGGTACCT	CCCAGGCTGA	200
	CTGCGCTATC	CTCATCATTC	CCTCCGGTAC	TGGTGAGTTC	GAGGCTGGTA	250
	TCTCCAAGGA	TGGCCAGACC	CGTGAGCACG	CTCTGCTGGC	TTTCACCCTC	300
10	GGTGTCAAGC	AGCTCATCGT	CGCCCTCAAC	AAGATGGACA	CCTGCAAGTG	350
	GTCCGAGGAT	CGTTACAACG	AAATTGTCAA	GGAAACCTCC	AACTTCATCA	400
	AGAAGGTCGG	CTACAACCCC	AAGGCCGTTT	CCTTCGTCCC	CATCTCTGGC	450
	TTCAACGGTG	ACAACATGCT	TGAGCCCTCC	TCCAAC TGCC	CCTGGTACAA	500
	GGGATGGGAG	AAGGAGACCA	AGGCCGGCAA	GGTCACTGGT	AAGACCCTCA	550
15	TCGAGGCCAT	CGACGCCATT	GAGCCCCCTG	TCCGTCCCTC	CAACAAGCCC	600
	CTCCGTCTTC	CCCTCCAGGA	TGTCTACAAG	ATCTCTGGTA	TCGGAACGGT	650
	CCCTGTCCGC	CGTGTGAGGA	CCGGTATCAT	CAAGCCCGGC	ATGGTCGTCA	700
	CCTTCGCCCC	CGCCAACGTC	ACCACTGAAG	TCAAGTCCGT	CGAGATGCAC	750
	CACCAGCAGC	TCCAGGAGGG	TGTCCCCGGT	GACAACGTCG	GTTTCAACGT	800
20	CAAGAACGTT	TCCGTCAAGG	AAGTCCGCCG	TGGTAACGTC	TGCGGTGACT	850
	CCAAGAACGA	TCCCCCTCAG	GGTGCTGCCT	CCTTCAACGC	CCAGGTCATC	900
	GTCCTCAACC	ACCCCGGTCA	GGTCGGCGCT	GGTTACGCCC	CCGTCCTCGA	950
	CTGCCACACT	GCCCACATTG	CTTGCAAGTT	CTCTGAGCTG	CTTGAGAAGA	1000
	TTGACCGCCG	TACCGGCAAG	TCTGTTGAGA	ACAACCCCAA	GTTTCATCAAG	1050
25	TCCGGTGATG	CCGCCATCGT	GAAGATGGTT	CCTTCCAAGC	CCATGTGTGT	1100
	CGAGTCCTTC	ACTGACTACC	CCCCTCTGGG	TCGTTTCGCC	GTCCGTGAC	1149

30 2) INFORMATION FOR SEQ ID NO: 405

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1151 bases
 (B) TYPE: Nucleic acid
 35 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

40 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Aspergillus niger*
 (B) STRAIN: ATCC 9508

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 405

45	CAAGCTCAAG	TCCGAGCGTG	AGCGTGGTAT	CACCATCGAC	ATTGCCCTCT	50
	GGAAGTTCCA	GACTGGCAAG	TATGAGGTCA	CCGTCATTGG	TATGTACTCA	100
	CAGAGTTCTC	TTTTTCATCAA	AGCAATATAC	TAACGTCCAT	CATAGACGCC	150
	CCCGGTCAAC	GTGACTTCAT	CAAGAACATG	ATCACTGGTA	CCTCCCAGGC	200
50	TGACTGCGCT	ATCCTCATCA	TTGCCTCCGG	TACTGGTGAG	TTCGAGGCTG	250
	GTATCTCCAA	GGATGGCCAG	ACTCGTGAGC	ACGCTCTGCT	TGCTTTCACC	300
	CTCGGTGTCC	GCCAGCTCAT	CGTTGCCCTC	AACAAGATGG	ACACCTGCAA	350
	GTGGTCCGAG	GACCGTTACA	ACGAAATCGT	TAAGGAGACC	TCCAAC TTCA	400
	TCAAGAAGGT	CGGATACAAC	CCCAAGGGTG	TTCCTTTCGT	CCCCATCTCC	450
55	GGTTTCAACG	GTGACAACAT	GCTCGAGCCC	TCCCCCAACT	GCCCCCTGGTA	500
	CAAGGGTTGG	GAGAAGGAGA	CCAAGGCCGG	CAAGGTCACC	GGTAAGACCC	550
	TCCTTGAGGC	CATCGACGCC	ATCGAGCCCC	CCGTCCGTCC	CTCCAACAAG	600
	CCCCTCCGTC	TTCCCCTCCA	GGATGTCTAC	AAGATCTCCG	GTATTGGAAC	650
	TGTTCCCGTC	GGTCGTGTGG	AGACCGGTAT	CATTGCCCTT	GGTATGGTGG	700
60	TGACCTTCGC	TCCCGCCAAC	GTCACCACTG	AAGTCAAGTC	CGTTGAGATG	750

	CACCACCAGC	AGCTCAAGGA	AGGTGTCCCC	GGTGACAACG	TTGGTTTCAA	800
	CGTCAAGAAC	GTTTCCGTCA	AGGAGGTTCC	CCGTGGTAAC	GTTGCCGGTG	850
	ACTCCAAGAA	CGACCCCCCT	CTTGGCTGTG	AGAGCTTCAC	CGCCCAGGTC	900
	ATCGTCCTCA	ACCACCCCGG	TCAGGTCGGC	GCTGGTTACG	CTCCCGTCCT	950
5	GGACTGCCAC	ACTGCTCACA	TTGCTTGCAA	GTTTCGCTGAG	CTCCTTGAGA	1000
	AGATTGACCG	CCGTACCGGA	AAGTCTGTTG	AATCTTCCCC	CAAGTTCATC	1050
	AAGTCCGGTG	ACGCTGCCAT	CGTCAAGATG	ATTCCCTCCA	AGCCCATGTG	1100
	TGTTGAGGCT	TTCCTGACT	ACCCCCCTCT	TGGTCGTTTC	GCCGTCGCG	1150
10	A					1151

2) INFORMATION FOR SEQ ID NO: 406

- 15 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1093 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Double
 - (D) TOPOLOGY: Linear

- 20 (ii) MOLECULE TYPE: Genomic DNA

- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Blastoschizomyces capitatus*
 - 25 (B) STRAIN: ATCC 10663

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 406

	GCTTAAAGCT	GAACGTGAAC	GTGGTATCAC	CATTGATATC	GCTCTCTGGA	50
30	AGTTCGAAAC	TCCTAAGTAC	TACGTTACTG	TTATTGATGC	TCCAGGTCAC	100
	CGTGATTTCA	TCAAGAACAT	GATTACTGGT	ACTTCCCAAG	CCGATTGCGC	150
	CATTCTTATC	ATTGCTGCCG	GTGTCGGTGA	ATTCGAAGCT	GGTATCTCCA	200
	AGGAAGGTCA	AACCAGAGAA	CACGCTCTTC	TCGCTTTCAC	CCTTGGTGTC	250
	AGACAACCTA	TCATTGCCAT	CAACAAGATG	GACTCTGTCA	AGTGGGACCA	300
35	AAAGAGATAC	GAAGAAATCG	TCAAGGAGGC	TTCCAACCTC	GTCAAGAAGG	350
	TTGGTTACAA	CCCCAAGTCT	GTTCCATTCG	TTCCTATCTC	TGGTTGGAAC	400
	GGTGACAACA	TGTTGGAACC	TACCACCAAC	GCCCCATGGT	ACAAGGGATG	450
	GACCAAGGAA	ACCAAGGCTG	GTGCCACTAA	GGGTATGACT	CTTATTGAAG	500
	CCATTGACGC	CATTGAACCA	CCAGTAAGAC	CATCCGACAA	GCCACTCCGT	550
40	CTCCCCTCC	AAGATGTTTA	CAAGATTGGT	GGTATCGGAA	CTGTGCCAGT	600
	CGGCCGTGTC	GAAACCGGTA	TCATCAAGGC	CGGTATGGTC	GTTACCTTTG	650
	CTCCACCAAT	GGTCACAAC	GAAGTTAAGT	CCGTTGAAAT	GCACCACGAA	700
	CAACTTGCTC	AAGGTAACCC	AGGTGACAAC	GTTGGTTTCA	ACGTCAAGAA	750
	CGTTTCCGTT	AAGGAAATCA	GACGTGGTAA	CGTCTGTGGT	GACTCCAAGA	800
45	ACGATCCACC	AAAGGGCTGC	GAATCTTTCA	ACGCTCAAGT	TATCGTCTTG	850
	AACCACCCTG	GTCAAATCTC	TGCTGGTTAC	TCTCCAGTTC	TCGATTGCCA	900
	CACTGCCCAC	ATTGCCTGCA	GATTCGACGA	ACTCCTTGAA	AAGATCGACC	950
	GTCGTTCTGG	TAAGAAGATT	GAAGACTCTC	CAAAGTTTGT	CAAGTCTGGT	1000
	GATGCCGCTA	TCGTCAAGAT	GATCCCAACC	AAGCCAATGT	GCGTTGAAAC	1050
50	CTTCACTGAA	TACCCACCAC	TTGGTCGTTT	CGCCGTCCGT	GAT	1093

2) INFORMATION FOR SEQ ID NO: 407

- 55 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1101 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Double
 - 60 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 5 (A) ORGANISM: *Candida albicans*
 (B) STRAIN: ATCC 10231

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 407

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10 CTTGGACAAA TTGAAGGCTG AAAGAGAAAG AGGTATCACC ATTGATATCG      50
   CTTTGTGGAA ATTCGAAACT CCAAATATACC ACGTTACCGT CATTGATGCT      100
   CCAGGTCACA GAGATTTTCAT CAAGAATATG ATCACTGGTA CTTCTCAAGC      150
   TGATTGTGCT ATTTTGATTA TTGCTGGTGG TACTGGTGAA TTCGAAGCCG      200
   GTATTTCTAA GGATGGTCAA ACCAGAGAAC ACGCTTTGTT GGCTTACACT      250
15 TTGGGTGTCA AACAATTGAT TGTTGCTGTC AACAAGATGG ACTCTGTCAA      300
   ATGGGACAAA AACAGATTTG AAGAAATCAT CAAGGAAACC TCCAACCTCG      350
   TCAAGAAGGT TGGTTACAAC CCAAAGACTG TTCCATTYGT TCCAATCTCT      400
   GGTGGAATG GTGACAACAT GATTGAACCA TCCACCAACT GTCCATGGTA      450
   CAAGGGTTGG GAAAAGGAAA CCAAATCCGG TAAAGTTACT GGTAAGACCT      500
20 TGTTAGAAGC TATTGACGCT ATTGAACCAC CAACCAGACC AACCGACAAA      550
   CCATTGAGAT TGCCATTGCA AGATGTTTAC AAGATCGGTG GTATTGGTAC      600
   TGTGCCAGTC GGTAGAGTTG AAAGTGGTAT CATCAAAGCC GGTATGGTTG      650
   TTTACTTTTCG CCCAGCTGGT GTTACCACTG AAGTCAAATC CGTTGAAATG      700
   CATCACGAAC AATTGGCTGA AGGTGTTCCA GGTGACAATG TTGGTTTCAA      750
25 CGTTAAGAAC GTTTCCGTTA AAGAAATTAG AAGAGGTAAC GTTTGTGGTG      800
   ACTCCAAGAA CGATCCACCA AAGGGTTGTG ACTCTTTCAA TGCCCAAGTC      850
   ATTGTTTTGA ACCATCCAGG TCAAATCTCT GCTGGTACT CTCCAGTCTT      900
   GGATTGTCAC ACTGCCCACA TTGCTTGTA AATTCGACACT TTGGTTGAAA      950
   AGATTGACAG AAGAACTGGT AAGAAATTGG AAGAAAATCC AAAAATTCGTC     1000
30 AAATCCGGTG ATGCTGCTAT CGTCAAGATG GTCCCAACCA AACCAATGTG     1050
   TGTGAAGCT TTTACTGACT ACCCACCATT AGGTAGATTC GCTGTCAGAG     1100
   A                                                                1101

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35

2) INFORMATION FOR SEQ ID NO: 408

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 1089 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

45

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Candida albicans*
 (B) STRAIN: ATCC 18804

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 408

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   GAAGGCTGAA AGAGAAAGAG GTATCACCAT TGATATCGCT TTGTGGAAAT      50
   TCGAAACTCC AAAATACCAC GTTACCGTCA TTGATGCTCC AGGTCACAGA      100
   GATTTTCATCA AGAATATGAT CACTGGTACT TCTCAAGCTG ATTGTGCTAT      150
55 TTTGATTATT GCTGGTGGTA CTGGTGAATT CGAAGCCGGT ATTTCTAAGG      200
   ATGGTCAAAC CAGAGAACAC GCTTTGTTGG CTTACACTTT GGGTGTCAAA      250
   CAATTGATTG TTGCTGTCAA CAAGATGGAC TCTGTCAAAT GGGACAAAAA      300
   CAGATTTGAA GAAATCATCA AGGAAACCTC CAACTTCGTC AAGAAGGTTG      350
   GTTACAACCC AAAGACTGTT CCATTGCTTC CAATCTCTGG TTGGAATGGT      400
60 GACAACATGA TTGAACCATC CACCAACTGT CCATGGTACA AGGGTTGGGA      450

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245

	AAAGGAAACC	AAATCCGGTA	AAGTTACTGG	TAAGACCTTG	TTAGAAGCTA	500
	TTGACGCTAT	TGAACCACCA	ACCAGACCAA	CCGACAAACC	ATTGAGATTG	550
	CCATTGCAAG	ATGTTTACAA	GATCGGTGGT	ATTGGTACTG	TGCCAGTCGG	600
	TAGAGTTGAA	ACTGGTATCA	TCAAAGCCGG	TATGGTTGTT	ACTTTCGCCC	650
5	CAGCTGGTGT	TACCACTGAA	GTCAAATCCG	TTGAAATGCA	TCACGAACAA	700
	TTGGCTGAAG	GTGTTCCAGG	TGACAAATGTT	GGTTTCAACG	TTAAGAACGT	750
	TTCCGTTAAA	GAAATTAGAA	GAGGTAACGT	TTGTGGTGAC	TCCAAGAACG	800
	ATCCACCAAA	GGGTTGTGAC	TCTTTCATG	CCCAAGTCAT	TGTTTTGAAC	850
	CATCCAGGTC	AAATCTCTGC	TGGTTACTCT	CCAGTCTTGG	ATTGTCACAC	900
10	TGCCCCACATT	GCTTGTAAT	TCGACACTTT	GGTTGAAAAG	ATTGACAGAA	950
	GAACTGGTAA	GAAATTGGAA	GAAAATCCAA	AATTCGTCAA	ATCCGGTGAT	1000
	GCTGCTATCG	TCAAGATGGT	CCCAACCAAA	CCAATGTGTG	TTGAAGCTTT	1050
	CACTGACTAC	CCACCATTAG	GTAGATTCGC	TGTCAGAGA		1089

15

2) INFORMATION FOR SEQ ID NO: 409

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 1101 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

25 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Candida albicans*
 (B) STRAIN: ATCC 56884

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 409

	CTTGGACAAA	TTGAAGGCTG	AAAGAGAAAG	AGGTATCACC	ATTGATATCG	50
	CTTTGTGGAA	ATTCGAAACT	CCAAAATACC	ACGTTACCGT	CATTGATGCT	100
35	CCAGGTCACA	GAGATTTTCAT	CAAGAATATG	ATCACTGGTA	CTTCTCAAGC	150
	TGATTGTGCT	ATTTTGATTA	TTGCTGGTGG	TACTGGTGAA	TTCGAAGCCG	200
	GTATTTCTAA	GGATGGTCAA	ACCAGAGAAC	ACGCTTTGTT	GGCTTACACT	250
	TTGGGTGTCA	AACAATTGAT	TGTTGCTGTC	AACAAGATGG	ACTCTGTCAA	300
	ATGGGACAAA	AACAGATTTG	AAGAAATCAT	CAAGGAAACC	TCCAACCTCG	350
40	TCAAGAAGGT	TGGTTACAAC	CCAAAGACTG	TTCCATTCGT	TCCAATCTCT	400
	GGTTGGAATG	GTGACAACAT	GATTGAACCA	TCCACCAACT	GTCCATGGTA	450
	CAAGGGTTGG	GAAAAGGAAA	CCAAATCCGG	TAAAGTTACT	GGTAAGACCT	500
	TGTTAGAAGC	TATTGACGCT	ATTGAACCAC	CAACCAGACC	AACCGACAAA	550
	CCATTGAGAT	TGCCATTGCA	AGATGTTTAC	AAGATCGGTG	GTATTGGTAC	600
45	TGTGCCAGTC	GGTAGAGTTG	AAACTGGTAT	CATCAAAGCC	GGTATGGTTG	650
	TTACTTTTCG	CCCAGCTGGT	GTTACCACTG	AAGTCAAATC	CGTTGAAATG	700
	CATCACGAAC	AATTGGCTGA	AGGTGTTCCA	GGTGACAATG	TTGGTTTCAA	750
	CGTTAAGAAC	GTTTCCGTTA	AAGAAATTAG	AAGAGGTAAC	GTTTGTGGTG	800
	ACTCCAAGAA	CGATCCACCA	AAGGGTTGTG	ACTCTTTCAA	TGCCCAAGTC	850
50	ATTGTTTTGA	ACCATCCAGG	TCAAATCTCT	GCTGGTACT	CTCCAGTCTT	900
	GGATTGTCAC	ACTGCCCACA	TTGCTTGTA	ATTGACACT	TTGGTTGAAA	950
	AGATTGACAG	AAGAACTGGT	AAGAAATTGG	AAGAAAATCC	AAAATTCGTC	1000
	AAATCCGGTG	ATGCTGCTAT	CGTCAAGATG	GTCCCAACCA	AACCAATGTG	1050
	TGTTGAAGCT	TTCACTGACT	ACCCACCATT	AGGTAGATTC	GCTGTCAGAG	1100
55	A					1101

60

2) INFORMATION FOR SEQ ID NO: 410

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1102 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Candida albicans*
 (B) STRAIN: ATCC 60193

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 410

```

15  CTTGGACAAA TTGAAGGCTG AAAGAGAAAG AGGTATCACC ATTGATATCG      50
    CTTTGTGGAA ATTCGAAACT CCAAAATACC ACGTTACCGT CATTGATGCT      100
    CCAGGTCACA GAGATTTTCAT CAAGAATATG ATCACTGGTA CTTCTCAAGC      150
    TGATTGTGCT ATTTTGATTA TTGCTGGTGG TACTGGTGAA TTCGAAGCCG      200
    GTATTTCTAA GGATGGTCAA ACCAGAGAAC ACGCTTTGTT GGCTTACACT      250
20  TTGGGTGTCA AACAATTGAT TGTTGCTGTC AACAAGATGG ACTCTGTCAA      300
    ATGGGACAAA AACAGATTG AAGAAATCAT CAAGGAAACC TCCAACCTCG      350
    TCAAGAAGGT TGTTACAAC CCAAAGACTG TTCCATTCGT TCCAATCTCT      400
    GGTGGAATG GTGACAACAT GATTGAACCA TCCACCAACT GTCCATGGTA      450
    CAAGGGTTGG GAAAAGGAAA CCAAATCCGG TAAAGTTACT GGTAAGACCT      500
25  TGTTAGAAGC TATTGACGCT ATTGAACCAC CAACCAGACC AACCGACAAA      550
    CCATTGAGAT TGCCATTGCA AGATGTTTAC AAGATCGGTG GTATTGGTAC      600
    TGTGCCAGTC GGTAGAGTTG AACTGGTAT CATCAAAGCC GGTATGGTTG      650
    TTAATTTTCG CCCAGCTGGT GTTACCCTG AAGTCAAATC CGTTGAAATG      700
    CATCACGAAC AATTGGCTGA AGGTGTTCCA GGTGACAATG TTGGTTTCAA      750
30  CGTTAAGAAC GTTTCCTGTA AAGAAATTAG AAGAGGTAAC GTTGTGGTG      800
    ACTCCAAGAA CGATCCACCA AAGGGTTGTG ACTCTTTCAT TGCCCAAGTC      850
    ATTGTTTTGA ACCATCCAGG TCAAATCTCT GCTGGTTACT CTCCAGTCTT      900
    GGATTGTCAC ACTGCCCACA TTGCTTGTA AATTCGACACT TTGGTTGAAA      950
    AGATTGACAG AAGAACTGGT AAGAAATTGG AAGAAAATCC AAAATTCGTC     1000
35  AAATCCGGTG ATGCTGCTAT CGTCAAGATG GTCCCAACCA AACCAATGTG     1050
    TGTGAAGCT TCACTGACT ACCCACCATT AGGTAGATTG GCTGTCAGAG     1100
    AT
  
```

40

2) INFORMATION FOR SEQ ID NO: 411

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1102 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

50

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Candida albicans*
 (B) STRAIN: ATCC 90028

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 411

```

60  CTTGGACAAA TTGAAGGCTG AAAGAGAAAG AGGTATCACC ATTGATATCG      50
    CTTTGTGGAA ATTCGAAACT CCAAAATACC ACGTTACCGT CATTGATGCT      100
    CCAGGTCACA GAGATTTTCAT CAAGAATATG ATCACTGGTA CTTCTCAAGC      150
    TGATTGTGCT ATTTTGATTA TTGCTGGTGG TACTGGTGAA TTCGAAGCCG      200
  
```

	GTATTTCTAA	GGATGGTCAA	ACCAGAGAAC	ACGCTTTGTT	GGCTTACACT	250
	TTGGGTGTCA	AACAATTGAT	TGTTGCTGTC	AACAAGATGG	ACTCTGTCAA	300
	ATGGGACAAA	AACAGATTG	AAGAAATCAT	CAAGGAAACC	TCCAACCTCG	350
	TCAAGAAGGT	TGGTTACAAC	CCAAAGACTG	TTCCATTCGT	TCCAATCTCT	400
5	GGTTGGAATG	GTGACAACAT	GATTGAACCA	TCCACCAACT	GTCCATGGTA	450
	CAAGGGTTGG	GAAAAGGAAA	CCAAATCCGG	TAAAGTTACT	GGTAAGACCT	500
	TGTTAGAAGC	TATTGACGCT	ATTGAACCAC	CAACCAGACC	AACCGACAAA	550
	CCATTGAGAT	TGCCATTGCA	AGATGTTTAC	AAGATCGGTG	GTATTGGTAC	600
	TGTGCCAGTC	GGTAGAGTTG	AAACTGGTAT	CATCAAAGCC	GGTATGGTTG	650
10	TTACTTTTCGC	CCCAGCTGGT	GTTACCACTG	AAGTCAAATC	CGTTGAAATG	700
	CATCACGAAC	AATTGGCTGA	AGGTGTTCCA	GGTGACAATG	TTGGTTTCAA	750
	CGTTAAGAAC	GTTTCCGTTA	AAGAAATTAG	AAGAGGTAAC	GTTTGTGGTG	800
	ACTCCAAGAA	CGATCCACCA	AAGGGTTGTG	ACTCTTTCAA	TGCCCAAGTC	850
	ATTGTTTTGA	ACCATCCAGG	TCAAATCTCT	GCTGGTTACT	CTCCAGTCTT	900
15	GGATTGTCAC	ACTGCCCACA	TTGCTTGTA	ATTTCGACACT	TTGGTTGAAA	950
	AGATTGACAG	AAGAACTGGT	AAGAAATTGG	AAGAAAATCC	AAAATTCGTC	1000
	AAATCCGGTG	ATGCTGCTAT	CGTCAAGATG	GTCCCAACCA	AACCAATGTG	1050
	TGTTGAAGCT	TTCACTGACT	ACCCACCATT	AGGTAGATTC	GCTGTCAGAG	1100
	AT					1102
20						

2) INFORMATION FOR SEQ ID NO: 412

- 25 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1101 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Double
 - (D) TOPOLOGY: Linear

30 (ii) MOLECULE TYPE: Genomic DNA

- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Candida dubliniensis*
 - 35 (B) STRAIN: NCPF 3108

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 412

	CTTGATAAAA	TTGAAGGCTG	AAAGAGAAAG	AGGTATCACC	ATTGATATCG	50
40	CTTTGTGGAA	ATTCGAAACT	CCAAAATACC	ACGTTACCGT	CATTGATGCT	100
	CCAGGTCACA	GAGATTTTCAT	CAAGAACATG	ATCACTGGTA	CTTCTCAAGC	150
	TGATTGTGCT	ATTTTGATTA	TTGCTGGTGG	TACTGGTGAA	TTCGAAGCCG	200
	GTATTTCTAA	GGATGGTCAA	ACCAGAGAAC	ACGCTTTGTT	GGCTTACACT	250
	TTGGGTGTCA	AACAATTGAT	TGTTGCTGTC	AACAAGATGG	ACTCTGTCAA	300
45	ATGGGACAAA	AACAGATTG	AAGAAATCAT	CAAGGAAACC	TCTAACCTCG	350
	TCAAGAAGGT	TGGTTACAAC	CCAAAGACTG	TTCCATTCGT	TCCAATCTCT	400
	GGTTGGAATG	GTGACAACAT	GATTGAAGCT	TCCACCAACT	GTCCATGGTA	450
	CAAGGGTTGG	GAAAAGGAAA	CCAAATCCGG	TAAGGTTACT	GGTAAGACCT	500
	TGTTAGAAGC	TATTGATGCT	ATTGAACCAC	CAACCAGACC	AACCGACAAA	550
50	CCATTGAGAT	TGCCATTGCA	AGATGTTTAC	AAGATCGGTG	GTATTGGTAC	600
	TGTGCCAGTC	GGTAGAGTTG	AAACTGGTGT	CATTAAAGCC	GGTATGGTTG	650
	TCACTTTTGC	CCCAGCTGGT	GTTACCACTG	AAGTCAAATC	CGTTGAAATG	700
	CATCACGAAC	AATTGGCTGA	AGGTGTTCCA	GGTGACAATG	TTGGTTTCAA	750
	CGTTAAGAAT	GTTTCTGTCA	AAGAAATTAG	AAGAGGTAAC	GTTTGTGGTG	800
55	ACTCCAAGAA	CGATCCACCA	AAGGGTTGTG	ACTCTTTCAA	TGCCCAAGTC	850
	ATTGTCTTGA	ACCATCCAGG	TCAAATCTCT	GCTGGTTACT	CTCCAGTCTT	900
	GGATTGTCAC	ACTGCCCACA	TTGCTTGTA	ATTTCGACACT	TTGGTTGAAA	950
	AGATTGACAG	AAGAACTGGT	AAGAAATTGG	AAGAAAATCC	AAAATTCGTC	1000
	AAATCCGGTG	ACGCTGCTAT	YGTCAAGATG	GTCCCAACCA	AACCAATGTG	1050
60	TGTTGAAGCT	TTCACTGACT	ACCCACCATT	AGGTAGATTC	GCTGTCAGAG	1100

5 2) INFORMATION FOR SEQ ID NO: 413

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1098 bases
(B) TYPE: Nucleic acid
10 (C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

15 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Candida catenulata*
(B) STRAIN: ATCC 10565

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 413

20 GGACAAGCTT AAGGCTGAGC GTGAGAGAGG TATCACCATT GACATTGCCT 50
TGTGGAAGTT CGAGACTCCC AAGTACCACG TCACTGTCAT TGACGCCCCC 100
GGTCACAGAG ATTTTCATCAA GAACATGATC ACTGGTACCT CGCAGGCTGA 150
CTGTGCTATC TTGATCATTG CTTCCGGTGT CGGTGAGTTC GAGGCTGGTA 200
25 TCTCCAAGGA CGGTCAGACC CGTGAGCACG CCTTGTGGC CTACACCTTG 250
GGTGTCAAGC AGTTGATCGT TGCCATCAAC AAGATGGACT CCGTCAAGTG 300
GGACAAGAAC AGATTGAGG AGATTGTCAA GGAGACCACC AACTTCGTCA 350
AGAAGGTTGG TTACAACCCC AAGGCTGTCC CCTTCGTCCC CATCTCTGGC 400
TGGAACGGTG ACAACATGAT TGAGGCCTCC ACCAACTGCC CCTGGTACAA 450
30 GGGCTGGGAG AAGGAGACCA AGGCCGGTAA GTCTACCGGT AAGACCTTGT 500
TGGAGGCCAT TGACGCCATT GAGCCCCCTA CCAGACCCAC CGACAAGCCC 550
TTGAGATTGC CCTTGCAGGA TGTCTACAAG ATCGGTGGTA TTGGTACGGT 600
GCCCCGTCGGC CGTGTGAGG CCGGTGTCAT CAAGCCCGGT ATGGTCGTCA 650
CCTTCGCCCC CGCTGGTGTC ACCACTGAAG TCAAGTCCGT CGAGATGCAC 700
35 CACGAGCAGT TGTCCGAGG TGTCCCCGGT GACAACGTTG GTTCAACGT 750
CAAGAACGTC TCTGTAAAG AGATCAGACG TGGTAACGTC TGCGGTGACT 800
CCAAGAACGA CCCCCCATG GGTGCTCTT CTTTCAACGC CCAGGTTATC 850
GTGTTGAACC ACCCCGGTCA GATCTCTGCC GGTACTCTC CCGTCTTGGA 900
CTGCCACACC GCCCACATTG CTTGCAAGTT CGCCGAGTTG ATCGAGAAGA 950
40 TTGACAGACG TACCGGTAAG TCCATGGAGG CTAACCCCAA GTTCGTCAAG 1000
TCTGGTGACG CCGCCATCGT CAAGATGGAG CCCACTAAGC CCATGTGTGT 1050
TGAGGCCTTC ACTGACTTCC CTCCTTTGGG TAGATTCGCC GTCAGAGA 1098

45

2) INFORMATION FOR SEQ ID NO: 414

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1102 bases
50 (B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

55

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Candida dubliniensis*
(B) STRAIN: NCPF 3949

60 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 414

	CTTGGATAAA	TTGAAGGCTG	AAAGAGAAAG	AGGTATCACC	ATTGATATCG	50
	CTTTGTGGAA	ATTCGAAACT	CCAAAATACC	ACGTTACCGT	CATTGATGCT	100
	CCAGGTCACA	GAGATTTCAT	CAAGAACATG	ATCACTGGTA	CTTCTCAAGC	150
5	TGATTGTGCT	ATTTTGATTA	TTGCTGGTGG	TACTGGTGAA	TTCGAAGCCG	200
	GTATTTCTAA	GGATGGTCAA	ACCAGAGAAC	ACGCTTTGTT	GGCTTACACT	250
	TTGGGTGTCA	AACAATTGAT	TGTTGCTGTC	AACAAGATGG	ACTCTGTCAA	300
	ATGGGACAAA	AACAGATTCTG	AAGAAATCAT	CAAGGAAACC	TCTAACTTCG	350
	TCAAGAAGGT	TGGTTACAAC	CCAAAGACTG	TTCCATTTCGT	TCCAATCTCT	400
10	GGTTGGAATG	GTGACAACAT	GATTGAAGCT	TCCACCAACT	GTCCATGGTA	450
	CAAGGGTTGG	GAAAAGGAAA	CCAAATCCGG	TAAGGTTACT	GGTAAGACCT	500
	TGTTAGAAGC	TATTGATGCT	ATTGAACCAC	CAACCAGACC	AACCGACAAA	550
	CCATTGAGAT	TGCCATTGCA	AGATGTTTAC	AAGATCGGTG	GTATTGGTAC	600
	TGTGCCAGTC	GGTAGAGTTG	AAACTGGTGT	CATTAAAGCC	GGTATGGTTG	650
15	TCACTTTTGC	CCCAGCTGGT	GTTACCACTG	AAGTCAAATC	CGTTGAAATG	700
	CATCACGAAC	AATTGGTTGA	AGGTGTTCCA	GGTGACAATG	TTGGTTTCAA	750
	CGTTAAGAAT	GTTTCTGTCA	AAGAAATTAG	AAGAGGTAAC	GTTTGTGGTG	800
	ACTCCAAGAA	CGATCCACCA	AAGGGTTGTG	ACTCTTTCAA	TGCCCAAGTC	850
	ATTGTCTTGA	ACCATCCAGG	TCAAATCTCT	GCTGGTTAYT	CTCCAGTCTT	900
20	GGATTGTCAC	ACTGCCCACA	TTGCTTGTA	ATTTCGACACT	TTGGTTGAAA	950
	AGATTGACAG	AAGAACTGGT	AAGAAATTGG	AAGAAAATCC	AAAATTCGTC	1000
	AAATCCGGTG	ACGCTGCTAT	YGTCAAGATG	GTCCCAACCA	AACCAATGTG	1050
	TGTTGAAGCT	TTCCTGACT	ACCCACCATT	AGGTAGATTC	GCTGTCAGAG	1100
	AT					1102
25						

2) INFORMATION FOR SEQ ID NO: 415

- 30 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1102 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Double
 - (D) TOPOLOGY: Linear

- 35 (ii) MOLECULE TYPE: Genomic DNA

- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Candida dubliniensis*
 - 40 (B) STRAIN: CBS 7987

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 415

	CTTGGATAAA	TTGAAGGCTG	AAAGAGAAAG	AGGTATCACC	ATTGATATCG	50
45	CTTTGTGGAA	ATTCGAAACT	CCAAAATACC	ACGTTACCGT	CATTGATGCT	100
	CCAGGTCACA	GAGATTTCAT	CAAGAACATG	ATCACTGGTA	CTTCTCAAGC	150
	TGATTGTGCT	ATTTTGATTA	TTGCTGGTGG	TACTGGTGAA	TTCGAAGCCG	200
	GTATTTCTAA	GGATGGTCAA	ACCAGAGAAC	ACGCTTTGTT	GGCTTACACT	250
	TTGGGTGTCA	AACAATTGAT	TGTTGCTGTC	AACAAGATGG	ACTCTGTCAA	300
50	ATGGGACAAA	AACAGATTYG	AAGAAATCAT	CAAGGAAACC	TCTAACTTCG	350
	TCAAGAAGGT	TGGTTACAAC	CCAAAGACTG	TTCCATTTCGT	TCCAATCTCT	400
	GGTTGGAATG	GTGACAACAT	GATTGAAGCT	TCCACCAACT	GTCCATGGTA	450
	CAAGGGTTGG	GAAAAGGAAA	CCAAATCCGG	TAAGGTTACT	GGTAAGACCT	500
	TGTTAGAAGC	TATTGATGCT	ATTGAACCAC	CAACCAGACC	AACCGACAAA	550
55	CCATTGAGAT	TGCCATTGCA	AGATGTTTAC	AAGATCGGTG	GTATTGGTAC	600
	TGTGCCAGTC	GGTAGAGTTG	AAACTGGTGT	CATTAAAGCC	GGTATGGTTG	650
	TCACTTTTGC	CCCAGCTGGT	GTTACCACTG	AAGTCAAATC	CGTTGAAATG	700
	CATCACGAAC	AATTGGTTGA	AGGTGTTCCA	GGTGACAATG	TTGGTTTCAA	750
	CGTTAAGAAT	GTTTCTGTCA	AAGAAATTAG	AAGAGGTAAC	GTTTGTGGTG	800
60	ACTCCAAGAA	CGATCCACCA	AAGGGTTGTG	ACTCTTTCAA	TGCCCAAGTC	850

	ATTGTCTTGA	ACCATCCAGG	TCAAATCTCT	GCTGGTTAYT	CTCCAGTCTT	900
	GGATTGTCAC	ACTGCCCCACA	TTGCTTGTAA	ATTCGACACT	TTGGTTGAAA	950
	AGATTGACAG	AAGAACTGGT	AAGAAATTGG	AAGAAAATCC	AAAATTTCGTC	1000
	AAATCCGGTG	ACGCTGCTAT	YGTCAAGATG	GTCCCAACCA	AACCAATGTG	1050
5	TGTTGAAGCT	TTCCTGACT	ACCCACCATT	AGGTAGATTC	GCTGTCAGAG	1100
	AT					1102

10 2) INFORMATION FOR SEQ ID NO: 416

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1094 bases
 (B) TYPE: Nucleic acid
 15 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

20 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Candida famata*
 (B) STRAIN: ATCC 62894

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 416

25	AATTGAAGGC	TGAAAGAGAA	AGAGGTATCA	CCATTGATAT	CGCTTTATGG	50
	AAATTGCAAA	CTCCAAAATA	CCACGTTACC	GTTATTGATG	CTCCAGGTCA	100
	CAGAGATTTT	ATCAAGAACA	TGATTACTGG	TACTTCTCAA	GCTGATTGTG	150
	CTATTTTTRAT	TATTGCTGGT	GGTGTCCGGT	AATTCGAAGC	CGGTATCTCT	200
30	AAGGATGGTC	AAACCAGAGA	ACACGCTTTA	TTGGCTTACA	CCTTAGGTGT	250
	TAGACAATTG	ATTGTTGCCG	TCAACAAGAT	GGACTCTGTT	AAATGGGACA	300
	AGGCTAGATT	CGAAGAAATC	ATCAAGGAAA	CCTCTAACTT	CGTCAAGAAG	350
	GTTGGTTACA	ACCCTAAGAC	TGTTCCCTTC	GTGCCAATTT	CTGGATGGAA	400
	CGGTGACAAC	ATGATTGAAG	CCTCCACCAA	CTGTCCATGG	TACAAGGGTT	450
35	GGGAAAAGGA	AACCAAGGCT	GGTAAATCTA	CTGGTAAGAC	TTTGTTAGAA	500
	GCCATTGATG	CCATTGAACC	ACCAACCAGA	CCAACCGAAA	AGCCATTGAG	550
	ATTACCATTA	CAAGATGTCT	ACAAGATCGG	TGGTATTGGT	ACTGTGCCAG	600
	TCGGTAGAGT	TGAAACCGGT	GTTATCAAGG	GTGGTATGGT	TGTTACCTTT	650
	GCCCCAGCCG	GTGTCACTAC	CGAAGTCAAA	TCCGTTGAAA	TGCACCACGA	700
40	ACAATTAGCT	GAAGGTGTTC	CAGGTGACAA	TGTTGGTTTC	AACGTCAAGA	750
	ACGTTTCCGT	TAAGGAAATC	AGAAGAGGTA	ACGTTTGTGG	TGACTCCAAG	800
	AACGACCCAC	CAAAGGGTGC	TGAATCTTTC	ACCGCTCAAG	TTATTGTCTT	850
	GAACCACCCA	GGTCARATCT	CTGCTGGTTA	CTCTCCAGTC	TTAGATTGTC	900
	ACACCGCCCA	CATTGCTTGT	AAATTTCGAT	CTTTACTCGA	AAAGATTGAC	950
45	AGAAGATCCG	GTAAGAAATT	AGAAGACGAA	CCAAAATTCG	TCAAGTCCGG	1000
	TGATGCTGCT	ATCGTCAAGA	TGGTCCCAAC	CAAACCAATG	TGTGTTGAAG	1050
	CTTTCCTACT	GA	ATACCCACCA	TTAGGTAGAT	TCGCTGTTAG	1094

50

2) INFORMATION FOR SEQ ID NO: 417

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1101 bases
 55 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

60

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Candida glabrata*
 (B) STRAIN: ATCC 66032

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 417

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TTTGACAAG TTGAAGGCTG AAAGAGAAAG AGGTATCACT ATCGATATCG      50
CTTTGTGGAA GTTCGAAACT CCAAAGTACC ACGTYACCGT TATCGATGCT      100
CCAGGTCACA GAGATTTCAT CAAGAACATG ATTACTGGTA CTTCTCAAGC      150
10 TGAAGTGTGCT ATCTTGATTA TTGCTGGTGG TGTCGGTGAA TTCGAAGCYG      200
GTATCTCCAA GGATGGTCAA ACCAGAGAAC ACGCTCTATT GGCTTTCACC      250
CTAGGTGTTA GACAATTGAT TGTGCTGCTC AACAAGATGG ACTCTGTCAA      300
GTGGGATGAA TCCAGATTCG CTGAAATCGT TAAGGAAACC TCCAACCTCA      350
TCAAGAAGGT CGGTTACAAC CCAAAGACTG TTCCATTCGT CCCAATCTCT      400
15 GGTGGAACG GTGACAACAT GATTGAAGCC ACCACCAACG CTTCTGGTA      450
CAAGGGTTGG GAAAAGGAAA CCAAGGCTGG TGTCGTCAAG GGTAAGACCT      500
TGTTGGAAGC CATTGACGCT ATCGAACCAC CAACCAGACC AACTGACAAG      550
CCATTGAGAT TGCCATTGCA AGATGTCTAC AAGATCGGTG GTATCGGTAC      600
GGTGCCAGTC GGTAGAGTCG AAACCGGTGT CATCAAGCCA GGTATGGTTG      650
20 TTACCTTCGC CCCAGCTGGT GTTACCACTG AAGTCAAGTC CGTTGAAATG      700
CACCACGAAC AATTGACTGA AGGTTTGCCA GGTGACAACG TTGGTTTCAA      750
CGTTAAGAAC GTTTCCGTTA AGGAAATCAG AAGAGGTAAT GTCTGTGGTG      800
ACTCCAAGAA CGACCCACCA AAGGCTGCTG CTTCTTTCAA CGCTACCGTC      850
ATTGTCTTGA ACCACCCAGG TCAAATCTCT GCTGGTTACT CTCCAGTTTT      900
25 GGAAGTGCAC ACCGCCACCA TTGCTTGTA GTTTGAAGAA TTGTTGGAAA      950
AGAACGACAG AAGATCCGGT AAGAAGTTGG AAGACTCTCC AAAGTTCTTG      1000
AAGTCCGGTG ACGCTGCTTT GGTAAAGTTC GTTCCATCCA AGCCAATGTG      1050
TGTCGAAGCT TTCTCCGACT ACCCACCATT GGGTAGATTC GCTGTCAGAG      1100
A
30

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2) INFORMATION FOR SEQ ID NO: 418

35 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1080 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

40

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Candida guilliermondii*
 45 (B) STRAIN: ATCC 6260

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 418

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AGAGAAAGAG GTATCACCAT TGACATTGCT TTGTGGAAAT TCGAGACTCC      50
50 AAAGTACCAC GTTACYGTCA TTGATGCCCC AGGTCACAGA GATTTCATCA      100
AGAACATGAT CACTGGTACT TCTCAAGCTG ACTGTGCTAT TTTGATTATT      150
GCTGGTGGTA CCGGTGAATT CGAAGCTGGT ATCTCTAAGG ATGGTCAAAC      200
CAGAGAGCAC GCTTTGTTGG CTTACACCTT GGGTGTTAGA CAATTGATTG      250
TTGCTGTCAA CAAGATGGAC TCCGTCAART GGGACAAGAA CAGATTYAG      300
55 GAAATCATCA AGGAAACCTC TAACTTCGTC AAGAAGGTTG GTTACAACCC      350
TAAGACTGTG CCATTTCGTC CTATCTCTGG ATGGAAYGGT GACAACATGA      400
TTGAGGCTTC TACCAACTGT CCTTGGTACA AGGGATGGGA GAAGGAGACC      450
AAGGCTGGTA AGTCCACCGG TAAGACTTTG TTGGAGGCCA TTGACGCCAT      500
TGAGCCACCT CAAAGACCAA CCGACAAGCC ATTGAGATTG CCATTGCAAG      550
60 ATGTYTACAA GATTGGTGGT ATTGGAACGG TGCCAGTCGG TAGAGTTGAA      600

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	ACCGGTATCA	TYAAGGCCGG	TATGGTTGTT	ACCTTTGCCC	CAGCTGGTGT	650
	YACCACTGAA	GTCAAGTCCG	TGGAAATGCA	CCACGAACAA	TTGGTTGAAG	700
	GTGTTCCAGG	TGACAATGTT	GGTTTCAACG	TTAAGAACGT	TTCCGTTAAG	750
	GAAATTAGAA	GAGGTAACGT	TTGTGGTGAC	TCCAAGAACG	ACCCACCAAA	800
5	GGGTTGTGAC	TCTTTCACCG	CTCAAGTTAT	TGTGTTGAAC	CACCCCTGGTC	850
	AAATCTCTGC	TGGTTACTCT	CCAGTTTTGG	ACTGTCACAC	CGCCACATT	900
	GCTTGTAAT	TCGACACCTT	GTTGGAGAAG	ATTGACAGAA	GAACCGGTAA	950
	GAAGATGGAG	GACAACCCCA	AGTTTGTCAA	GTCCGGTGAC	GCTTCTATCG	1000
	TCAAGATGGT	GCCATCCAAG	CCAATGTGTG	TTGAGGCTTT	CACCGACTAC	1050
10	CCACCATTGG	GAAGATTCGC	CGTCAGAGAC			1080

2) INFORMATION FOR SEQ ID NO: 419

15

(i) SEQUENCE CHARACTERISTICS:

20

- (A) LENGTH: 751 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

25

- (A) ORGANISM: *Candida haemulonii*
- (B) STRAIN: ATCC 22991

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 419

30	TCTGTCAAGT	GGGACAAGGC	CAGATACGAG	GAAATCGTCA	AGGAGACCTC	50
	TAACCTTCGTC	AAGAAGGTTG	GTTACAACCC	TAAGACTGTT	CCATTCGTCC	100
	CAATCTCTGG	TTGGAACGGT	GACAACATGA	TTGAGGCTTC	TACCAACTGT	150
	GACTGGTACA	AGGGTTGGGA	GAAGGAGACC	AAGTCTGGTA	AGTCCACCGG	200
	TAAGACCTTG	TTGGAGGCCA	TTGACGCCAT	TGAGCCACCA	ACCAGACCAA	250
35	CCGACAAGCC	ATTGAGATTG	CCATTGCAGG	ATGTCTACAA	GATTGGTGTT	300
	ATCGGAAGCTG	TGCCAGTCGG	CAGAGTTGAG	ACCGGTGTTA	TCAAGGCCGG	350
	TATGGTTGTC	ACCTTCGCCC	CAGCTGGTGT	CACCACTGAA	GTCAAGTCTG	400
	TCGAGATGCA	CCACGAGCAG	TTGCCAGAGG	GTGTCCCAGG	TGACAACGTT	450
	GGTTTCAACG	TCAAGAACGT	TTCCGTTAAG	GAAATCAGAA	GAGGTAACGT	500
40	CTGTGGTGAC	TCCAAGCAGG	ACCCACCAAA	GGGCTGTGAC	TCTTTCACCG	550
	CTCAGGTTAT	TGTGTTGAAC	ACCCAGGTC	AGATCTCTTC	TGGTTACTCT	600
	CCAGTTTTGG	ACTGTCACAC	TGCCCACATT	GCTTGTAAGT	TCGACACCTT	650
	GGTTGAGAAG	ATCGACAGAA	GAACCGGTAA	GAAGTTGGAA	GATGAGCCAA	700
	AGTTCATCAA	GTCCGGTGAC	GCTGCTATCG	TCAAGATGGT	CCCAACCAAG	750
45	C					751

2) INFORMATION FOR SEQ ID NO: 420

50

(i) SEQUENCE CHARACTERISTICS:

55

- (A) LENGTH: 1102 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

60

- (A) ORGANISM: *Candida inconspicua*

(B) STRAIN: ATCC 16783

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 420

5	TCTTGACAAG	TTAAAGGCTG	AAAGAGAAAG	AGGTATCACT	ATTGATATTG	50
	CTTTATGGAA	ATTCGAAACT	CCAAAGTATC	ACGTTACCGT	CATTGATGCT	100
	CCAGGTCACA	GAGATTTTCA	TAAGAACATG	ATTACTGGTA	CTTCTCAAGC	150
	AGATTGTGCT	ATTTTGTGTA	TTGCTGGTGG	TGTCGGTGAA	TTCGAAGCTG	200
	GTATTTCCAA	GGATGGTCAA	ACTAGAGAAC	ACGCTTTATT	AGCATTCACC	250
10	TTAGGTGTGA	AGCAATTGAT	TGTTGCTATC	AACAAGATGG	ATTCTGTAA	300
	GTGGGATGAA	AAGAGATTTG	AAGAAATTGT	CAAGGAAACC	CAAAACTTCA	350
	TCAAGAAGGT	TGGTTACAAC	CCAAAGACTG	TTCCATTTCG	TCCAATTTCT	400
	GGTTGGAATG	GTGACAACAT	GATTGAACCA	TCTTCTAACT	GTCCATGGTA	450
	CAAGGGTTGG	ACTAAGGAAA	CCAAGGCAGG	TGTTGTCAAG	GGTAAGACCT	500
15	TATTAGAAGC	TATTGATGCT	ATTGAACCAC	CTGTCAGACC	AACTGATAAG	550
	CCATTAAGAT	TACCATTACA	AGATGTTTAC	AAGATTGGTG	GTATTGGTAC	600
	TGTGCCAGTC	GGTAGAGTTG	AAACCGGTAT	TATTAAGCCA	GGTATGGTTG	650
	TTGTTTTTCG	ACCATCTGGT	GTTACCACTG	AAGTCAAGTC	CGTTGAAATG	700
	CACCATGAAC	AATTAGAAGA	AGGTGTCCCA	GGTGACAATG	TTGGTTTCAA	750
20	CGTCAAGAAC	GTCTCTGTGA	AGGATATCAA	GAGAGGTAAC	GTTTGTGGTG	800
	ACTCCAAGAA	TGACCCACCA	CAAGGTTGTG	CTTCCTTCAA	TGCTCAAGTC	850
	ATTGTCTTGA	ACCACCCTGG	TCAAATTTCT	GCTGGTTACT	CTCCAGTTTT	900
	AGATTGTCAC	ACTGCCCACA	TTGCATGTAA	ATTTCGATGAA	TTAATTGAAA	950
	AGATTGACAG	AAGAACTGGT	AAGTCCGTTG	AAGACCATCC	AAAGTCTGTT	1000
25	AAGTCTGGTG	ATGCAGCTAT	CGTTAAGATG	GTTCCAACCA	AGCCAATGTG	1050
	TGTTGAAGCT	TTCACTGAAT	ACCCACCATT	AGGTAGATTC	GCAGTCAGAG	1100
	AT					1102

30

2) INFORMATION FOR SEQ ID NO: 421

(i) SEQUENCE CHARACTERISTICS:

	(A)	LENGTH: 1099 bases
35	(B)	TYPE: Nucleic acid
	(C)	STRANDEDNESS: Double
	(D)	TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

40

(vi) ORIGINAL SOURCE:

	(A)	ORGANISM: <i>Candida kefyr</i>
	(B)	STRAIN: ATCC 28838

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 421

	TGGACAAGTT	AAAGGCTGAA	AGAGAAAGAG	GTATCACCAT	CGATATCGCT	50
	TTGTGGAAGT	TCGAAACTCC	AAAGTACCAA	GTTACCGTTA	TCGATGCTCC	100
	AGGTCACAGA	GATTTTCATCA	AGAACATGAT	TACTGGTACT	TCTCAAGCTG	150
50	ACTGTGCTAT	CTTGATTATT	GCTGGTGGTG	TCGGTGAATT	CGAAGCCGGT	200
	ATCTCCAAGG	ATGGTCAAAC	CAGAGAACAC	GCTTTGTTGG	CTTACACCTT	250
	GGGTGTTAGA	CAATTGATTG	TTGCTATCAA	CAAGATGGAC	TCTGTAAAGT	300
	GGGATGAATC	TCGTTACCAA	GAAATTGTGA	AGGAAACCTC	CAACTTCATC	350
	AAGAAGGTCG	GTTACAACCC	AAAGAATGTT	CCATTTCGTCC	CAATCTCTGG	400
55	TTGGAACGGT	GACAACATGA	TTGAAGCCAC	CACCAACGCT	CCATGGTACA	450
	AGGGTTGGGA	AAAGGAAACC	AAGGCTGGTA	CCGTCAAGGG	TAAGACCTTG	500
	TTGGAAGCTA	TTGACGCTAT	CGAACCACCA	ACCAGACCAA	CTGACAAGCC	550
	ATTGAGATTG	CCATTGCAAG	ATGTCTACAA	GATCGGTGGT	ATTGGTACTG	600
	TGCCAGTCGG	TAGAGTCGAA	ACCGGTGTCA	TCAAGCCAGG	TATGGTTGTT	650
60	ACCTTCGCCC	CAGCCGGTGT	CACTACCGAA	GTTAAGTCCG	TCGAAATGCA	700

	CCACGAACAA	TTGGAAGAAG	GTCTACCAGG	TGACAACGTC	GGTTTCAACG	750
	TCAAGAACGT	TTCCGTTAAG	GAAATCAGAA	GAGGTAACGT	CTGTGGTGAC	800
	TCCAAGAACG	ATCCACCAAA	GGCTGCTGCT	TCTTTCAACG	CCACTGTTAT	850
	CGTCTTGAAC	CACCCAGGTC	AAATCTCTGC	TGGTTACTCT	CCAGTTTTGG	900
5	ATTGTCACAC	TGCTCACATT	GCTTGTAAGT	TCGACGAATT	GTTGGAAAAG	950
	AACGACAGAA	GATCCGGTAA	GAAGTTGGAA	GACTCTCCAA	AGTTCTTGAA	1000
	GTCTGGTGAC	GCTGCTTTGG	TTAAGTTCGT	TCCATCTAAG	CCAATGTGTG	1050
	TTGAAGCATT	CTCTGACTAC	CCACCATTGG	GTAGATTCGC	TGTCAGAGA	1099

10

2) INFORMATION FOR SEQ ID NO: 422

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 1095 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

20 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Candida krusei*
 (B) STRAIN: ATCC 34135

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 422

	AAGTTAAAGG	CAGAAAGAGA	AAGAGGTATC	ACTATTGATA	TTGCTTTATG	50
	GAAGTTYGAA	ACTCCAAART	ACCACGTTAC	CGTTATTGAT	GCTCCAGGTC	100
30	ACAGAGATTT	CATCAAGAAC	ATGATTACCG	GTACTTCTCA	AGCTGATTGT	150
	GCTATTTTGA	TTATTGCTGG	TGGTGTCGGT	GAATTCGAAG	CTGGTATCTC	200
	CAAGGATGGT	CAAAC TAGAG	AACACGCTCT	ATTGGCTTTC	ACCTTAGGTG	250
	TTAGACAATT	GATTGTTGCT	ATCAACAAGA	TGGATTCCGT	TAARTGGGAT	300
	GAAAACAGAT	TTGAAGAAAT	TGTCAAGGAA	ACCCAAAAC T	TCATCAAGAA	350
35	GGTTGGTTAC	AACCCAAAGA	CTGTTCCATT	CGTTCCAATY	TCTGGTTGGA	400
	ATGGTGACAA	CATGATTGAA	GCATCCACCA	ACTGTCCATG	GTACAAGGGT	450
	TGGACTAAGG	AAACCAAGGC	AGGTGTTGTT	AAGGGTAAGA	CCTTATTAGA	500
	AGCAATCGAT	GCTATTGAAC	CACCTGTCAG	ACCAACCGAA	AAGCCATTAA	550
	GATTACCATT	ACAAGATGTT	TACAAGATTG	GTGGTATTGG	TACTGTGCCA	600
40	GTCCGTTAGG	TCGAAACCGG	TGTCATTAAAG	CCAGGTATGG	TTGTCACTTT	650
	TGCTCCAGCA	GGTGTCACCA	CCTGAAGTCAA	GTCCGTTGAA	ATGCACCATG	700
	AACAATTAGA	ACAAGGTGTT	CCAGGTGATA	ACGTTGGTTT	CAACGTTAAG	750
	AACGTTTCTG	TCAAGGATAT	CAAGAGAGGT	AACGTTTGTG	GTGACTCCAA	800
	GAACGACCCA	CCAATGGGTG	CAGCTTCCTT	CAATGCTCAA	GTCATTGTCT	850
45	TGAACCACCC	TGGTCAAATT	TCCGCTGGTT	ACTCTCCAGT	CTTGGATTGT	900
	CACACTGCCC	ACATTGCATG	TAAGTTCGAC	GAATTAATCG	AAAAGATTGA	950
	CAGAAGAACT	GGTAAGTCTG	TTGAAGACCA	TCCAAAGTCY	GTCAAGTCTG	1000
	GTGATGCAGC	TATCGTCAAG	ATGGTCCCAA	CCAAGCCAAT	GTGTGTTGAA	1050
	GCTTTCACTG	AATAYCCACC	ATTAGGTAGA	TTCGCAGTCA	GAGAT	1095

50

2) INFORMATION FOR SEQ ID NO: 423

(i) SEQUENCE CHARACTERISTICS:

- 55 (A) LENGTH: 1104 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

60

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 5 (A) ORGANISM: *Candida lambica*
(B) STRAIN: ATCC 24750

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 423

10	CTTGACAAG CTTAAGGCTG AAAGAGAAAG AGGTATCACC ATTGATATCG	50
	CTTTATGGAA GTTCGAAACT CCAAAGTACC ACGTTACCGT CATTGACGCT	100
	CCAGGTCACA GAGATTTTCAT CAAGAACATG ATTACTGGTA CCTCTCAAGC	150
	AGATTGTGCT ATTTTTRATYA TTGCTGGTGG TGTCGGTGAA TTCGAAGCTG	200
	GTATCTCTAA GGATGGTCAA ACCAGAGAAC ACGCTCTTCT TGCATTCACT	250
	CTTGGTGTGA GACAATTGAT TGTTGCTATC AACAAAGATGG ACTCTGTCAA	300
15	GTGGGACGAA TCCAGATTCG ATGAAATTTG TAAGGAAACC GCWAACTTCA	350
	TCAAGAAGGT TGGTTACAAC CCAAAGACTG TTCCATTCGT CCCAATCTCT	400
	GGTTGGAACG GTGACAACAT GATTGAACCA TCTGCTAACT GTCCATGGTA	450
	CAAGGGATGG ACTAAGGAAA CCAAGGCTTC CGGTGTCGTC AAGGGTAAGA	500
	CCCTTCTTGA AGCAATTGAT GCTATTGAGC CACCTGTCAG ACCAACTGAC	550
20	AAGGCTTTGA GATTGCCATT RCAAGATGTC TACAAGATTG GTGGTATTGG	600
	TACTGTGCCA GTCGGTAGAG TTGAAACCGG TATCATCAAG CCAGGTATGA	650
	TTGTCGTTTT CGCTCCAACC GGTGTTACTA CTGAAGTTAA GTCCGTTGAA	700
	ATGCACCATG AACAATTAGA AGAAGGTGTC CCAGGTGACA ATGTTGGTTT	750
	CAACGTCAAG AACGTCTCTG TTAAGGATAT TAAGAGAGGT AACGTCTGTG	800
25	GTGACTCCAA GAACGACCCA CCAATGGGTT GTGCTTCCTT CAATGCTCAA	850
	GTCATTGTTT TTAACCACCC AGGTCAAATT TCTGCTGGTT ACTCACCAGT	900
	TCTTGACTGT CACACTGCCC ACATTGCATG TAAGTTCGAY GAATTACTCG	950
	AAAAGATTGA CAGAAGAACC GGTAAGGCTA CTGAAGACCA TCCAAAGTCT	1000
	GTCAAGTCTG GTGATGCAGC TATCGTCAAG ATGGTTCCAA CCAAGCCAAT	1050
30	GTGTGTYGAA GCTTTCCTG ACTACCCACC ATTAGGTAGA TTCGCTGTYA	1100
	GAGA	1104

35 2) INFORMATION FOR SEQ ID NO: 424

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 1098 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

45 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Candida lusitaniae*
(B) STRAIN: ATCC 66035

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 424

50	GGACAAGTTG AAGGCTGAGA GAGAAAGAGG TATCACCATC GATATCGCTT	50
	TGTGGAAGTT CGAGACTCCA AAGTACCACG TTACCGTCAT TGACGCTCCA	100
	GGTCACAGAG ATTTTCATCAA GAACATGATC ACTGGTACTT CCCAAGCTGA	150
	CTGTGCTATC TTGATTATCG CTGGTGGTGT CGGTGAGTTC GAAGCCGGTA	200
55	TCTCTAAGGA CGGTCAAACC AGAGAGCACG CTTTGTTGGC TTACACCTTG	250
	GGTGTCAGC AGTTGATTGT TGCTGTCAAC AAGATGGACT CCGTCAAGTG	300
	GGACCAATCT AGATTGAGG AAATCATCAA GGAAACCTCT AACTTCGTCA	350
	AGAAGGTTGG TTACAACCCT AAGACTGTTC CATTCGTCCC AATCTCTGGT	400
	TGGAACGGTG ACAACATGAT TGAGCCATCY ACCAACTGCC CATGGTACAA	450
60	GGGTTGGGAG AAGGAGACCA AGTCYGGTAA GTCCACCGGT AAGACCTTGT	500

	TGGAGGCCAT	TGACGCCATT	GAGCCACCTT	CGAGACCAAC	CGACAAGCCA	550
	TTGAGATTGC	CATTGCAAGA	TGTCTACAAG	ATYGGTGGTA	TTGGTACTGT	600
	GCCAGTCGGT	AGAGTTGAGA	CCGGTGTCTAT	CAAGGCCGGT	ATGGTTGTCA	650
	CCTTTGCTCC	AGCTGGTGTC	ACCACTGAAG	TCAAGTCCGT	GGAAATGCAC	700
5	CACGAACAAT	TGGCTGAGGG	TGTCCCAGGT	GACAACGTTG	GTTTCAACGT	750
	CAAGAACGTT	TCCGTCAAGG	AAATCAGAAG	AGGTAACGTC	TGTGGTGACT	800
	CCAAGAACGA	CCCACCAAAG	GCTGCTGCTT	CYTTCACTGC	TCAAGTYATY	850
	GTCTTGAACC	ACCCAGGTCA	AATCTCCTCY	GGTACTCTC	CAGTYTTGGA	900
	CTGTACACT	GCYCACATTG	CTTGTAAGTT	CGACACCTTG	ATTGAGAAGA	950
10	TCGACAGAAG	AACYGGTAAG	AAGTTGGAAG	AAGAGCCAAA	GTTTCATCAAG	1000
	TCYGGTGACG	CTGCTATCGT	CAAGATGGTC	CCAACCAAGC	CAATGTGYGT	1050
	YGAAGCTTTC	ACCGACTACC	CACCATTGGG	TAGATTTCGT	GTCAGAGA	1098

15

2) INFORMATION FOR SEQ ID NO: 425

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1101 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

25

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Candida norvegensis*
 (B) STRAIN: ATCC 22977

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 425

	TCTTGACAAG	TTAAAGGCTG	AAAGAGAAAG	AGGTATCACT	ATTGATATTG	50
	CTTTATGGAA	ATTTCGAACT	CCAAAATACC	ACGTTACCGT	TATTGATGCT	100
	CCAGGTCACA	GAGATTTTCAT	TAAGAACATG	ATTACTGGTA	CTTCCCAAGC	150
35	TGATTGTGCT	ATCTTAATTA	TTGCTGGTGG	TGTCGGTGAA	TTCGAAGCTG	200
	GTATCTCCAA	GGATGGTCAA	ACCAGAGAAC	ACGCTTTATT	AGCATTCCACC	250
	TTAGGTGTTA	AGCAATTAAT	TGTTGCTATC	AACAAGATGG	ACTCTGTAA	300
	GTGGGATGAA	AAGAGATTG	AAGAAATTGT	CAAGGAAACC	CAAAACTTCA	350
	TCAAGAAGGT	TGGTTACAAC	CCAAAGACTG	TTCCATTTCGT	TCCAATTTCT	400
40	GGTTGGAATG	GTGACAACAT	GATTGAACCA	TCTACTAACT	GTCCATGGTA	450
	CAAGGGTTGG	ACTAAGGAAA	CCAAGGCAGG	TGTTGTAAAG	GGTAAGACCT	500
	TATTAGAAGC	TATTGATGCT	ATTGAACCAC	CTGTCAGACC	AACTGACAAG	550
	CCATTAAGAT	TACCATTACA	AGATGTTTAC	AAGATTGGTG	GTATTGGTAC	600
	TGTGCCAGTC	GGTAGAGTTG	AAACCGGTGT	TATTAAGCCA	GGTATGGTTG	650
45	TTGTTTTTCGC	ACCATCTGGT	GTTACCACTG	AAGTCAAGTC	CGTTGAAATG	700
	CACCATGAAC	AATTAGAACA	AGGTGTCCCA	GGTGACAATG	TTGGTTTCAA	750
	CGTCAAGAAC	GTCTCTGTTA	AGGATATTAA	GAGAGGTAAC	GTTTGTGGTG	800
	ACTCCAAGAA	CGACCCACCA	CAAGGTTGTG	CTTCCTTCAA	TGCTCAAGTC	850
	ATTGTCTTGA	ACCACCCTGG	TCAAATTTCT	GCAGGTTACT	CTCCAGTTTT	900
50	AGATTGTCAC	ACTGCCCACA	TTGCATGTAA	GTTTCGATGAA	TTAATCGAAA	950
	AGATTGACAG	AAGAACTGGT	AAGTCCGTTG	AAGACCATCC	AAAGTCTGTT	1000
	AAGTCTGGTG	ATGCAGCTAT	CGTTAAGATG	GTTCCAACCA	AGCCAATGTG	1050
	TGTTGAAGCT	TTCACTGAAT	ACCCACCATT	AGGTAGATTC	GCAGTCAGAG	1100
	A					1101

55

2) INFORMATION FOR SEQ ID NO: 426

(i) SEQUENCE CHARACTERISTICS:

257

- (A) LENGTH: 1095 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

5

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Candida parapsilosis*
 (B) STRAIN: ATCC 90018

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 426

	CAAATTGAAG	GCTGAAAGAG	AAAGAGGTAT	CACCATTGAT	ATCGCTTTGT	50
15	GGAAATTCGA	AACTCCAAAA	TACCATGTTA	CTGTTATTGA	TGCTCCAGGT	100
	CACAGAGATT	TCATCAAGAA	TATGATTACT	GGTACTTCTC	AAGCTGATTG	150
	TGCTATTTTG	ATTATTGCTG	GTGGTACTGG	TGAATTCGAA	GCTGGTATCT	200
	CTAAGGATGG	TCAAACCAGA	GAACACGCTT	TGTTGGCTTA	CACCTTGGGT	250
	GTTAAGCAAT	TGATTGTTGC	CATCAACAAG	ATGGACTCAG	TCAAATGGGA	300
20	CAAGAACAGA	TACGAAGAAA	TTGTCAAGGA	AACTTCCAAC	TTCGTCAAGA	350
	AGGTTGGTTA	CAACCCTAAA	GCTGTCCCAT	TCGTCCCAAT	CTCTGGTTGG	400
	AACGGTGACA	ATATGATTGA	ACCATCAACC	AACTGTCCAT	GGTACAAGGG	450
	TTGGGAAAAG	GAAACTAAAG	CTGGTAAGGT	TACCGGTAAG	ACCTTGTTGG	500
	AAGCTATCGA	TGCTATCGAA	CCACCAACCA	GACCAACTGA	CAAGCCATTG	550
25	AGATTGCCAT	TGCAAGATGT	CTACAAGATT	GGTGGTATTG	GAAGTGTGCC	600
	AGTTGGTAGA	GTTGAAACCG	GTATCATCAA	GGCTGGTATG	GTTGTTACTT	650
	TTGCCCCAGC	TGGTGTTACC	ACTGAAGTCA	AGTCCGTTGA	AATGCACCAC	700
	GAACAATTGA	CTGAAGGTGT	CCCAGGTGAC	AATGTTGGTT	TCAACGTCAA	750
	GAACGTTTCA	GTTAAGGAAA	TCAGAAGAGG	TAACGTTTGT	GGTGACTCCA	800
30	AGAACGATCC	ACCAAAGGGA	TGTGAYTCCT	TCAATGCTCA	AGTTATTGTC	850
	TTGAACCAAC	CAGGTCAAAT	CTCTGCTGGT	TACTCACCAG	TCTTGGATTG	900
	TCACACTGCC	CACATTGCTT	GTAAATTCGA	CACTTTGATT	GAAAAGATTG	950
	ACAGAAGAAC	CGGTAAGAAA	TTGGAAGATG	AACCAAAATT	CATCAAGTCC	1000
	GGTGATGCTG	CYATCGTCAA	GATGGTCCCA	ACCAAGCCAA	TGTGTGTTGA	1050
35	AGCTTTCACT	GACTACCCAC	CATTGGGAAG	ATTGCTGTT	AGAGA	1095

2) INFORMATION FOR SEQ ID NO: 427

40

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 752 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

45

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Candida rugosa*
 (B) STRAIN: ATCC 96275

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 427

55	CTCCGTCAAG	TGGTCTCAGT	CTCGTTTCGA	GGAGATCGTC	AAGGAGGTTT	50
	CCAACCTCAT	CAAGAAGGTT	GGTTACAAGC	CCGATGAGGT	TCCTTTCGTC	100
	CCCATCTCTG	GCTGGAACGG	CGACAACATG	CTTGAGCCCT	CCACCAACTG	150
	CCCCTGGTAC	AAGGGATGGA	CCAAGAAGAC	CAAGAAGGGT	GAGGTCAAGG	200
	GTAAGACTCT	TCTCGAGGCC	ATTGACGCCA	TCGAGCCCCC	CTCCCGTCCT	250
60	ACCGACAAGC	CCCTCCGCTT	GCCTCTTCAG	GATGTCTACA	AGATCGGCGG	300

	TATCGGTACG	GTACCTGTCG	GCCGTGTCGA	GACCGGTATC	ATCAAGCCCCG	350
	GCATGGTTCG	CACTTTCGCC	CCCGCTGGTG	TCACCACTGA	AGTGAAGTCC	400
	GTCGAGATGC	ACCACGAGCA	GATCCCCGAG	GGTCTCCCCG	GTGACAACGT	450
	CGGTTTCAAC	GTCAAGAACG	TTACCGTCAA	GGATATCCGC	CGTGGTAACG	500
5	TCTGCGGTGA	CTCCAAGAAC	GACCCCCCCA	AGGGCTGCTC	TTCCTTCACT	550
	GCCCAGGTCA	TCGTTTTC	CCACCCCGGT	CAGATCTCCA	ACGGTTACTC	600
	CCCCGTTTTC	GACTGCCACA	CCGCCACAT	TGCCTGCCGC	TTCGACGAGA	650
	TCCAGTCCAA	GATGGACCGT	CGTACTGGTA	AGACCCTTGA	GGAGAACCCC	700
	AAGTTCATCA	AGGCTGGTGA	CTCCGCTATC	GTCAAGATGG	TTCCCTCCAA	750
10	GC					752

2) INFORMATION FOR SEQ ID NO: 428

15

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1093 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 20 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 25 (A) ORGANISM: *Candida sphaerica*
 (B) STRAIN: ATCC 2504

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 428

30	AGTTAAAGGC	TGAAAGAGAA	AGAGGTATCA	CCATCGATAT	CGCTTTGTGG	50
	AAGTTCGAAA	CTCCAAAGTA	CCAAGTTACC	GTTATCGATG	CTCCAGGTCA	100
	CAGAGATTTC	ATCAAGAACA	TGATTACTGG	TACTTCTCAA	GCTGACTGTG	150
	CTATCTTGAT	TATTGCTGGT	GGTGTCGGTG	AATTCGAAGC	CGGTATCTCC	200
	AAGGATGGTC	AAACCAGAGA	ACACGCTTTG	TTGGCTTTCA	CCTTGGGTGT	250
35	TAGACAATTG	ATTGTTGCTG	TTAACAAGAT	GGATTCCGTT	AAGTGGGATG	300
	AATCTCGTTT	CCAAGAAATT	GTCAAGGAAA	CCTCTAACTT	CATCAAGAAG	350
	GTCGGTTACA	ACCCAAAGAC	TGTTCCATTC	GTCCCAATCT	CTGGTTGGAA	400
	CGGTGACAAC	ATGATTGAAG	CCACCACCAA	TGCTTCATGG	TACAAGGGTT	450
	GGGAAAAGGA	AACCAAGTCC	GGTGTCGTCA	AGGGTAAGAC	CTTGTTGGAA	500
40	GCTATTGACG	CTATCGAACC	ACCATCCAGA	CCAAC TGACA	AGCCATTGAG	550
	ATTGCCATTG	CAAGATGTCT	ACAAGATTGG	TGGTATCGGA	ACTGTGCCAG	600
	TCGGTAGAGT	CGAAACCGGT	GTTATCAAGC	CAGGTATGAT	TGTTACCTTT	650
	GCCCCAGCCG	GTGTTACTAC	TGAAGTTAAG	TCCGTCGAAA	TGCACCACGA	700
	ACAATTGGAA	GAAGGTCTAC	CAGGTGACAA	CGTCGGTTTC	AACGTCAAGA	750
45	ACGTTTCCGT	TAAGGAAATC	AGAAGAGGTA	ACGTCTGTGG	TGACTCCAAG	800
	AACGATCCAC	CAAAGGCTGC	TGCTTCTTTC	AACGCCACTG	TTATCGTCTT	850
	GAACCATCCA	GGTCAAATCT	CTGCTGGTTA	CTCTCCAGTT	TTGGATTGTC	900
	ACACTGCTCA	CATTGCTTGT	AAGTTCGACG	AATTGTTGGA	AAAGAACGAT	950
	AGAAGATCCG	GTAAGAAGTT	GGAAGACTCT	CCAAAGTTCT	TGAAGTCCGG	1000
50	TGATGCTGCT	TTGGTTAAGT	TCGTTCCATC	TAAGCCAATG	TGTGTTGAAG	1050
	CCTTCTCTGA	CTACCCACCT	CTAGGTAGAT	TCGCTGTCAG	AGA	1093

55 2) INFORMATION FOR SEQ ID NO: 429

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1094 bases
 (B) TYPE: Nucleic acid
 60 (C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

5 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Candida tropicalis*

(B) STRAIN: ATCC 13803

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 429

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10 AAATTGAAGG CTGAAAGAGA AAGAGGTATC ACCATTGATA TCGCTTTGTG      50
   GAAATTCGAA ACTCCAAAAT ACCACGTTAC CGTTATTGAT GCTCCAGGTC      100
   ACAGAGATTT CATCAAGAAC ATGATTACTG GTACTTCCCA AGCTGATTGT      150
   GCTATTTTGA TTATTGCTGG TGGTACTGGT GAATTCTGAAG CTGGTATTTT      200
15 TAAAGATGGT CAAACCAGAG AACACGCTTT GTTGGCTTAC ACCTTGGGTG      250
   TCAAACAATT GATTGTTGCT GTCAACAAGA TGGACTCTGT TAAATGGGAC      300
   AAAACAGAT TTGAAGAAAT TATCAAGGAA ACTTCTAACT TCGTCAAGAA      350
   GGTGTTGTTAC AACCTAAGG CTGTTCCATT CGTTCCAATC TCTGGTTGGA      400
   ATGGTGACAA CATGATTGAA GCTTCTACCA ACTGTCCATG GTACAAGGGT      450
20 TGGGAAAAAG AAACCAAGGC TGGTAAGGTT ACCGGTAAGA CTTTGTGTTGGA      500
   AGCCATTGAT GCTATTGAAC CACCTTCAAG ACCAACTGAC AAGCCATTGA      550
   GATTGCCATT GCAAGATGTT TACAAGATTG GTGGTATTGG TACTGTGCCA      600
   GTCGGTAGAG TTGAACTGG TGTCAACAAA GCCGGTATGG TTGTTACTTT      650
   CGCCCCAGCT GGTGTTACCA CTGAAGTCAA ATCCGTCGAA ATGCACCACG      700
25 AACAATTGGC TGAAGGTGTC CCAGGTGACA ATGTTGGTTT CAACGTTAAG      750
   AACGTTTCTG TTAAAGAAAT TAGAAGAGGT AACGTTTGTG GTGACTCCAA      800
   GAACGATCCA CCAAAGGGTT GTGACTCTTT CAACGCTCAA GTTATTGTCT      850
   TGAACCACCC AGGTCAAATC TCTGCTGGTT ACTCTCCAGT CTTGGATTGT      900
   CACACTGCTC ATATTGCTTG TAAATTCGAC ACCTTGGTTG AAAAGATTGA      950
30 CAGAAGAACT GGTAAGAAAT TGGAAGAAAA TCCAAAATTC GTCAAATCCG      1000
   GTGATGCTGC TATTGTCAAG ATGGTTCCAA CCAAACCAAT GTGTGTTGAA      1050
   GCTTTCCTG ACTACCCACC ATTAGGTAGA TTCGCTGTCA GAGA              1094

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35 2) INFORMATION FOR SEQ ID NO: 430

(i) SEQUENCE CHARACTERISTICS:

40 (A) LENGTH: 1095 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

45 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Candida utilis*

(B) STRAIN: Csp 388

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 430

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   CAAGCTTAAA GCTGAGAGAG AGAGAGGTAT CACTATCGAC ATTGCTCTCT      50
   GGAAGTTCTG GACTCCAAAG TACCACGTTA CTGTCATTGA TGCCCCAGGT      100
   CACAGAGATT TCATCAAGAA CATGATTACT GGTACCTCCC AGGCTGACTG      150
55 TGCTATTCTT ATCATTGCCG GTGGTGTGTTG TGAGTTCGAG GCTGGTATCT      200
   CTAAGGATGG TCAGACCAGA GAGCACGCTT TGCTCGCTTT CACCCTTGGT      250
   GTTAGACAGA TGATTGTTGC TATCAACAAG ATGGACTCTG TCAAGTGGGA      300
   CGAGAAGAGA TTCGAGGAGA TCGTTAAGGA GACCTCTAAC TTCATCAAGA      350
   AGGTTGGTTA CAACCCAAAG ACTGTTCCAT TTGTCCCAAT TTCYGGTTGG      400
60 AACGGTGACA ACATGATTGA GGCCTCTACC AACTGTCCAT GGTACAAGGG      450

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	TTGGGAGAAG	GAGACCAAGG	CTGGTGTGTG	CAAGGGTAAG	ACCTTGCTCG	500
	ATGCCATTGA	CGCCATTGAG	CCACCAACAA	GACCAACTGA	CAAGCCATTG	550
	AGATTGCCAC	TCCAGGATGT	CTACAAGATT	GGTGGTATCG	GAAGCTGTTCC	600
	AGTCGGTAGA	GTCGAGACCG	GTGTCATCAA	GCCAGGTATG	GTTGTTACCT	650
5	TTGCCCCATC	CGGTGTCACC	ACTGAGGTTA	AGTCCGTCGA	GATGCACCAC	700
	GAGCAGCTTG	CTGAGGGTAT	CCCAGGTGAC	AACGTTGGTT	TCAACGTTAA	750
	GAACGTCTCT	GTTAAGGAGA	TCAGAAGAGG	TAACGTTGCC	GGTGACTCCA	800
	AGAACGACCC	ACCACAGGGT	GCTGAGTCCT	TCAACGCTCA	GGTCATTGTC	850
	TTGAACCACC	CAGGTCAGAT	CTCTGCTGGT	TACTCTCCAG	TTTTGGACTG	900
10	TCACACCGCC	CACATTGCTT	GTAAGTTCTC	TGAGCTTTTG	GAGAAGATTG	950
	ACAGAAGATC	CGGTAAGTCC	CTTGAGGCCT	CTCCAAAGTT	CGTCAAGTCT	1000
	GGTGATGCCG	CTATCGTCAA	GATGGTTCCA	TCCAAGCCAT	TGTGTGTTGA	1050
	GGCCTTCACT	GACTACCCAC	CACTCGGTAG	ATTCGCTGTC	AGAGA	1095

15

2) INFORMATION FOR SEQ ID NO: 431

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 1085 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

25 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Candida viswanathii*
 (B) STRAIN: ATCC 28269

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 431

	GCTGAAAGAG	AAAGAGGTAT	CACCATCGAT	ATCGCTTTGT	GGAAATTCGA	50
	AACTCCAAAR	TACCACGTTA	CCGTCATTGA	YGCTCCAGGT	CACAGAGATT	100
35	TCATCAAGAA	CATGATYACT	GGTACTTCTC	AAGCTGATTG	TGCTATYTTG	150
	ATTATCGCTG	GTGGTACTGG	TGAATTCGAA	GCTGGTATYT	CTAAGGATGG	200
	TCAAACGAGA	GAACACGCTT	TGTTGGCCTA	CACCTTGGGT	GTCAAGCAAT	250
	TGATTGTTGC	TGTCAACAAG	ATGGACTCTG	TCAAATGGGA	CAAGAACAGA	300
	TTCGAAGAAA	TCATCAAGGA	AACCTCCAAC	TTCGTCAAGA	AGGTTGGTTA	350
40	CAACCCAAAG	ACTGTTCCAT	TCGTCCCAAT	CTCTGGTTGG	AACGGTGACA	400
	ACATGATTGA	AGCCTCCACC	AAC TGCCCAT	GGTACAAGGG	TTGGGAAAAG	450
	GAAACCAAGG	CTGGTAAGGT	TACCGGTAAG	ACTTTGTTGG	AAGCCATTGA	500
	CGCTATCGAA	CCACCAACCA	GACCAACTGA	CAAGCCATTG	AGATTGCCAT	550
	TGCAAGATGT	CTACAAGATT	GGTGGTATCG	GAAGCTGTCC	AGTCGGTAGA	600
45	GTTGAAACTG	GTGTCATCAA	GGCCGGTATG	GTTGTCACTT	TYGCCCCAGC	650
	TGGTGTTACC	ACTGAAGTCA	AGTCCGTTGA	AATGCACCAC	GAACAATTGG	700
	CTGAAGGTGT	CCCAGGTGAC	AACGTTGGTT	TCAACGTCOA	GAACGTTTCC	750
	GTCAAGGAAA	TCAGAAGAGG	TAACGTCTGT	GGTGACTCCA	AGAACGACCC	800
	ACCAAAGGGT	TGTGASTCTT	TCAACGCTCA	AGTCATTGTC	TTGAACCACC	850
50	CAGGTCAAAT	CTCTGCTGGT	TACTCTCCAG	TCTTGGATTG	TCACACTGCC	900
	CACATTGCTT	GTAAGTTTGA	CACCTTGCTT	GAAAAGATTG	ACAGAAGAAC	950
	CGGTAAGAAG	TTGGAAGAAA	ACCCAAAGTT	TGTCAACTCC	GGTGACGCTG	1000
	CTATCGTCAA	GATGGTCCCA	ACCAAGCCAA	TGTGTGTTGA	AGCYTTCAC	1050
	GACTACCCAC	CATTGGGTAG	ATTCGCTGTC	AGAGA		1085

55

2) INFORMATION FOR SEQ ID NO: 432

(i) SEQUENCE CHARACTERISTICS:

60

- (A) LENGTH: 1072 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

5

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Candida zeylanoides*
 (B) STRAIN: ATCC 7351

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 432

	AGGTATTACC	ATTGACATTG	CCTTGTGGAA	GTTTCGAGACC	CCCAAGTACC	50
15	AGGTCACCGT	CATTGACGCT	CCTGGCCACA	GAGATTTCAT	TAAGAACATG	100
	ATCACTGGTA	CCTCCCAGGC	TGACTGTGCC	ATCTTGATCA	TTGCTGGTGG	150
	TGTTGGTGAG	TTCGAGGCTG	GTATCTCCAA	GGATGGCCAG	ACCAGAGAGC	200
	ACGCCTTGCT	TGCCTACACC	TTGGGTGTCA	AGCAATTGAT	TGTTGCTGTC	250
	AACAAGATGG	ACTCCGTCAA	GTGGGACAAG	AACAGATTCTG	AGGAGATTGT	300
20	CAAGGAGACC	TCCAACCTCG	TCAAGAAGGT	TGGCTACAAC	CCCAAGACTG	350
	TCCCCTTCGT	TCCCATCTCC	GGTTGGAACG	GTGACAACAT	GATTGAGGCC	400
	TCCACCAACT	GCCCTTGCTA	CAAGGGTTGG	GAGAAGGAGA	CCAAGGCCGG	450
	TAAGGTCACT	GGTAAGACCT	TGTTGGAGGC	TATTGACGCC	ATTGAGCCCC	500
	CCACCAGACC	CACCGACAAG	CCCTTGAGAT	TGCCCTTGCA	GGATGTCTAC	550
25	AAGATTGGTG	GTATTGGAAC	GGTGCCCGTT	GGCAGAGTTG	AGACCGGCAT	600
	CATCAAGGCC	GGTATGGTTG	TCACCTTTGC	CCCCGCTGGT	GTCACTACTG	650
	AAGTGAAGTC	TGTCGAGATG	CACCACGAGC	AATTGGCTGA	GGGTGTCCCA	700
	GGTGACAATG	TTGGTTTCAA	CGTGAAGAAC	GTTTCCGTGA	AGGAGATCAG	750
	AAGAGGTAAC	GTTTGCGGTG	ACTCCAAGAA	CGACCCCCCG	AAGGCTGCTG	800
30	CTTCTTTCAA	CGCCCAGGTT	ATCGTCTTAA	ACCACCCCCG	TCAAATCTCT	850
	GCTGGTTACT	CTCCGGTTTT	GGATTGCCAC	ACTGCCCCAC	TTGCTTGCGAG	900
	ATTCGACCAG	TTGATTGAGA	AGATCGACAG	AAGAACCGGT	AAGAAGATGG	950
	AGGACGACCC	TAAGTTCATC	AAGTCCGGTG	ACGCTGCCAT	CGTCAAGATG	1000
	GTTCTTTCCA	AGCCCATGTG	TGTTGAGGCC	TTCCTGACT	ACCCTCCCTT	1050
35	GGTTCGTTTC	GCTGTCAGAG	AC			1072

2) INFORMATION FOR SEQ ID NO: 433

40

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 751 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

45

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Coccidioides immitis*
 (B) STRAIN: Silveira

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 433

55	AGCACCAACT	GGTCCGAGCC	TCGTTTCAAC	GAAATCGTCA	AGGAAGTCTC	50
	CAACTTCATC	AAGAAGGTCG	GATACAACCC	CAAGGCTGTT	CCATTCGTCC	100
	CCATCTCTGG	TTTCGAAGGT	GACAACATGA	TTCAACCCTC	CACCAACGCT	150
	CCTTGGTACA	AGGGCTGGAA	CAAGGAGACC	GCCTCTGGCA	AGCACACTGG	200
	CAAGACCCTC	CTCGACGCCA	TTGATGCCAT	CGACCCCCCA	ACCCGCCCCA	250
60	CCGAGAAGCC	CCTCCGTCTC	CCACTTCAGG	ATGTGTACAA	GATCTCTGGT	300

	ATCGGAACAG	TCCCAGTCGG	CCGTGTTCGAA	ACCGGTGTTA	TCAAGCCTGG	350
	TATGGTTGTG	ACCTTCGCTC	CTTCCAACGT	CACCACTGAA	GTCAAGTCCG	400
	TCGAAATGCA	CCACCAGCAG	CTCACCAGG	GTAACCCTGG	TGACAACGTT	450
	GGCTTCAACG	TCAAGAACGT	CTCTGTCAAG	GAAGTCCGCC	GCGGTAACGT	500
5	CGCTGGTGAC	TCCAAGAACG	ACCCACCAA	GGGCTGCGAC	TCCTTCAACG	550
	CCCAGGTCAT	CGTCCTCAAC	CACCCCTGGT	AAGTCGGTGC	TGGTTATGCC	600
	CCAGTCCTTG	ACTGCCACAC	TGCCCACATT	GCTTGCAAGT	TCTCCGAGCT	650
	CCTCGAGAAG	ATCGACCGCC	GTACCGGTAA	ATCCGTTGAG	AACAACCCCA	700
	AGTTCATCAA	GTCTGGTGAT	GCCGCTATCG	TCAAGATGGT	TCCATCCAAG	750
10	C					751

2) INFORMATION FOR SEQ ID NO: 434

15

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1146 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Cryptococcus albidus*
 (B) STRAIN: ATCC 66030

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 434

30	AAGCTCAAGG	CCGAGCGAGA	GCGAGGTATC	ACCATCGACA	TCGCCTTGTC	50
	GAAGTTCGAG	ACCCCCAAGT	ACAATGTCAC	CGTCATTGAC	GCCCCCGGTC	100
	ACCGAGACTT	CATCAAGAAC	ATGATCACCG	GTACCTCGCA	GGCCGACTGT	150
	GCCATCCTCA	TCATCGCCTC	CGGTATCGGA	GAGTTCGAGG	CTGGTATCTC	200
	CAAGGACGGT	CAGACCCGAG	AGCACGCCCT	TTTGGCCTTC	ACCCTCGGTG	250
35	TCCGACAGCT	CATCATTGCC	ATCAACAAGA	TGGACACCTG	CAAGGTTAGT	300
	TCGCAGGTCC	TGGTCTCTGT	ACGAATCTTG	CTGACCCCTT	TTACAGTGGT	350
	CCGAAGACCG	ATACAACGAA	ATCGTCAAGG	AGGCTTCCGG	TTTCATCAAG	400
	AAGGTCCGGAT	ACAACCCCAA	GACCGTTCCC	TTCGTCCCA	TCTCCGGATG	450
	GCACGGAGAC	AACATGTTGG	AGGAGTCCAC	CAACATGCCC	TGGTACAAGG	500
40	GATGGCACAA	GGAGTCCAAG	GCCGGTGTTG	TCAAGGGAAA	GACCTTGCTC	550
	GAGGCCATCG	ACGCCATCGA	GCCCCCTACC	CGACCTTCCG	ACAAGCCCTT	600
	GCGATTGCCC	CTCCAGGATG	TCTACAAGAT	CGGTGGTATC	GGTACGGTGC	650
	CCGTCGGTCG	AGTCGAGACC	GGTGTCAATC	AGGCTGGTAT	GGTCGTCACC	700
	TTCGCCCCTG	CCAACGTCAC	CACCGAAGTC	AAGTCCGTCG	AAATGCACCA	750
45	CGAACAGCTC	GCTGAGGGTG	TTCCCGGTGA	CAACGTCGGT	TTCAACGTCA	800
	AGAACGTTTC	CGTCAAGGAC	ATCCGACGAG	GAAACGTCTG	CTCCGACTCG	850
	AAGAACGACC	CCGCTATGGA	GTCTGCTTCC	TTCAACGCTC	AGGTCATTGT	900
	CTTGAACCA	CCGGGTCAGA	TCGGTGCCGG	CTACTCCCCC	GTTTTGGACT	950
	GCCACACCGC	TCACATTGCC	TGCAAGTTTCG	CTGAGCTCGT	TGAGAAGATC	1000
50	GACCGACGAA	CCGGTAAGGT	CATGGAGGCC	GCCCCCAAGT	TCGTCAAGTC	1050
	CGGTGACGCC	GCCATCGTCA	AGTTGATCCC	GTCCAAGCCC	ATGTGTGTGC	1100
	AGTCCTACTC	CGAGTACCCC	CCCTTGGGTC	GATTCGCCGT	CCGAGA	1146

55

2) INFORMATION FOR SEQ ID NO: 435

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1095 bases
 (B) TYPE: Nucleic acid

60

- (C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

5

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Exophiala jeanselmei*
(B) STRAIN: ATCC 64755

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 435

	CAAGCTGAAG	GCCGAGCGTG	AGCGTGGTAT	CACCATCGAT	ATCGCCTTGT	50
	GGAAGTTCGA	GACTCCCAAG	TACTATGTCA	CTGTCATCGA	CGCCCCCTGGT	100
	CATCGTGA	TTATCAAGAA	CATGATCACT	GGTACTTCCC	AGGCTGACTG	150
15	CGCCATTCTC	ATCATTGCCG	CCGGTACTGG	TGAATTCGAA	GCCGGTATCT	200
	CCAAGGATGG	TCAGACTCGT	GAGCACGCTC	TGCTCGCCTA	CACCCTGGGT	250
	GTC AAGCAGC	TCATTGTCGC	CATCAACAAG	ATGGACACCA	CCAAGTG GTC	300
	CGAGGATCGT	TTCAACGAAA	TCATCAAGGA	GACTTCCAGC	TTCATCAAGA	350
	AGGTCGGCTA	CAACCCCAAG	TCCGTTCCCT	TCGTCCCCAT	CTCCGGCTTC	400
20	AACGGTGACA	ACATGATCGA	TGTCTCCACC	AACTGCCCCT	GGTACAAGGG	450
	CTGGGAGAAG	GAGACCAAGG	CTGGCAAGGC	CTCTGGCAAG	ACTCTCCTCG	500
	AGGCCATCGA	CGCCATCGAC	CCCCCCTC	GTCCCACCGA	CAAGCCTCTC	550
	CGTCTTCCTC	TCCAGGATGT	CTACAAGATC	TCTGGTATCG	GAACGGTGCC	600
	CGTCGGTCTG	GTTGAGACTG	GTGTCATCAA	GGCCGGTATG	GTCGTTACCT	650
25	TCGCTCCTGC	CAACGTCACC	ACTGAAGTCA	AGTCCGTCGA	AATGCACCAC	700
	GAACAAC TCG	CCGAGGGTGT	TCCAGGTGAC	AACGTTGGTT	TCAACGTCAA	750
	GAACGTCTCC	GTCAAGGAGG	TTCGTCGTGG	AAACGTCTGC	GGTGACTCCA	800
	AGAACGACCC	ACCCAAGGGT	GCTGATTCCCT	TCAACGCCCA	GGTCATCGTC	850
	TTGAACCAACC	CTGGTCAAGT	CGGTGCTGGC	TACGCCCCAG	TGTTGGATTG	900
30	CCACACTGCC	CACATTGCTT	GCAAGTTCTC	TGAGCTTCTC	GAGAAGATTG	950
	ACCGCCGTAC	CGGTAAATCC	ATCGAAAACA	ACCCCAAGTT	CATCAAGTCT	1000
	GGTGACGCTG	CCATCGTCAA	GATGGTTCCC	AGCAAGCCCA	TGTGTGTTGA	1050
	GGCCTTCACT	GACTACCCAC	CTCTTGGTCG	TTTCGCCGTC	CGTGA	1095

35

2) INFORMATION FOR SEQ ID NO: 436

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 1113 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

45 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Fusarium oxysporum*
(B) STRAIN: WSA-212

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 436

	AAGCTCAAGG	CCGAGCGTGA	GCGTGGTATC	ACCATCGATA	TTGCTCTCTG	50
	GAAGTTCGAG	ACTCCTCGCT	ACTATGTCAC	CGTCATTGGT	ATGTTGTCGC	100
55	TCATGCTTCA	TTCTACTTCT	CTTCGTACTA	ACACATCACT	CAGACGCTCC	150
	CGGTCACCGT	GATTTTCATCA	AGAACATGAT	CACTGGTACT	TCCCAGGCCG	200
	ATTGCGCCAT	TCTCATCAT	GCCGCCGGTA	CTGGTGAGTT	CGAGGCTGGT	250
	ATCTCCAAGG	ATGGCCAGAC	CCGTGAGCAC	GCTCTTCTTG	CCTACACCCT	300
	TGGTGTCAAG	AACCTCATCG	TCGCCATCAA	CAAGATGGAC	ACCACCAAGT	350
60	GGTCTGAGGC	CCGTTACCAG	GAGATCATCA	AGGAGACCTC	CTCTTTTCATC	400

	AAGAAGGTCG	GCTACAACCC	CAAGGCTGTC	GCTTTCGTCC	CCATCTCCGG	450
	TTTCAACGGT	GACAACATGC	TTACCCCCTC	CACCAACTGC	CCCTGGTACA	500
	AGGGTTGGGA	GCGTGAGATC	AAGTCCGGCA	AGCTCACTGG	CAAGACCCTC	550
	CTCGAGGCCA	TTGACTCCAT	CGAGCCCCCC	AAGCGTCCCG	TTGACAAGCC	600
5	CCTTCGTCTT	CCCCTTCAGG	ATGTCTACAA	GATCGGTGGT	ATTGGAACGG	650
	TTCCCCGTCG	CCGTATCGAG	ACTGGTGTCA	TCAAGCCCGG	TATGGTCGTT	700
	ACCTTCGCTC	CTTCCAACGT	CACCACTGAA	GTCAAGTCCG	TCGAGATGCA	750
	CCACGAGCAA	CTCACTGAGG	GCCAGCCCGG	TGACAACGTT	GGTTTCAACG	800
	TGAAGAACGT	CTCCGTCAAG	GACATCCGAC	GTGGTAACGT	CGCTGGTGAC	850
10	TCCAAGAACG	ACCCCCCTAT	GGGTGCCGCT	TCTTTCACCG	CCCAGGTCAT	900
	CGTCCTCAAC	CACCCCGGTC	AGGTCGGTGC	TGGTTACGCT	CCCGTCCTCG	950
	ATTGTACAC	TGCCCACATT	GCCTGCAAGT	TCGCCGAGAT	CCAGGAGAAG	1000
	ATCGACCGCC	GAACCGGTAA	GGCTACTGAG	GCCGCCCCCA	AGTTCATCAA	1050
	GTCTGGTGAC	TCCGCCATCG	TCAAGATGGT	TCCCTCCAAG	CCCATGTGTG	1100
15	TTGAGGCTTT	CAC				1113

2) INFORMATION FOR SEQ ID NO: 437

20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 726 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 25 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 30 (A) ORGANISM: *Geotrichum* spp.
 (B) STRAIN: LEV-4

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 437

35	GGTCCGAGGA	CAGATTCAAC	GAGATTGTCA	AGGAGACTTC	CAACTTCATC	50
	AAGAAGGTTG	GTTAYAACCC	CAAGACTGTT	GCTTTCGTCC	CCATCTCTGG	100
	TTGGAACGGT	GACAACATGA	TTGAGCCCTC	CACCAACTGC	CCCTGGTACA	150
	AGGGATGGCA	GAAGGAGACC	AAGGCTGGTG	TACTAAGGG	TAAGACCCTC	200
	CTTGAGGCCA	TCGATGCCAT	TGAGCCCCCT	GTCAGACCTT	CCGACAAGCC	250
40	CCTCCGTCTT	CCCCTCCAGG	ATGTCTACAA	GATCGGTGGT	ATCGGAAGCTG	300
	TGCCCGTCGG	CCGTGTCGAA	ACCGGTGTCA	TCAAGGCCGG	TATGGTCGTC	350
	ACCTTCGCCC	CCGCTGGTGT	CACCACTGAA	GTCAAGTCCG	TCGAGATGCA	400
	CCACGAGCTC	CTCACTGAGG	GTCTCCCCCG	TGACAACGTT	GGTTTCAACG	450
	TCAAGAACGT	CTCCGTAAAG	GATATCAGAC	GTGGTAACGT	CTGCCGTGAC	500
45	TCCAAGAACG	ATCCCCCCTA	GGCTTGCGCT	TCTTTCACCG	CCCAGGTCAT	550
	TATCTTCAAC	CACCCTGGTC	AGATCTCTGC	TGGATACTCT	CCCGTCCTTG	600
	ATTGCCACAC	CGCCCATATT	GCTTGCAAGT	TCGACACTTT	GATCGAGAAG	650
	ATTGACCGTC	GTAAGGTAA	GAAGACTGAG	GACTCCCCCA	AGTTCGTCAA	700
50	GGCCGGTGAT	GCTGCTATCG	TCAAGA			726

2) INFORMATION FOR SEQ ID NO: 438

55

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 754 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 60 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Histoplasma capsulatum*
 (B) STRAIN: G186A5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 438

10	CACCACCAAG	TGGTCCGAGT	CCCGTTTCAA	CGAAATCATC	AAGGAGGTTT	50
	CCAACTTCAT	CAAGAAGGTC	GGATATAACC	CCAAGGCTGT	TCCCTTCGTG	100
	CCAATCTCTG	GTTTCGAGGG	TGACAACATG	ATTGAACCCT	CCCCCAACTG	150
	CACATGGTAC	AAGGGCTGGA	ACAAGGAGAC	TGCCTCTGGC	AAGTETTETG	200
	GTAAACCCT	TCTCGATGCC	ATTGACGCCA	TTGAACCCCC	AACCCGTCCT	250
	ACCGATAAGC	CCCTCCGTCT	TCCCCTCCAG	GATGTGTACA	AAATCTCTGG	300
15	TATTGGCACT	GTTCCCGTCG	GACGTGTTGA	GACTGGTGTC	ATCAAGCCCG	350
	GTATGGTCGT	GACTTTCGCT	CCCTCCAACG	TCACCACTGA	AGTCAAGTCC	400
	GTCGAAATGC	ACCACCAACA	ACTCCAGGCT	GGTTACCCTG	GCGACAACGT	450
	CGGCTTCAAC	GTCAAGAACG	TTTCAGTCAA	GGAAGTCCGC	CGTGGCAACG	500
	TTGCTGGCGA	CTCCAAAAT	GATCCCCCTA	AGGGCTGCGA	ATCCTTCAAT	550
20	GCCCAGGTCA	TCGTCCTTAA	CCACCCCGGC	CAGGTTGGCG	CTGGTTATGC	600
	CCCAGTCCTC	GACTGCCACA	CTGCCCACAT	TGCTTGCAAG	TTCTCTGAGC	650
	TTATTGAGAA	GATCGACCGC	CGTACCGGAA	AGTCTGTTGA	GAACAACCCC	700
	AAGTTCATCA	AGTCTGGTGA	TGCTGCTATC	GTCAAGATGG	TTCCCTCCAA	750
	GCCC					754

2) INFORMATION FOR SEQ ID NO: 439

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 743 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Issatchenkia orientalis*
 (B) STRAIN: ATCC 6258

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 439

45	TGGGATGAAA	ACAGATTTGA	AGAAATTGTC	AAGGAAACCC	AAAACCTTCAT	50
	CAAGAAGGTT	GGTTACAACC	CAAAGACTGT	TCCATTCGTT	CCAATCTCTG	100
	GTTGGAATGG	TGACAACATG	ATTGAAGCAT	CCACCAACTG	TCCATGGTAC	150
	AAGGGTTGGA	CTAAGGAAAC	CAAGGCAGGT	GTTGTTAAGG	GTAAGACCTT	200
	ATTAGAAGCA	ATCGATGCTA	TTGAACCACC	TGTCAGACCA	ACCGAAAAGC	250
	CATTAAGATT	ACCATTACAA	GATGTTTACA	AGATTGGTGG	TATTGGTACT	300
50	GTGCCAGTCG	GTAGAGTCGA	AACCGGTGTC	ATTAAGCCAG	GTATGGTTGT	350
	CACTTTTGCT	CCAGCAGGTG	TCACCACCGA	AGTCAARTCC	GTTGAAATGC	400
	ACCATGAACA	ATTAGAACAA	GGTGTTCAG	GTGATAACGT	TGGTTTCAAC	450
	GTTAAGAACG	TCTCTGTCAA	GGATATCAAG	AGAGGTAACG	TTTGTGGTGA	500
	CTCCAAGAAC	GACCCACCAA	TGGGTGCAGC	TTCYTTCAAT	GCTCAAGTCA	550
55	TTGTCTTGAA	CCACCCTGGT	CAAATTTCCG	CTGGTTACTC	TCCAGTCTTG	600
	GATTGTCACA	CTGCCCACAT	TGCATGTAAG	TTGACGAAT	TAATCGAAAA	650
	GATTGACAGA	AGAAGTGGTA	AGTCTGTTGA	AGACCATCCA	AAGTCYGTCA	700
	AGTCTGGTGA	TGCAGCTATC	GTCAAGATGG	TCCCAACCAA	GCC	743

2) INFORMATION FOR SEQ ID NO: 440

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 1091 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

10 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Malassezia furfur*
 (B) STRAIN: ATCC 42132

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 440

CAAGCTCAAG GCTGAGCGTG AGCGTGGTAT CACCATCGAC ATTGCTCTGT 50
 GGAAGTTCTGA GACCCCTAAG TACCACGTTA CCGTCATTGA CGCTCCTGGT 100
 20 CACCGTGACT TCATCAAGAA CATGATTACG GGTACCTCGC AGGCTGACTG 150
 CGCTATCCTC ATCATTGCCG GTGGTACCGG TGAGTTCGAG GCTGGTATCT 200
 CGAAGGACGG TCAGACCCGT GAGCACGCTC TGCTCGCTTT CACCCTGGGT 250
 GTGCGTCAGC TCATTGTGGC CGTCAACAAG ATGGACACCA CCAAGTACTC 300
 GGAGGACCGC TTCAACGAGA TTGTCCGCGA AGTGTCGAAC TTCATCAAGA 350
 25 AGGTCGGTTT CAACCCCAAG ACTGTTGCCT TCGTCCCAT CTCGGGCTGG 400
 CACGGTGACA ACATGATCGA GGCCACCACC AACATGCCTT GGTACAAGGG 450
 CTGGGAGAAG GAGACCAAGT CGGGCAAGGT CACTGGTAAG ACTCTGCTGG 500
 ACGCCATCGA CGCCATCGAG CCCCCGACCC GCCCCACTGA CAAGCCCCCTG 550
 CGTCTCCCTC TGCAGGATGT GTACAAGATC GGTGGTATCG GTACTGTCCC 600
 30 TGTCGGTTCGT GTTGAGACCG GTGTGATCAA GCCCGGTATG GTTGTGACCT 650
 TCGTCCCTC GAACGTCACC ACTGAAGTTA AGTCGGTTGA GATGCACCAC 700
 GAGTCGCTCC CTGAGGGTCT CCCCGGTGAC AACGTTGGTT TCAACGTGAA 750
 GAACGTCTCG GTTAAGGACA TTCGCCGTGG TAACGTTGCC TCGGACTCGA 800
 AGAACGACCC CGCTCAGGAG GCTGCTTCGT TCAACGCGCA GGTCAATTGTC 850
 35 ATGAACCACC CTGGTCAGAT CAGCAACGGT TACTCGCCCG TGCTTGACTG 900
 CCACACTGCG CACATTGCCT GCCGCTTCAA CAACATCCTC CAGAAGATCG 950
 ACCGTCGCTC GGGTAAGGTG CTTGAGGAGA ACCCCAAGTT CATCAAGTCG 1000
 GGTGACGCTG CCATGGTGGA GATGATCCCC ACCAAGCCCA TGTGTGTGGA 1050
 40 GTCGTTCAAC GAGTACCCCC CTCTGGGTCG TTTGCTGTG C 1091

2) INFORMATION FOR SEQ ID NO: 441

(i) SEQUENCE CHARACTERISTICS:

- 45 (A) LENGTH: 749 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Malassezia pachydermatis*
 55 (B) STRAIN: ATCC 42756

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 441

ACCACCAAGT ACTCGGAGGA CCGCTTCAAC GAGATTATTC GCGAGACTTC 50
 60 GAACCTCATC AAGAAGGTCG GTTACAACCC GAAGACTGTT GCCTTCGTCC 100

	CGATCTCGGG	CTGGCACGGT	GACAACATGA	TTGAGGCGAC	CACCAACATG	150
	CCGTGGTACA	AGGGCTGGGA	GAAGGAGACC	AAGTCGGGCA	AGGCCACTGG	200
	TAAGACCTTT	CTGGACGCTA	TTGACGCCAT	TGAGCCGCCG	ACGCGCCCGA	250
	CCGACAAGCC	TCTCCGTCTT	CCTCTCCAGG	ATGTGTACAA	GATCGGTGGT	300
5	ATCGGTACYG	TCCCAGTCCG	CCGTGTTGAG	ACCGGTGTTA	TCAAGCCCGG	350
	TATGGTTGTG	ACCTTCGCTC	CGTCGAACGT	CACSACTGAA	GTTAAGTCGG	400
	TCGAGATGCA	CCACGAGCAG	ATCCCTGAGG	GTCTTCCGGG	TGACAACGTT	450
	GGTTTCAACG	TGAAGAACGT	GTCGGTCAAG	GACATTCGCC	GTGGTAACGT	500
	CGCCTCGGAC	TCGAAGAACG	ACCCGGCTCA	GGAGGCTGCC	TCGTTCAATG	550
10	CTCAGGTCAT	TGTGATGAAC	CACCCTGGTC	AGATCAGCAA	CGGTTACTCG	600
	CCRG TGCTCG	ACTGCCACAC	TGCTCACATT	GCCTGCCGCT	TCAACAACAT	650
	CCTCCAGAAG	ATCGACCGTC	GTTCCGGTAA	GGTTCTYGAA	GAGAACCCCA	700
	AGTTCATCAA	GTCGGGTGAC	GCTGCCATGG	TTGAGATGAT	CCCGACCAA	749

15

2) INFORMATION FOR SEQ ID NO: 442

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 1150 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

25 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Malbranchea filamentosa*
 (B) STRAIN: ATCC 48174

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 442

	ACTGAAGGCC	GAGCGTGAGC	GTGGTATCAC	CATCGATATC	GCCCTCTGGA	50
	AGTTCGAGAC	CCCCAAGTAC	CATGTCACCG	TCATTGGTAC	GTTTCGACATG	100
35	TTCGACCTTT	TGCCTAGTGT	CCCCTTCTAA	CCACAGTTTA	TAGACGCCCC	150
	TGGCCATCGT	GATTTTCGTCA	AGAACATGAT	CACCTGGTACT	TCCCAGGCTG	200
	ATTGCGCTAT	CCTCATCATT	GCTTCCGGCA	CTGGTGAATT	CGAGGCTGGT	250
	ATCTCCAAGG	ATGGCCAGAC	CCGTGAGCAC	GCTCTGCTTT	CCTTCACCCT	300
	CGGTGTTAGG	CAGCTCATTG	TCGCCCTCAA	CAAGATGGAC	ACTGTCAACT	350
40	TCGCTGAGGC	CCGTTACAAC	GAGATTGTCA	AGGAAGTCTC	CAACTTCATC	400
	AAGAAGGTCG	GCTACAACCC	CAAGGCCGTT	CCTTTCGTCC	CCATCTCCGG	450
	TTTCGAGGGT	GACAACATGA	TCGAGGCCTC	CACCCGCATT	CCTTGGTACA	500
	AGGGCTGGAA	CAAGGAGACC	GCCAGTGGCA	AGAGCACCGG	CAAGACCCTY	550
	CTCGAGGCCA	TTGATGCCAT	CGAACCCCCG	GTCCGTCCCA	CCGACAAGCC	600
45	CCTYCGTCTC	CCTCTTCAGG	ATGTGTACAA	GATCTCCGGT	ATTGGCACTG	650
	TTCCTGTCGG	TCGTGTTGAG	ACTGGTGTCA	TCAAGCCTGG	TATGGTCGTT	700
	ACTTTCGCCC	CCGCCAACGT	CACCACTGAA	GTCAAGTCCG	TCGAGATGCA	750
	CCACCAGCAG	CTCCAGGCCG	GTAACCCCCG	TGACAACGTC	GGCTTCAACG	800
	TCAAGAACGT	TTCCGTCAAG	GAAGTCCGCC	GTGGCAACGT	TGCCTCCGAC	850
50	TCCAAGAACG	ACCCCGCCAA	GGGCTGCGAC	TCCTTCAACG	CCCAGGTCAT	900
	CGTCCTTAAC	CACCCCGGTC	AGGTCCGGTG	TGGATACGCT	CCCGTCCTCG	950
	ATTGCCACAC	TGCCACATT	GCTTGCAAGT	TCTCTGAGCT	TCTTGAGAAG	1000
	ATCGATCGCC	GTACCGGTAA	ATCCGTTGAG	GACCACCCCA	AGTTCATCAA	1050
	GTCTGGTGAT	GCCGCTATCG	TCAAGATGGT	TCCCTCCAAG	CCTATGTGCG	1100
55	TTGAGGCTTT	CAC TGACTAC	CCTCCCCCTG	GTCGTTTCGC	CGTCCGTGAC	1150

2) INFORMATION FOR SEQ ID NO: 443

60

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1099 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Metschnikowia pulcherrima*
 (B) STRAIN: DSM 70336

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 443

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15  GGACAAGTTG AAGGCTGAGA GAGAGAGAGG TATCACCATC GACATTGCCT      50
    TGTGGAAGTT CGAGACTCCT AAGTACCACG TCACCGTYAT TGACGCCCCA      100
    GGTCACAGAG ATTCATCAA GAACATGATC ACTGGTACTT CCCAGGCTGA      150
    CTGTGCIATC TTGATTATCG CYGGTGGTGT TGGTGAGTTC GAGGCTGGTA      200
    TCTCCAAGGA TGGCCAGACC AGAGAGCACG CTTTGTGGC YTACACCTTG      250
20  GGTGTTAGAC ARTTGATTGT TGCCGTCAAC AAGATGGACT CTGTCAAGTG      300
    GGACAAGAAC AGATTTGAGG AGATCATCAA GGAGACCTCT AACTTCGTCA      350
    AGAAGGTTGG TTACAACCCT AAGACYGTGC CATTCTGCC AATYTCTGGT      400
    TGGAACGGTG ACAACATGAT TGAGGCTTCC ACTAACTGCC CATGGTACAA      450
    GGGTTGGGAG AAGGAGACCA AGGCCGGTAA GTCTWCCGGT AAGACCTTGT      500
25  TGGAGGCCAT TGACGCCATT GAGCCACCAA CCAGACCTAC CGACAAGGCC      550
    TTGAGATTGC CTTTGCAGGA TGTCTACAAG ATCGGTGGTA TCGGAACGGT      600
    GCCAGTCGGC CGTGTCGAGA CCGGTGTCAT TAAGGCCGGT ATGGTTGTYA      650
    CCTTYGCCCC AGCTGGTGTC ACCACTGAGG TCAAGTCCGT CGAGATGCAC      700
    CACGAGCAGT TGGTCGAGGG TCTTCCAGGT GACAAYGTTG GTTTCAACGT      750
30  CAAGAACGTC TCCGTAAAGG AGATCAGAAG AGGTAACGTC TGTGGTGA      800
    CCAAGCAGGA CCCACCAAAG GGTGCCGCTT CTTTCACCGC YCAGGTTATT      850
    GTGTTGAACC ACCCTGGTCA GATCTCCTCT GGTTACTCTC CAGTGTGGA      900
    CTGYCACACC GCCCACATTG CCTGTAARTT CGACACCTTG TTGGAGAAGA      950
    TTGACAGAAG AACTGGTAAG TCCTTGAGT CYGAGCCTAA GTTCGTCAAG      1000
35  TCGGGTGACG CCGCCATTGT CAAGATGGTG CCAACCAAGC CAATGTGTGT      1050
    TGAGGCTTTC ACCGACTACC CACCTTTGGG TAGATTCGCC GTCAGAGAC      1099
  
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2) INFORMATION FOR SEQ ID NO: 444

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1153 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Paecilomyces lilacinus*
 (B) STRAIN: ATCC 42570

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 444

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55  CAAGCTCAAG GCCGAGCGTG AGCGTGGTAT CACCATCGAC ATTGCCCTCT      50
    GGAAGTTCGA GACTCCCAAG TACTATGTCA CCGTCATTGG TACGTCGACT      100
    CGCGCGAGAC TGGTCGCAAT TTCCACGTCG CTAACGTGCT TGAACAGACG      150
    CTCCCGGCCA CCGTGACTTC ATCAAGAACA TGATCACTGG TACCTCCCAG      200
60  GCTGACTGCG CTATCCTCAT TATCGCTGCC GGCCTGGTG AGTTCGAGGC      250
  
```

	TGGTATCTCC	AAGGATGGCC	AGACCCGTGA	GCACGCTCTG	CTCGCCTACA	300
	CCCTCGGTGT	TAAGCAGCTC	ATCGTCGCTA	TCAACAAGAT	GGACACCACC	350
	AAGTGGTCTG	AGGCCCGTTT	CCAGGAGATC	ATCAAGGAGA	CCTCCAACCTT	400
	CATCAAGAAG	GTCGGCTACA	ACCCCAAGAC	CGTCGCTTTC	GTCCCCATCT	450
5	CTGGTTTCCA	CGGCGACAAC	ATGCTTTCCC	CCTCCACCAA	CTGCCCCTGG	500
	TACAAGGGCT	GGGAGAAGGA	GACCAAGGCT	GGCAAGTCCA	CCGGCAAGAC	550
	CCTCCTTGAG	GCCATCGACT	CCATCGAGCC	CCCCAAGCGC	CCCAGCGACA	600
	AGCCCCCTCG	CCTTCCCCTT	CAGGATGTGT	ACAAGATCGG	CGGTATCGGC	650
	ACAGTCCCTG	TCGGCCGTAT	CGAGACTGGT	GTCATCAAGC	CCGGCATGGT	700
10	CGTGACCTTC	GCTCCTTCCA	ACGTCAACCAC	CGAAGTCAAG	TCCGTTGAGA	750
	TGCACCACGA	GCAGCTCTCC	GAGGGTGTCC	CCGGTGACAA	CGTCGGCTTC	800
	AACGTCAAGA	ACGTCTCCGT	CAAGGAGATC	CGTCGTGGCA	AEGTEGECGG	850
	TGACTCCAAG	AACGACCCCC	CTCTGGGTGC	CGCTTCTTTC	GATGCCCAGG	900
	TCATCGTCCT	CAACCACCCC	GGCCAGGTGC	GTGCTGGCTA	CGCCCCCGTC	950
15	CTCGACTGCC	ACACCGCCCA	CATTGCCTGC	AAGTTCGCCG	AGATCAAGGA	1000
	GAAGATCGAC	CGCCGTACCG	GCAAGTCTGT	CGAGTCCGCC	CCCAAGTTCA	1050
	TCAAGTCTGG	CGACTCTGCC	ATCGTCAAGA	TGATTCCCTC	CAAGCCCATG	1100
	TGCGTTGAGG	CTTTCACCGA	CTACCCTCCT	CTGGGCCGCT	TCGCCGTCCG	1150
	TGA					1153
20						

2) INFORMATION FOR SEQ ID NO: 445

- 25 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 763 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Double
 - (D) TOPOLOGY: Linear

- 30 (ii) MOLECULE TYPE: Genomic DNA

- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Paracoccidioides brasiliensis*
 - 35 (B) STRAIN: ATCC 32071

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 445

	TACCACTAAG	TGGTCCGAGA	CCCGATTCAA	TGAAATTATC	AAGGAAGTCA	50
40	CCAATTTTCAT	TAAGAAGGTC	GGATATAACC	CCAAGACTGT	TCCTTTCGTT	100
	CCCATTCTCTG	GTTTCGAGGG	TGACAACATG	ATCGAGCCCT	CTGCCAACTG	150
	CCCATGGTAC	AAGGGCTGGT	CCAAGGAGAC	TGCTCAGGGC	AAGTACTCTG	200
	GCAAGACCCT	TCTTGAGGCC	ATCGACGCCA	TTGAGCCCCC	CACCCGTCCT	250
	ACCGATAAAC	CTCTCCGTCT	TCCCCTCCAG	GATGTCTACA	AGATCTCCGG	300
45	TATTGGCACT	GTTTCTGTCTG	GACGTGTTGA	GACTGGAGTC	ATCAAGCCCCG	350
	GTATGGTCGT	GACCTTCGCT	CCCGCCAACG	TCACCACTGA	AGTCAAGTCC	400
	GTCGAAATGC	ACCACCAGCA	GCTTACCGCC	GGTAACCCCCG	GTGACAACGT	450
	CGGCTTCAAC	GTCAAGAATG	TTTCCGTCAA	AGAAGTCCGC	CGTGGTAACG	500
	TTGCCGGTGA	CTCTAAGAAT	GATCCCCCAA	AGGGCTGCGA	TTCCTTCAAT	550
50	GCCCAGGTCA	TCGTCTCTCAA	CCACCCTGGT	CAGGTTGGCG	CTGGTTATGC	600
	CCCAGTCCTC	GACTGCCATA	CTGCCCACAT	TGCCTGCAAA	TTCGCTGAGC	650
	TCCTTGAGAA	GATTGATCGA	CGAACCGGAA	AGTCTGTTGA	GAACAACCCC	700
	AAGTTCATCA	AGTCCGGTGA	TGCTGCTATC	GTCAAGATGA	TTCCTTCCAA	750
	GCCCATGTGC	GTC				763
55						

2) INFORMATION FOR SEQ ID NO: 446

- 60 (i) SEQUENCE CHARACTERISTICS:

270

- (A) LENGTH: 1346 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

5

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Penicillium marneffe*
 (B) STRAIN: ATCC 64101

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 446

	AAGCTCAAGG	CTGAGCGTGA	GCGTGGTATC	ACCATCGATA	TTGCTCTCTG	50
15	GAAGTTCCAG	ACTGCCAAGT	ACGAGGTTAC	CGTCATTGAC	GCCCCCGGTC	100
	ACCGTGATTT	CATCAAGAAC	ATGATCACTG	GTACCTCCCA	GGCCGATTGC	150
	GCTATTCTCA	TCATTGCCTC	TGGTACTGGT	GAATTCGAGG	CTGGTATCTC	200
	CAAGGATGGC	CAGACTCGTG	AGCACGCTCT	TTTGGCTTTC	ACCCTCGGTG	250
	TCCGTCAGCT	CATTGTTGCC	CTCAACAAGA	TGGACACTTG	CAAGTGGTCT	300
20	CAGGGTGAGT	ACTCGTACCT	GCGTTTGGCC	TTGAATATCT	TACTAATGCA	350
	CCATAGATCG	TTACAACGAA	ATTGTCAAGG	AGACTTCCAA	CTTCATCAAG	400
	AAGGTCGGAT	ACAACCCCAA	GAACGTTCCCT	TTCGTTCCCTA	TCTCCGGTTT	450
	CAACGGTGAC	AACATGCTTG	AGCCCTCCCC	CAACTGCCCC	TGGTACAAGG	500
	GTTGGGAGAA	GGAGACCAAG	GCCGGTAAGG	TCACTGGTAA	GACCCTCCTC	550
25	GAGGCCATCG	ACGCCATTGA	GCCCCCTACC	CGTCCCGCCA	ACAAGGTTAG	600
	TCCCTCCTCG	ACTACTCAAA	CCCTCCTCAT	AAGTTCAGAT	TACTGACTCG	650
	TTCACAGCCC	CTCCGTCTTC	CCCTCCAGRA	TGTCTACAAG	ATCGGTGGTA	700
	TTGGAACGGT	TCCCGTCGGT	CGTGTGAGA	CTGGTACCAT	CGTTCCTGGT	750
	ATGGTTGTCA	CCTTGTAAGT	CACTCTCCTC	GCTTATCCTA	CCTGAAATCA	800
30	TCATGTGCTA	ACTTGACACT	CAGCGCTCCC	GCCAACGTCA	CCACTGAAGT	850
	CAAGAGTGTT	GAAATGCACC	ACCAGCAGCT	CACTGCCGGT	CAGCCCGGTG	900
	ACAACGTTGG	TTTCAACGTG	AAGAACGTCT	CCGTCAAGGA	AATCCGTCTG	950
	GGTAACGTTG	CTGGTGACAG	CAAGAACGAC	CCCCCTGCCG	GTGCTGCCTC	1000
	CTTCAACGCC	CAGGTCATCG	TCCTCAACCA	CCCCGGTCAG	GTCGGTGCTG	1050
35	GTTACGCCCC	AGTCCTCGAT	TGCCACACTG	CCCACATTGC	TTGCAAGTTC	1100
	GCTGAGCTCC	TCGAGAAGAT	TGACCGTCGT	ACCGGAAAGT	CTGTTGAGGA	1150
	CCACCCCAAG	TTCATCAAGT	CCGGTGACGC	TGCCATCGTC	AAGATGATTC	1200
	CTTCCAAGCC	CATGTGTGTT	GAGGCTTTCA	CCGAGTACCC	TCCTCTCGGT	1250
	CGTTTCGCCG	TTCGCGAGTA	AGTTTTATCT	CCGTTGTCTA	TTTTCCATCC	1300
40	TTCCCTTCTC	CTCCGTCTTC	CATATATACT	TTTTCAGTTA	TATGTG	1346

2) INFORMATION FOR SEQ ID NO: 447

45

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1094 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Pichia anomala*
 (B) STRAIN: ATCC 18205

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 447

60	AAGTTAAAAG	CTGAACGTGA	AAGAGGTATC	ACTATTGATA	TTGCTTTATG	50
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	GAAATTCGAA	ACTCCAAAAT	ACCATGTTAC	CGTTATTGAT	GCTCCAGGTC	100
	ACAGAGATTT	CATCAAAAAT	ATGATTACTG	GTACTTCCCA	AGCTGATTGT	150
	GCTATYTTAA	TTATTGCCGG	TGGTATTGGT	GAATTCGAAG	CTGGTATCTC	200
	AAAAGATGGT	CAAACCAGAG	AACACGCTTT	NTTAGCTTAC	ACCTTAGGTG	250
5	TTAAACAATT	GATTGTTGCT	ATCAACAAGA	TGGATTCCGT	TAAATGGGAT	300
	GAATCTCGTT	TCGAAGAAAT	TGTCAAGGAA	ACYTCAAAC	TTATCAAGAA	350
	AGTTGGTTAC	AACCCAAAAA	CTGTTCCATT	CGTTCCAATC	TCAGGTTGGA	400
	ATGGTGATAA	CATGATTGAA	CCATCAWCTA	ACTGTCCATG	GTACAAAGGT	450
	TGGAAAAAAG	AAACCAAAGC	TGGTGAAGCT	AAAGGTAAAA	CTTTATTAGA	500
10	AGCCATTGAT	GCTATTGACC	CACCATCAAG	ACCAACTGAT	AAACCATTAC	550
	GTTTACCATT	ACAAGATGTT	TACAARATTG	GTGGTATTGG	TACTGTGCCA	600
	GTCCGGTAGAG	TTGAAACCGG	TGTTATCAAA	CCAGGTATGG	TTGTTACCTT	650
	TGCCCCAGCT	GGTGTTACCA	CTGAAGTCAA	ATCTGTTGAA	ATGCATCATG	700
	AACAATTGAC	TGAAGGTTTA	CCAGGTGACA	ATGTTGGTTT	CAACGTTAAG	750
15	AATGTTTCTG	TTAAAGAAAT	CCGTCGTGGT	AACGTCTGTG	GTGACTCTAA	800
	AAACGATCCA	CCAAAAGCTG	CTGAATCATT	CAATGCTCAA	GTTATTGTCT	850
	TAAACCATCC	AGGTCAAATC	TCTGCTGGTT	ACTCTCCAGT	TTTAGATTGT	900
	CACACTGCTC	ACATTGCTTG	TAAATTTGAC	ACTTTAATTG	AAAAAATTGA	950
	CAGACGTACT	GGTAAGAAAT	TAGAAGAAGC	TCCAAAATTC	ATCAAATCAG	1000
20	GTGATGCTGC	TATTGTTAAA	TTTGTTCCAT	CAAAACCATT	ATCAGTTGAA	1050
	GCTTTCAC	ACTACCCACC	ATTAGGTCGT	TTCGCTGTCA	GAGA	1094

25 2) INFORMATION FOR SEQ ID NO: 448

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1100 bases
 (B) TYPE: Nucleic acid
 30 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

35 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Pichia anomala*
 (B) STRAIN: ATCC 2149

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 448

40	CTTAGATAAG	TTAAAAGCTG	AACGTGAAAG	AGGTATCACT	ATTGATATTG	50
	CTTTATGGAA	ATTTCGAACT	CCAAAATACC	ATGTTACCGT	TATTGATGCT	100
	CCAGGTCACA	GAGATTTTCAT	CAAAAATATG	ATTACTGGTA	CTTCCCAAGC	150
	TGATTGTGCT	ATMTTAATTA	TTGCCGGTGG	TATTGGTGAA	TTCGAAGCTG	200
45	GTATCTCAAA	AGATGGTCAA	ACCAGAGAAC	ACGCTTTRTT	AGCTTACACC	250
	TTAGGTGTTA	AACAATTGAT	TGTTGCTATC	AACAAGATGG	ATTCCGTTAA	300
	ATGGGATGAA	TCTCGTTTCG	AAGAAATTGT	CAAGGAAACY	TCAAACCTTA	350
	TCAAGAAAGT	TGGTACAACC	CAAAAACGTG	TCCATTCGTT	CCAATCTCAG	400
	GTTGGAATGG	TGATAACATG	ATTGAACCAT	CAACTAACTG	TCCATGGTAC	450
50	AAAGGTTGGA	AAAAAGAAAC	CAAAGCTGGT	GAAGCTAAAG	GTAAAACCTT	500
	ATTAGAAGCC	ATTGATGCTA	TTGATCCACC	ATCAAGACCA	ACTGATAAAC	550
	CATTACGTTT	ACCATTACAA	GATGTTTACA	ARATTGGTGG	TATTGGTACT	600
	GTGCCAGTCG	GTAGAGTTGA	AACCGGTGTT	ATCAAACCAG	GTATGGTTGT	650
	TACCTTTGCC	CCAGCTGGTG	TTACCACTGA	AGTCAAATCT	GTTGAAATGC	700
55	ATCATGAACA	ATTGACTGAA	GGTTTACCAG	GTGACAATGT	TGGTTTCAAC	750
	GTTAAGAATG	TTTCTGTAA	AGAAATCCGT	CGTGGTAACG	TCTGTGGTGA	800
	CTCTAAAAAC	GATCCACCAA	AAGCTGCTGA	ATCATTCAAT	GCTCAAGTTA	850
	TTGTCTTAAA	CCATCCAGGT	CAAACTCTCTG	CTGGTTACTC	TCCAGTTTAA	900
	GATTGTCACA	CTGCTCACAT	TGCTTGTAAG	TTTGACACTT	TAATTGAAAA	950
60	AATTGACAGA	CGTACTGGTA	AGAAATTAGA	AGAAGCTCCA	AAATTCATCA	1000

AATCAGGTGA TGCTGCTATT GTTAAATTTG TTCCATCAAA ACCATTATCA 1050
 GTTGAAGCTT TCACTGACTA CCCACCATTA GGTCGTTTCG CTGTCAGAGA 1100

5

2) INFORMATION FOR SEQ ID NO: 449

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1201 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Pseudallescheria boydii*
 (B) STRAIN: ATCC 44331

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 449

CAAGCTCAAG GCCGAGCGTG AGCGTGGTAT CACCATCGAT ATCGCCCTCT 50
 GGAAGTTCGA GACCCCAAG TACCAGGTCA CCGTCATTGG TATGTCTTTG 100
 TGCTTTTGT GCTTTTGTG CCTGTGCCTC GCACAATTCC AGCCCTCGAT 150
 25 AATTATGAAC CTCGTACTAA TATGTCGTTT TCCCACTACC CACAGACGCC 200
 CCCGGCCATC GTGATTTCAT CAAGAACATG ATTACTGGTA CCTCCCAGGC 250
 TGATTGCGCC ATTCTCATCA TTGCCTCCGG TACTGGTGAG TTCGAGGCTG 300
 GCATCTCCAA GGATGGCCAG ACCCGTGAGC ACGCTCTTCT CGCCTTCACC 350
 CTCGGTGTCA AGAACCTCAT TGTTGCCATC AACAAGATGG ACACCAACAA 400
 30 CTGGTCCGAG GACCGATACA AGGAGATCAT CAAGGAGACC TCCAAC TTCA 450
 TCAAGAAGGT CGGCTACAAC CCCAAGGCCG TTCCTTTCGT CCCCATCTCC 500
 GGTTCACCG GAGACAACAT GCTTACCCCC TCCACCAACT GCCCCTGGTA 550
 CAAGGGTTGG GTCCGTGAGG TCAAGGGTAA CACCCTTACC GGCAAGACCC 600
 TTCTCGAGGC CATCGACTYC ATCGAGCCCC CCAAGCGTCC CACCGAGAAG 650
 35 CCCCTCCGTC TTCCCCTTCA GGACGTCTAC AAGATCGGTG GTATTGGCAC 700
 TGTGCCCCGTC GGCCGTATCG AGACCGGTAT CCTCAAGCCC GGTATGGTCG 750
 TCACCTTCGC TCCCTCCAAC GTCACCACTG AAGTCAAGTC CGTCGAGATG 800
 CACCACGAGC AGCTTACCGA GGGTGTCCCC GGTGACAACG TTGGTTTCAA 850
 CGTGAAGAAC GTCTCCGTCA AGGATATCCG CCGTGGCAAC GTCTGCGGTG 900
 40 ACTCCAAGAA CGACCCCCC GCTGCTGCCG CCTCTTTCCA GGCCAGGTC 950
 ATTGTCTCTA ACCACCCCGG CCAGATCGGT GCTGGTTACG CTCCCGTTCT 1000
 TGACTGCCAC ACTGCCACA TTGCTTGCAA GTTCGCCGAG CTCCTTGAGA 1050
 AGATCGACCG CCGTACCGGT AAGTCGGTCG AGAACAACCC CAAGTTCGTC 1100
 AAGTCTGGTG ATGCCGCAT CGTCAAGATG GTTCCCTCCA AGCCCATGTG 1150
 45 TGTTGAGTCC TTCACCGAGT ACCCCCCTCT CGGTCGTTTC GCCGTCCGTG 1200
 A 1201

2) INFORMATION FOR SEQ ID NO: 450

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1095 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Rhizopus oryzae*
 (B) STRAIN: ATCC 56015

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 450

5 CAAGCTTAAG GCTGAACGTG AACGTGGTAT CACCATCGAT ATTGCTCTCT 50
 GGAAGTTTCGA AACCCCCAAG TACCAAATTA CCGTTATTGA TGCTCCCGGT 100
 CACCGTGATT TCATCAAGAA CATGATTACC GGTACTTCTC AAGCCGATTG 150
 TGCTATTCTT ATCATTGCTG GTGGTACTGG TGAATTCGAA GCTGGTATCT 200
 10 CCAAGGATGG TCAAACCCGT GAACACGCCC TTTTGGCTTT CACTCTCGGT 250
 GTCCGTC AAT TGATTGTTGC TGTCAACAAG ATGGATACCA CCAAGTGGTC 300
 CGAAGCTCGT TTCAACGAAA TYGTCAAGGA AGTTTCTTCC TTCATCAAGA 350
 AGATTGGTTA CAACCCCAAG TCTGTTCCCT TCGTCCCCAT CTCTGGTTGG 400
 CACGGTGACA ACATGTTGGA AGAATCTACC AACATGCCCT GGTACAAGGG 450
 15 ATGGAACAAG GAAACCAAGG CTGGTGCCAA GTCTGGTAAG ACCCTCTTGG 500
 ATGCCATTGA CAACATTGAC CCTCCTACCC GTCCTGTTGA CAAGCCTCTC 550
 CGTCTTCCTC TTCAAGATGT TTACAAGATT GGTGGTATCG GTACTGTCCC 600
 CGTCGGTCGT GTCGAACTG GTGTCATCAA GGCTGGTATG GTTGTACCT 650
 TCGCTCCTGC TGCTGTCACC ACTGAAGTTA AGTCCGTCGA AATGCACCAC 700
 20 GAAACCCTCA CTGAAGGTCT CCCC GG TGAC AACGTCGGTT TCAACGTCAA 750
 GAACGTCTCC GTCAAGGATA TCCGTCGTGG TAACGTCTGT TCTGACTCCA 800
 AGAACGACCC CGCCAAGGAA GCCGGTTCCT TCACCGCTCA AGTCATTATC 850
 TTGAACCACC CTGGTCAAAT TGGTGCTGGT TACGCTCCYG TTTTGGATTG 900
 TCACACTGCT CACATTGCCT GTAAGTTCGC TGAATTGATC GAAAAGATTG 950
 25 ACAGACGTTT CGGTAAGTCC TTGGAAGCTA CTCCCAAGTT CGTCAAGTCT 1000
 GGTGACTCTG CCATCGTCAA GATGATCCCC TCCAAGCCCA TGTGTGTTGA 1050
 AGCTTACACT GACTACCCCTC CTCTCGGTG TTTGCTGTT CGTGA 1095

30

2) INFORMATION FOR SEQ ID NO: 451

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1092 bases
 35 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

40

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Rhodotorula minuta*
 (B) STRAIN: ATCC 10658

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 451

GCTGAAGGCC GAGCGAGAGC GTGGTATCAC CATCGATATC GCTCTATGGA 50
 AGTTCGAGAC CCCC AAGTAC AACGTCACCG TCATTGACGC TCCAGGACAT 100
 CGTGATTTCA TCAAGAGTGA GTTAACCATA ACATCAAACA GTGTTGCAAA 150
 50 CATCAGCTAA TGCATGTTAT GCGTCCAGAC ATGATTACTG GTACTTCCCA 200
 GGCCGATTGC GCTATTCTCA TCATCGCCAC CGGTGTGTTGGT GAGTTCGAGG 250
 CTGGTATCTC CAAGGATGGC CAGACCCGAG AGCACGCCCT TCTCGCCTTC 300
 ACCCTCGGTG TCAGACAGCT CATCGTTGCC TTGAACAAGA TGGACTCGGT 350
 CAAGGTAGGC TAACTTCACA ACGTCGGCTT CCCATCATTC ATTCACTTAC 400
 55 CTGTCTTGTC TTCCACCCTC CAGTTCTCCG AGTCCCGATA CGATGAAATC 450
 GTCAAGGAGA CATCCGGTTT CATCAAGAAG GTCGGATTG ACCCCAAGGG 500
 TGTTCCCTTC GTCCCATCT CAGGATGGCA CGGAGACAAC ATGATCGAGG 550
 AGTCCACCAA CATGCCTTGG TACAAGGGAT GGAAGAAGAC CACCAAGACC 600
 GGCGAGTACA AGGGAAAGAC CCTGCTCGAG GCCATCGACT CCATCGAGCC 650
 60 CCCCACCCGT CCTACCGACA AGCCTCTCCG ACTTCCCTC CAGGATGTCT 700

	ACAAGATTGG	TGGTATCGGA	ACAGTGCCAG	TCGGACGAGT	CGAGACTGGT	750
	ACCATCAAGG	CTGGTATGGT	CGTCACCTTC	GCTCCTTCAG	CTGTCACCAC	800
	CGAAGTCAAG	TCTGTTGAGA	TGCACCACGA	GCAGCTCGAG	GCTGGTCTTC	850
	CAGGTGACAA	CGTCGGATTC	AACATCAAGA	ACGTTTCAGT	CAAGGATATC	900
5	CGAAGAGGAA	ACGTCTGCGG	TGACTCCAAG	AACGATCCCC	CCAAGGAGGC	950
	TGCTTCCTTC	ACCGCCCAGG	TCATTGTCCT	CAACCACCCC	GGTCAAATCG	1000
	GTAACGGATA	CTCTCCAGTT	CTCGATTGCC	ACACTGGTGA	GTCATTCTTC	1050
	CATATTAGTT	TGAACTCTTT	TGAACAATAC	TAACGTGAAT	CATTATACTT	1100
	TTCAGCCCAC	ATTGCATGCA	AGTTCGACAC	CCTCCTAGAG	AAGATTGACC	1150
10	GACGATCCGG	AAAGTCCATC	GAAGATACCC	CCAAGTTCGT	CAAGTCTGGT	1200
	GACGCCGCCA	TCGTCAAGAT	GGTCCCCACC	AAGCCAATGT	GCGTTGAGGC	1250
	TTTCACCGAC	TACCCACCTC	TTGGACGATT	CGCCGTCCGT	GA	1292

15

2) INFORMATION FOR SEQ ID NO: 452

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1289 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

25

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Sporobolomyces salmonicolor*
 (B) STRAIN: ATCC 32311

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 452

	AAGCTCAAGG	CCGAGCGTGA	GCGTGGTATC	ACCATCGATA	TCGCTCTCTG	50
	GAAGTTCGAG	ACCCCCAAGG	TGCGTTCTCA	CCCCGGCTGA	GGAGCACGCA	100
	CGCGAGGGCT	CACGCTGCGC	CTCTTACAGT	ACATGATCAC	CGTCATCGAC	150
35	GCCCCGGGTC	ACCGTGACTT	CATCAAGAAC	ATGATCACCG	GTACCTCGCA	200
	GGCCGACTGC	GCCATCCTCA	TCATCGCCCG	CGGTACCGGT	GAGTTCGAGG	250
	CTGGTATCTC	GAAGGACGGC	CAGACCCGCG	AGCACGCCCT	CCTCGCCTTC	300
	ACCTTCGGTG	TCCGTGAGCT	CATCGTCGCC	ATCAACAAGA	TGGACACGAC	350
	CAAGTACTCG	GAGGCCCCGT	TCGAGGAGAT	CATCAAGGAG	ACCTCCAAC	400
40	TCATCAAGAA	GGTCGGCTTC	AACCCCAAGA	ACGTCCCCTT	CGTCCCCATC	450
	TCGGGATGGC	ACGGTGACAA	CATGATTGAG	GAGACCGCCA	ACATGCCCTG	500
	GTACAAGGGA	TGGAAGAAGG	AGACCAAGGC	CGGTGAGGTC	AAGGGCAAGA	550
	CCCTCCTCGA	CGCCATCGAC	GCGATCGAGC	CCCCTTCGCG	CCCTACCGAC	600
	AAGCCCCCTC	GTCTTCCCCT	CCAGGTTCGT	TTCCCTGCTC	GCGGTTTACG	650
45	CTGCTACTTC	GAGCTGACCC	GCGAGCTCTG	CCCGAACAGG	ATGTCTACAA	700
	GATCGGTGGT	ATCGGCACAG	TCCCCGTCGG	CCGTGTCGAG	ACCGGCACGA	750
	TCAAGGCCGG	TATGGTCGTC	GTCTTCGCCC	CGGCCAACGT	CACCACTGAG	800
	GTCAAGTCGG	TCGAGATGCA	CCACGAGCAG	CTCGAGGCTG	GTCTCCCGGG	850
	AGACAACGTC	GGCTTCAAGT	GCGTCTCATC	ATGTTTTTGC	TTCGCTCGGC	900
50	CATTTTTTCA	GTCCTGACCC	CGTTTTGCC	CTCGACAGCG	TCAAGAACGT	950
	TTCCGTTAAG	GACATCCGTC	GCGGTAACGT	CTGCGGTGAC	TCGAAGAACG	1000
	ACCCCCCA	GGAGGCCGCT	TCCTTCAAGG	CCCAGGTCAT	CGTCATGAAC	1050
	CACCCCGGTC	AGATCGGCAA	CGGTTACGCT	CCCGTTCTCG	ACTGCCACAC	1100
	CGCCACATT	GCCTGCAAGT	TCGACACCCT	CCTCGAGAAG	ATCGACCGTC	1150
55	GCTCGGGCAA	GTCGATTGAG	GACCTCCCCA	AGTTCGTCAA	GTCGGGTGAC	1200
	GCCGCCATCG	TCAAGATGGT	TCCCTCCAAG	CCGATGTGTG	TCGAGTCGTT	1250
	CGCCGAGTAC	CCCCCTCTCG	GACGTTTCGC	CGTCCGTGA		1289

60

2) INFORMATION FOR SEQ ID NO: 453

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 1070 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

10

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Sporothrix schenckii*
(B) STRAIN: WSA-148

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 453

GTGAGCGCGG TATCACCATC GATATTGCTC TGTGGAAGTT CGAGACCCCC 50
AAGTACTACG TCACCGTCAT TGACGCCCCC GGTCATCGCG ATTTTCATCAA 100
GAACATGATC ACTGGTACCT CGCAGGCCGA CTGCGCCATT CTCATCATTG 150
20 CCGCTGGTAC TGGTGAGTTC GAGGCTGGTA TCTCCAAGGA TGGCCAGACT 200
CGTGAGCAGC CTCTGCTCGC CTACACCCTG GGTGTGCGGC AGCTGATCGT 250
CGCCATCAAC AAGATGGACA CGGCCAAGTG GGCTGAGGCT CGTTACCAGG 300
AGATCATCAA GGAGACCTCC AACTTCATCA AGAAGGTCGG CTACAACCCC 350
AAGACTGTTG CCTTCGTCCC CATCTCGGGC TTCCACGGCG ACAACATGCT 400
25 TACTCCCTCG ACCAACTGCC CCTGGTACAA GGGCTGGGAG AAGGAGGGCA 450
AGAGCGGCAA GGTTACCGGT AAGACTCTGC TGGACGCCAT TGACGCCGTC 500
GAGCCCCCA AGCGCCCCAC GGACAAGCCC CTGCGTCTGC CCCTCCAGGA 550
TGTCTACAAG ATCGGCGGTA TCGGCACTGT CCCTGTGCGC CGTATCGAGA 600
CTGGTGTCTT GAAGCCCGGC ATGGTCGTCA CCTTTGCCCC GTCCAACGTC 650
30 ACCACTGAAG TCAAGTCCGT CGAGATGCAC CACGAGCAGC TTGTTGAGGG 700
TGTTCCCGGC GACAACGTCG GCTTCAACGT CAAGAACGTC TCCGTCAAGG 750
AGATCCGTCG TGGCAACGTT GCCGGTGACT CCAAGAACGA CCCCCCTCG 800
GGCGCCGCCA CCTTCAACGC CCAGGTCATT GTCCTGAACC ACCCCGGCCA 850
GGTCGGCAAC GGCTACGCCC CGGTTCTGGA CTGCCACACC GCCCACATTG 900
35 CCTGCAAGTT CACCGAGATC CTTGAGAAGA TCGACCGCCG TACCGGCAAG 950
TCGGTTGAGA ACAACCCCAA GTTCATCAAG TCGGGTGACG CCGCCATTGT 1000
CAAGCTGACG CCCTCGAAGC CCATGTGCGT TGAGGCCTTC ACTGACTACC 1050
CCCCCTCTGG CCGTTTCGCC 1070

40

2) INFORMATION FOR SEQ ID NO: 454

(i) SEQUENCE CHARACTERISTICS:

- 45 (A) LENGTH: 1092 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

50

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Stephanoascus ciferrii*
(B) STRAIN: ATCC 52550

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 454

CTTAAGTCTG AGCGTGAGAG AGGTATCACC ATCGATATTG CTCTCTGGAA 50
ATTTCGAGACT CCTAAGTACA ACGTTACCGT CATTGATGCT CCAGGTCACA 100
60 GAGATTTTCAT CAAGAACATG ATTACTGGTA CCTCCCAGGC CGATCTTGCC 150

	ATCCTTATCA	TTGCTGGTGG	TGTCGGTGAG	TTGAGGCTG	GTATCTCCAA	200
	GGACGGTCAG	ACCAGAGAGC	ACGCTCTTCT	TTCTTTCACC	CTTGGTGTCA	250
	GAAACATGAT	TGTTGCTGTC	AACAAGATGG	ACTCCGTCAA	GTGGTCTGAG	300
	GATCGTTTCA	ACGAAATTGT	CAAGGAGACC	TCCAACCTCG	TCAAGAAGGT	350
5	TGGTTACAAC	CCTAAGAATA	TTGCTTTCGT	TCCTATCTCC	GGTTGGAACG	400
	GTGACAATAT	GATTGAGCCA	TCCACCAACT	GCCCATGGTA	CAAGGGTTGG	450
	GAGCGTGAGA	CCAAGAACGG	TACTGCCAAG	GGTAAGACCA	TCTTGAGAGC	500
	CATTGACTCT	ATGGAGCCAC	CTTCCAGACC	AGTTGACAAG	CCTCTCCGTC	550
	TTCCTCTTCA	GGACGTTTAC	AAGATTGGTG	GTATTGGTAC	GGTGCCAGTT	600
10	GGTCGTGTTG	AGACTGGTGT	TATCAAGCCA	GGTATGGTTG	TTACCTTTGC	650
	CCCAGCTGGT	GTCACCACTG	AAGTCAAGTC	TGTCGAGATG	CACCACGAAC	700
	AGATCCCAAG	AGGTACCCCA	GGTGACAACG	TTGGTTTCAA	CGTCAAGAAC	750
	GTCTCCGTCA	AGGAAATCAG	ACGTGGTAAC	GTTACTGGTG	ACTCCAAGAA	800
	CGACCCACCA	AAGGGCTGCG	ACTCTTTCAA	CGCTCAGGTC	ATCATCTTCA	850
15	ACCACCCTGG	TCAGATCTCT	GCTGGTTACG	CTCCAGTTTT	GGACTGCCAC	900
	ACTGCTCACA	TTGCTTGCAA	GTTTGAGGAG	CTCATTGAGA	AGATTGACAG	950
	ACGTTCCGGT	AAGAAGGTCG	AAGACTCTCC	TAAGTTCGTC	AAGGCCGGTG	1000
	ATGCCGCCAT	TGTCAAGATG	GTTCCATCCA	AGCCAATGTG	TGTTGAAACC	1050
	TTCAGTGAGT	ACCCACCTCT	TGGTCGTTTC	GCCGTCCGTG	AC	1092
20						

2) INFORMATION FOR SEQ ID NO: 455

25 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1149 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

30

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Trichophyton mentagrophytes*
 (B) STRAIN: WSA-225

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 455

	GCCGAGCGTG	AGCGTGGTAT	CACCATCGAT	ATCGCCCTCT	GGAAGTTCGA	50
40	GACCCCCAAG	TACAATGTCA	CCGTCATTGG	TATGTTTTCT	CTTTACCTTT	100
	CCCCTCCATC	GTCTTGCTGT	GCCATAACTA	ACGAGAGTAG	ACGCCCCCGG	150
	TCACCGTGAC	TTCATCAAGA	ACATGATCAC	TGGTACCTCC	CAGGCCGACT	200
	GTGCTATTCT	CATCATTGCT	GCCGGTACTG	GTGAGTTCGA	GGCTGGTATC	250
	TCCAAGGATG	GCCAGACCCG	TGAGCACGCT	CTGCTCGCCT	TCACCCTTGG	300
45	TGTCAAGCAG	CTCATCGTTG	CCATCAACAA	GATGGACACC	ACCAACTGGT	350
	CCGAGGACCG	TTTCAAGGAA	ATCATCAAGG	AAGTCACCAA	CTTCATCAAG	400
	AAGGTTGGCT	ACGACCCCAA	GGGTGTTCCA	TTCGTTCCAA	TCTCTGGTTT	450
	CAACGGTGAC	AACATGATTG	AGGCCTCCAC	CAACTGCCCA	TGGTACAAGG	500
	GATGGAACAA	GGAGACTAAG	GCCGGTGGTG	CCAAGACTGG	CAAGACCCTC	550
50	CTCGAGGCCA	TCGATGCCAT	CGACATGCCA	ACCCGTCCTA	CCGACAAGCC	600
	CCTCCGTCTC	CCACTCCAGG	ATGTCTACAA	GATCTCTGGT	ATCGGAACTG	650
	TACCAGTCGG	TCGTGTTGAG	ACCGGTATCA	TCAAGCCCGG	TATGGTCGTC	700
	ACCTTCGCCC	CTGCCAACGT	CACCACTGAA	GTCAAGTCCG	TCGAAATGCA	750
	CCACCAGCAG	CTTCAGCAGG	GTGTCCCCCG	TGACAACGTC	GGCTTCAACG	800
55	TCAAGAACGT	TTCCGTCAAG	GAAGTCCGCC	GTGGTAACGT	TGCCGGTGAC	850
	TCCAAGAACG	ACCCACCATC	CGGCTGTGCC	TCCTTCAACG	CCCAGGTCAT	900
	CGTCCTCAAC	CACCCCGGCC	AGATCGGTGC	TGGTTACGCC	CCAGTCCTCG	950
	ACTGCCACAC	TGCTCACATT	GCTTGCAAGT	TCGCTGAGCT	CCTCGAGAAG	1000
	ATTGACCGCC	GTACCGGTAA	ATCCGTCGAA	GCCAACCCCA	AGTTCGTCAA	1050
60	GTCTGGTGAT	GCCGCTATCG	CCAAGATGGT	TCCCTCCAAG	CCTATGTGCG	1100

TTGAGGCTTT CACTGACTAC CCCCCACTTG GTCGTTTCGC' CGTCCGTA' 1149

5 2) INFORMATION FOR SEQ ID NO: 456

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1101 bases
 (B) TYPE: Nucleic acid
 10 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

15 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Trichosporon cutaneum*
 (B) STRAIN: ATCC 62965

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 456

20 TCTTGACAAG CTAAAGCTG AACGTGAACG TGGTATCACC ATTGATATCG 50
 CTCTCTGGAA GTTCGAAACT CCTAAGTACT ACGTTACTGT TATTGATGCT 100
 CCAGGTCACC GTGATTTCAT CAAGAACATG ATTACTGGTA CTTCCCAAGC 150
 CGACTGCGCC ATTCTTATCA TTGCTGCCGG TGTCGGTGAA TTCGAAGCTG 200
 25 GTATCTCCAA GGAAGGTCAA ACCAGAGAAC ACGCTCTTCT CGCTTTCACC 250
 CTTGGTGTCA GACAACTTAT CATTGCCATC AACAAGATGG ACTCTGTCAA 300
 GTGGGACCAA AAGAGATACG AAGAAATCGT CAAGGAGGCT TCCAACCTCG 350
 TCAAGAAGGT TGGTTACAAC CCCAAGTCTG TTCCATTCGT TCCTATCTCT 400
 GGTGGAACG GTGACAACAT GTTGGAACCT ACCACCAACG CCCCATGGTA 450
 30 CAAGGGATGG ACCAAGGAAA CCAAGGCTGG TGCCACTAAG GGTATGACTC 500
 TTATTGAAGC CATTGACGCC ATTGAACCAC CAGTAAGACC ATCCGACAAG 550
 CCACTCCGTC TCCCACTCCA AGATGTTTAC AAGATTGGTG GTATCGGAAC 600
 TGTGCCAGTC GGCCGTGTCG AAACCGGTAT CATCAAGGCC GGTATGGTCG 650
 TCACCTTTGC TCCACCAATG GTCACAACTG AAGTTAAGTC CGTTGAAATG 700
 35 CACCACGAAC AACTTGCTCA AGGTAACCCA GGTGACAACG TTGGTTTCAA 750
 CGTCAAGAAC GTTTCGGTTA AGGAAATCAG ACGTGGTAAAC GTCTGTGGTG 800
 ACTCCAAGAA CGATCCACCA AAGGGCTGCG AATCTTTCAA CGCTCAAGTT 850
 ATCGTCTTGA ACCACCCTGG TCAAATCTCT GCTGGTTACT CTCCAGTTCT 900
 CGATTGCCAC ACTGCCCACA TTGCCTGCAG ATTGACGAA CTCCTTGAAA 950
 40 AGATCGACCG TCGTTCCGGT AAGAAGATTG AAGACTCTCC AAAGTTTGTC 1000
 AAGTCTGGTG ATGCCGCTAT CGTCAAGATG ATCCCAACCA AGCCAATGTG 1050
 CGTTGAAACC TTCACTGAAT ACCCACCCT TGGTCGTTTC GCCGTCCGTG 1100
 A 1101

45

2) INFORMATION FOR SEQ ID NO: 457

(i) SEQUENCE CHARACTERISTICS:

- 50 (A) LENGTH: 1085 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

55 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Wangiella dermatitidis*
 60 (B) STRAIN: WSA-229

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 457

	GTTGAAGGCC	GAGCGTGAGC	GTGGTATCAC	CATCGATATC	GCCCTCTGGA	50
	AGTTCGAGAC	CCCCAAGTAC	TATGTACACG	TCATCGACGC	CCCGGGTCAT	100
5	CGTGAAGTTA	TCAAGAACAT	GATCACTGGT	ACCTCGCAGG	CCGACTGCGC	150
	CATCTTGATC	ATTGCCGCCG	GTACCGGTGA	ATTCTGAAGCC	GGTATCTCCA	200
	AGGATTGGTCA	GACCCGTGAG	CACGCTCTGC	TCGCCTACAC	CTTGGGTGTC	250
	AAGCAGCTCA	TCGTGCGCCAT	CAACAAGATG	GACACCACCA	AGTGGTCCGA	300
	GGAGCGTTTC	AACGAAATCA	TCAAGGAGAC	TTCCAACCTC	ATCAAGAAGG	350
10	TCGGCTACAA	CCCCAAGGCC	GTTCCCTTTCG	TCCCCATCTC	CGGCTTCAAC	400
	GGTGACAACA	TGATTGAGGT	CTCCACCAAC	TGCCCCGTGGT	ACAAGGGATG	450
	GGAGAAGGAG	TCCAAGGCTG	GCAAGGCCAC	CGGCAAGACC	CTCCTCGAGG	500
	CCATTGACGC	CATCGACCCA	CCCACCCGTC	CCACCGACAA	GCCTCTCCGT	550
	CTCCCTCTCC	AGGATGTCTA	CAAGATCTCT	GGTATCGGAA	CGGTTCCTGT	600
15	CGGTCGTGTC	GAGACCGGTA	CCATCAAGGC	CGGTATGGTC	GTCACCTTCG	650
	CTCCGGCCAA	CGTCACCACT	GAAGTCAAGT	CCGTCGAAAT	GCACCACGAG	700
	CAGCTCGCCG	AGGGTCTGCC	AGGTGACAAC	GTTGGCTTCA	ACGTCAAGAA	750
	CGTCTCCGTC	AAGGAGGTTC	GTCGTGGTAA	CGTTGCCGGT	GACTCCAAGA	800
	ACGACCCGCC	CAAGGGTGCC	GAGTCCTTCA	ACGCCCAGGT	CATTGTCCTC	850
20	AACCACCTTG	GTCAGATCGG	TGCCGGCTAC	GCTCCAGTCT	TGGATTGCCA	900
	CACTGCCCAC	ATTGCTTGCA	AGTTCGCCGA	GTTGCTCGAG	AAGATCGACC	950
	GTCGTACCGG	AAAGTCCATC	GAGAACAACC	CCAAGTTCAT	CAAGTCTGGT	1000
	GATGCTGCCA	TCGTCAAGAT	GATTCCCAGC	AAGCCCATGT	GTGTCGAGGC	1050
	TTTCACCGAC	TATCCTCCTC	TGGGTCGTTT	CGCTG		1085
25						

2) INFORMATION FOR SEQ ID NO: 458

30 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 492 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Aspergillus fumigatus*
 (B) STRAIN: DAL-95

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 458

	TGTCTTCATC	CGGAATTGAT	TGTGAGTCGT	TCCACATGCT	CACCTAGTTT	50
45	TCGCTCGATC	TTTTCACTAA	CGCAAACCAT	GTAACAAC	ATTGCCAAGG	100
	CCCACGGTGG	TTACTCCGTC	TTCACTGGTG	TTGGTGAGCG	TACTCGTGAG	150
	GGTAACGATC	TGTACCACGA	AATGCAGGAG	ACTGGTGTCA	TTCAGCTCGA	200
	GGGTGAATCC	AAGGTCGCAC	TGGTGTTCGG	ACAGATGAAC	GAGCCCCCGG	250
	GTGCCCCGTG	CCGTGTCGCC	CTTACCGGTC	TGACCATTCG	CGAGTACTTC	300
50	CGTGACGAGG	AGGGTCAGGA	CGTGCTGCTC	TTCATTGACA	ACATTTTCCG	350
	TTTCACCCAG	GCCGGTTCTG	AGGTGTCTGC	CCTTCTCGGT	CGTATCCCCT	400
	CTGCCGTCGG	TTACCAGCCC	ACCCTGGCCG	TCGACATGGG	TGGTATGCAG	450
	GAGCGTATCA	CCACCACCAA	GAAGGGTTCT	ATTACCTCCG	TC	492
55						

2) INFORMATION FOR SEQ ID NO: 459

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1154 bases

60

- (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

5 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Blastoschizomyces capitatus*
 (B) STRAIN: ATCC 10663

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 459

	GTCCGTGGTC	AAGAAGTTAT	TGACACTGGT	GCCCCAATTA	CCATTCCTGT	50
	TGGTCGTGGT	ACTCTTGGA	GAATTATCAA	CGTCATTGGT	GAACCAATTG	100
15	ACGAACGTGG	TCCTATCAAG	GCTTCTAAGT	ATGCTCCTAT	CCATACTGAA	150
	CCACCAACCT	TTGCTGAACA	ATCTACTTCT	GCTGAAGTTC	TTGAAACTGG	200
	TATCAAGGTT	GTCGATCTTC	TTGCTCCTTA	CGCCCGTGGT	GGTAAGATTG	250
	GTCTTTTCGG	TGGTGCTGGT	GTCGGTAAGA	CTGTCTTCAT	TCAAGAAGTT	300
	ATTAACAACA	TTGCCAAGGC	TCACGGTGGT	TTCTCTGTCT	TCACTGGTGT	350
20	CGGTGAAAGA	ACCCGTGAAG	GTAACGATCT	TTACCGTGAA	ATGAAGGAAA	400
	CTGGTGTCAT	CAACCTCGAA	GGTGACTCCA	AGGTCGCTCT	CGTTTTCGGT	450
	CAAATGAACG	AACCTCCAGG	TGCCCCGTGCC	CGTGTCGCTT	TGACTGGTCT	500
	TACCATTGCC	GAATACTTCC	GTGATGAAGA	AGGACAAGAT	GTCTTGCTTT	550
	TCGTTGACAA	CATTTTCAGA	TTCACCCAAG	CCGGTTCTGA	AGTCTCTGCT	600
25	CTTTTGGGTC	GTATTCCATC	TGCCGTCGGT	TACCAACCTA	CCCTTGCTAC	650
	CGATATGGGT	GCCCTCCAAG	AACGTATTAC	CACCACCCAA	AAGGGTTCCG	700
	TCACATCTGT	CCAAGCCGTC	TATGTCCCAG	CAGACGATTT	GACTGATCCT	750
	GCCCCAGCCA	CCACTTTCGC	TCACTTGGAC	GCCACCACTG	TCTTGCTCTCG	800
	TTCCATTTCC	GAATTGGGTA	TCTACCCAGC	TGTCGATCCT	CTCGATTCCA	850
30	AGTCTCGTCT	TTTGGATCCT	GAAGTTATTG	GACACGAACA	CTACGAAGTT	900
	GCCACTCAAG	TTCAACAAAC	CCTCCAAGCT	TACAAGTCTC	TCCAAGATAT	950
	CATTGCCATT	TTGGGTATGG	ATGAATTGTC	TGAAGCTGAT	AAGCTTACTG	1000
	TCGAACGTGC	CCGTAAGATC	CAAAGATTCC	TTTCCCAACC	ATTCGCTGTT	1050
	GCCGAAGTTT	TCACTGGTAT	CGAAGGTCGT	CTCGTTCCAT	TGAAGGAAAC	1100
35	CGTCAGATCT	TTCAAGGAAA	TCCTTGAAGG	TAAGTACGAT	CACCTTCCAG	1150
	AAGC					1154

40 2) INFORMATION FOR SEQ ID NO: 460

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1295 bases
 (B) TYPE: Nucleic acid
 45 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

50 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Candida albicans*
 (B) STRAIN: ATCC 18804

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 460

55	CCAATTCGAC	GAAGGAAACT	TGCCAGCTAT	TTTGAATGCT	TTGACTTTGA	50
	AGAACGGTGA	CCAAGACTTG	GTCTTGGAAG	TTGCTCAACA	TTTGGGTGAA	100
	AACACCGTCA	GAGCTATTGC	TATGGATGGT	ACTGAAGGTT	TAGTCAGAGG	150
	TACCGAAGTC	AACGATACCG	GTGCCCCAAT	CTCCGTCCCA	GTCGGTAGAG	200
60	GTAATTTAGG	TAGAATCATC	AATGTTGTTG	GTGAACCAAT	TGATGACAGA	250

	GGTCCAATTG	AATGTAAGGA	AAAGAAACCA	ATTCACGCTG	AACCACCATC	300
	ATTTCGTTGAA	CAATCCACTG	CTGCCGARAT	TTTGGAAACC	GGTATCAAGG	350
	TTGTCGACTT	GTTGGCCCCA	TACGCCAGAG	GTGGTAARAT	TGGTTTATTC	400
	GGTGGTGCTG	GTGTCGGTAA	GACCGTCTTT	ATCCAAGAAT	TGATTAACAA	450
5	CATTGGCCAAA	GCCCCATGGT	GTTTCTCTGT	CTTTACCGGT	GTGCGTGAAA	500
	GAACCAGAGA	AGGTAACGAT	TTGTACCGTG	AAATGAAAGA	AACCGGTGTC	550
	ATCAACTTGG	AAGGTGACTC	CAAGGTCGCT	TTGGTCTTCG	GTCAAATGAA	600
	CGAACCACCA	GGTGCTAGAG	CTAGAGTTGC	TTGACTGGT	TTGACCATTG	650
	CTGAATACTT	CAGAGATGAA	GAAGGTCAAG	ATGTCTTGTT	GTTTCATTGAT	700
10	AACATTTTCA	GATTCACCCA	AGCTGGTTCC	GAAGTGTCTG	CTTTGTTAGG	750
	TCGTATTCCA	TCTGCTGTCG	GTTATCAACC	AACCTTAGCC	ACTGATATGG	800
	GTCTTTTGCA	AGAACGTATT	ACCACCACCA	AGAAAGGTTC	CGTCACCTCT	850
	GTCCAAGCTG	TCTATGTCCC	AGCTGATGAT	TTGACCGATC	CTGCTCCAGC	900
	CACTACATTC	GCCCATTGGG	ATGCCACTAC	TGTCTTGTCT	AGAGGTATTT	950
15	CTGAATTGGG	TATCTACCCA	GCTGTGATC	CATTGGATTG	CAAATCCAGA	1000
	TTATTGGACG	CTTCTGTTGT	TGGTCAAGAA	CATTACGATG	TCGCTACTGG	1050
	TGTTCAACAA	ACTTTACAAG	CTTACAAATC	CTTACAAGAT	ATCATTGCTA	1100
	TTTTGGGTAT	GGATGAATTG	TCTGAAGCTG	ATAAATTGAC	TGTCGAAAGA	1150
	GCCCGTAAGA	TCCAAAGATT	CTTGTCTCAA	CCATTGCTG	TTGCTGAAGT	1200
20	TTTCACTGGT	ATCCCAGGTA	GATTAGTCAG	ATTGCAAGAC	ACTGTCAAAT	1250
	CATTCAAGGA	TGTTTTGGAA	GGTAAATACG	ATAACTTGCC	AGAAA	1295

25 2) INFORMATION FOR SEQ ID NO: 461

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1277 bases
 (B) TYPE: Nucleic acid
 30 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

35 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Candida dubliniensis*
 (B) STRAIN: NCPF 3949

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 461

40	TAAGTTGCCA	GCTATTTTGA	ATGCTTTGAC	TTTGAAGAAC	GGTGACCAAG	50
	ATTAGTTTT	GGAAGTTGCT	CAACATTTGG	GTGAAAACAC	CGTCAGAGCT	100
	ATTGCTATGG	ATGGTACTGA	AGGTTTAGTC	AGAGGTACTG	AAGTCAACGA	150
	TACCGGTGCC	CCAATCTCCG	TTCCAGTCGG	TAGAGGTACC	TTAGGTAGAA	200
45	TCATCAATGT	TGTTGGTGAA	CCAATTGATG	ACAGAGGTCC	AATTGAATGT	250
	AAGGAAAAGA	AACCAATTCA	TGCAGAACCA	CCATCCTTCG	TTGAGCAATC	300
	CACTGCTGCC	GAAATTTTGG	AAACCGGTAT	CAAGGTTGTC	GACTTATTGG	350
	CCCCATACGC	CAGAGGTGGT	AAGATTGGTT	TGTTGCGGTG	TGCTGGTGTC	400
	GGTAAGACCG	TCTTTATCCA	AGAATTGATT	AACAACATTG	CTAAAGCCCA	450
50	TGGTGGTTTC	TCCGTCTTTA	CCGGTGTCCG	TGAAAGAACC	AGAGAAGGTA	500
	ACGATTTGTA	CCGTGAAATG	AAAGAAACCG	GTGTCATCAA	CTTAGAAGGT	550
	GACTCCAAGG	TCGCTTTGGT	CTTTGGACAA	ATGAACGAAC	CACCAGGTGC	600
	TAGAGCTAGA	GTTGCTTTGA	CTGGTTTGAC	TATTGCTGAA	TACTTCAGAG	650
	ATGAAGAAGG	TCAAGATGTC	TTGTTGTTCA	TCGATAACAT	TTTCAGATTG	700
55	ACCCAAGCTG	GTTCCGAAGT	GTCTGCTTTG	TTAGGTCGTA	TTCCATCTGC	750
	CGTCGGTTAT	CAACCAACCT	TAGCTACTGA	TATGGGTCTT	TTGCAAGAAC	800
	GTATTACCAC	CACCAAGAAA	GGTCCCGTCA	CCTCTGTCCA	AGCTGTCTAT	850
	GTCCCAGCTG	ATGATTTGAC	CGATCCTGCT	CCAGCCACCA	CATTCGCCCA	900
	TTTGATGCC	ACTACTGTCT	TGTCTAGAGG	TATTTCTGAA	TTGGGTATTT	950
60	ACCCAGCTGT	CGATCCATTG	GATTCCAAAT	CCAGATTATT	GGACGCTGCC	1000

	GTTGTTGGTC	AAGAACATTA	TGATGTCGCT	ACTGGTGTTT	AAACAACTTT	1050
	GCAAGCTTAC	AAATCCTTAC	AAGATATCAT	TGCTATTTTG	GGTATGGATG	1100
	AATTGTCTGA	AGCTGATAAA	TTGACTGTCG	AAAGAGCCCG	TAAGATTCAA	1150
	AGATTCTTGT	CTCAACCATT	CGCCGTTGCT	GAAGTTTTC	CTGGTATTCC	1200
5	AGGTAGATTA	GTCAGATTGC	AAGACACTGT	CAAATCATTC	AAGGATGTTT	1250
	TGGAAGGTAA	ATACGATCAC	TTGCCAG			1277

10 2) INFORMATION FOR SEQ ID NO: 462

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1278 bases
 (B) TYPE: Nucleic acid
 15 (C) STRANDEDNESS: Double.
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

20 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Candida famata*
 (B) STRAIN: ATCC 62894

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 462

25	GTA	ACTTGCC	AGCTATTTTG	AACGCTTTGA	CCTTGAAGAA	CGGTGAAAAC	50
	GAC	TTAGTTT	TAGAAGTTGC	CCAACATTTG	GGTGAAAACA	CCGTCAGAGC	100
	TAT	TGCTATG	GATGGTACTG	AAGGTTTAGT	TAGAGGTACT	CCAGTTACCG	150
	ATT	CTGGTGC	TCCAATTTCT	GTCCCAGTCG	GTAGAGGTAC	TTTAGGTAGA	200
30	ATC	TTGAACG	TTATTGGTGA	ACCAATTGAT	GAACAAGGTC	CAGTTGATGC	250
	CAAG	GAAACC	AGACCAATTC	ACCAAGACCC	ACCAGCATTC	GTTGATCAAT	300
	CCAC	CAAGGC	TGAAGTTTTC	GAAACTGGTA	TCAAGGTTGT	CGATTTATTA	350
	GCCC	CTTACG	CTAGAGGTGG	TAAGATTGGT	TTATTCCGTG	GTGCCGGTGT	400
	CGGT	AAGACC	GTCTTTATCC	AAGAATTGAT	TAACAACATT	GCCAAGGCCC	450
35	ATG	GTGTTT	CTCTGTTTTT	ACTGGTGTCG	GTGAAAGAAC	CAGAGAAGGT	500
	AAC	GATTTAT	ATAGAGAAAT	GAAGGAAACT	GGTGTCATTA	ACTTGAAGG	550
	TGAC	TCCAAG	GTGCGCTTGG	TTTTCGGTCA	AATGAACGAA	CCACCAGGTG	600
	CTAG	AGCTAG	AGTTGCTTTA	ACCGGTTTAA	CCATTGCCGA	ATACTTCAGA	650
	GACG	AAGAAG	GTCAAGATGT	GTTATTGTTC	GTCGATAACA	TTTTTAGATT	700
40	CAC	CCAAGCC	GGTTCCGAAG	TGTCTGCTTT	GTTAGGTCGT	ATTCCATCGG	750
	CTGT	CGGTTA	TCAACCAACC	TTAGCCACTG	ATATGGGTCT	TTTACAAGAA	800
	AGA	ATTACCA	CCACCACCAA	GGGTTCCGTT	ACTTCTGTCC	AAGCTGTCTA	850
	CGT	CCCAGCC	GATGATTTAA	CCGATCCTGC	TCCAGCTACC	ACTTTCGCCC	900
	ACT	TGGATGC	TACCACTGTG	TTGTCTCGTG	GTATCTCTGA	ATTGGGTATT	950
45	TAC	CCAGCTG	TCGATCCATT	GGATTCCAAA	TCCAGATTGT	TAGATGCTGA	1000
	TAT	CGTTGGT	AAAGAACACT	ACGAAGTTGC	CACTGGTGTC	CAACAAACCT	1050
	TACA	AGCTTA	CAAATCTTTA	CAAGATATCA	TTGCTATTTT	AGGTATGGAT	1100
	GAAT	TGTCTG	AAGCCGATAA	ATTGACTGTC	GAAAGAGCCA	GAAAGATCCA	1150
	AAG	ATTCTTG	TCTCAACCAT	TCGCCGTTGC	CGAAGTTTTC	ACCGGTATCC	1200
50	CAG	G	GTAGATT	AGTTAGATTG	CAAGACACTG	TTAAATCTTT	1250
	TTAG	AAGGTA	AATATGATCA	CTTACCAG			1278

55 2) INFORMATION FOR SEQ ID NO: 463

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1154 bases
 (B) TYPE: Nucleic acid
 60 (C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

5 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Candida glabrata*

(B) STRAIN: ATCC 66032

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 463

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10 TCTGGTCAGA GGCGAGAAGG TCGTCGACAC AGGTGCCCCA ATCTCCGTCC      50
CTGTCCGCAG AGAGACCCTG GGCAGAATCA TCAACGTTAT CGGTGAACCT      100
ATCGACGAGC GTGGCCCAAT CAACTCAAAG TTGAGAAAGC CTATCCACGC      150
CGACCCCTCT TCCTTCGCAG AACAGTCCAC CGCCGCCGAA GTCCTGGAAA      200
15 CAGGTATCAA GGTCGTCGAC TTGCTGGCCC CTTACGCCAG AGGTGGTAAG      250
ATCGGTCTGT TCGGTGGTGC CGGTGTCGGT AAGACCGTGT TCATCCAAGA      300
ACTGATCAAC AACATCGCAA AGGCTCACGG TGGTTTCTCC GTGTTCACAG      350
GTGTCGGTGA AAGAACCAGA GAAGGTAACG ATTTGTACAG AGAAATGAAG      400
GAAACCGGTG TCATCAACTT GGAAGGTGAC TCTAAGGTCG CCTTGGTCTT      450
20 CGGCCAAATG AACGAACCAC CAGGAGCCAG AGCCAGAGTC GCCTTGACCG      500
GTTTGACCAT CGCAGAATAC TTCAGAGATG AAGAAGGTCA AGATGTCCTG      550
CTGTTTCGTCG ACAACATTTT CAGATTACCC CAAGCCGGTT CAGAAGTCTC      600
CGCTTTGCTA GGTCTGATCC CATCCGCCGT CGGTTATCAA CCAACCTTGG      650
CCACCGATAT GGGTCTGTTG CAAGAAAGAA TTACCACCAC AAAGAAGGGT      700
25 TCCGTCACTT CCGTCCAAGC CGTCTACGTG CCTGCAGATG ATTTAACAGA      750
TCCTGCCCCT GCCACTACTT TCGCGCACTT GGACGCCACC ACCGTCTTGT      800
CCAGAAGTAT CTCAGAATTG GGTATCTACC CAGCTGTCGA CCCATTGGAC      850
TCCAAGTCTA GATTGCTAGA CGCTGCCGTT GTCGGTGAAG AGCATTACAA      900
CGTCGCCACA AAGGTCCAAG AAAC TT TACA AACTTACAAG TCTCTGCAAG      950
30 ATATCATCGC CATTTTGGGT ATGGATGAAT TGTCGGAACA AGATAAGCTA     1000
ACTGTGCAAA GAGCAAGAAA GATCCAAAGA TTCTTGTCCTC AACCATTTCGC     1050
TGTCGCTGAA GTTTTCACCG GTATCGAAGG TAAGCTGGTC AGATTGAAGG     1100
ACACCATCTC CTCTTTCAAG GCTGTCTTGG AAGGTAAGTA CGATGATCTT     1150
CCAG
35

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2) INFORMATION FOR SEQ ID NO: 464

40 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1293 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

45

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Candida guilliermondii*

50 (B) STRAIN: ATCC 6260

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 464

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55 CCACTACGAG GACGGTAACC TTCCTGCTAT TTTCAACGCC TTGACTCTTA      50
AGAACGGTGA CCAAACTTG GTTTTGAAG TTGCCAGCA TTTGGGTGAA      100
AACACCGTCA GAACCATTGC TATGGATGGT ACTGAAGGTT TGGTTAGAGG      150
TGCCAGCGTC ACTGACACTG GTGCTCCTAT CTCTGTGCCT GTTGGTCGTG      200
GTA CTTTGGG TCGTATCATC AACGTTATTG GTGAGCCAAT TGACGAGCGT      250
GGACCAATCG AGTCCAAGCA AAAGAAGCCC ATTCACGCTG AACCACCATC      300
60 GTTCGTCGAA CAATCCACTT CTGCCGAGGT TTTGGA AACC GGTATCAAGG      350

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	TTGTCGACTT	GTTGGCTCCA	TACGCCAGAG	GTGGTAAGAT	TGGATTGTTCT	400
	GGTGGTGCCG	GTGTCGGTAA	GACTGTGTTT	ATCCAAGAGT	TGATTAACAA	450
	CATTGCCAAG	GCTCACGGTG	GTTTCTCCGT	GTTACCGGT	GTCGGTGAAA	500
	GAACCAGAGA	AGGTAACGAT	TTGTACCGTG	AAATGAAGGA	AACTGGTGTC	550
5	ATCAACTTGG	AAGGTGAATC	CAAGGTGGCC	TTGGTGTTCTG	GTCAAATGAA	600
	CGAACCTCCA	GGAGCTAGAG	CCAGAGTTGC	CCTTACCGGT	TTGACCATCG	650
	CTGAATACTT	CAGAGATGAG	GAGGGTCAAG	ATGTGTTGTT	GTTCCGTCGAC	700
	AACATTTTCA	GATTCACCTCA	AGCTGGTTCT	GAAGTGTCGG	CTTTGTTGGG	750
	TCGTATTTCCT	TCGGCTGTCTG	GTTACCAACC	TACTTTGGCC	ACCGATATGG	800
10	GTTTGTTGCA	AGAGCGTATT	ACCACCACCA	AGAAGGGTTC	CGTCACCTCT	850
	GTCCAAGCTG	TCTATGTGCC	AGCCGATGAT	TTGACCGATC	CTGCTCCTGC	900
	TACTACTTTT	GCTCACTTGG	ATGCTACCAC	TGTGTTGTCT	AGAGGTATCT	950
	CCGAGTTGGG	TATTTACCCA	GCTGTGCATC	CTTTGGATTC	CAAGTCGAGA	1000
	TTGTTGGATG	CCTCTGTTGT	CGGTGAGGAG	CACTACTCGG	TTGCTTCTAA	1050
15	CGTTCAACAA	ACCTTGCAAG	CTTACAAGTC	TTTGCAAGAT	ATCATTGCCA	1100
	TTTTGGGTAT	GGACGAATTG	TCGGAAGCTG	ACAAGTTGAC	CGTCGAGAGA	1150
	GCCCGTAAGA	TCGAGAGATT	CTTGTCTCAA	CCATTTGCTG	TTGCCGAAGT	1200
	TTTCACTGGT	ATCAGTGGTA	AGTTGGTCAG	ATTGGAGGAC	ACTATCAGAT	1250
	CTTCAAGGA	AGTCTTGGA	GGTAAGTACG	ATCACTTGCC	AGA	1293
20						

2) INFORMATION FOR SEQ ID NO: 465

- 25 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1293 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Double
 - (D) TOPOLOGY: Linear

- 30 (ii) MOLECULE TYPE: Genomic DNA

- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Candida haemulonii*
 - 35 (B) STRAIN: ATCC 22991

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 465

	CACTTTGACG	ATGGTAACTT	GCCAGCCATT	TTCAACGCCT	TGAAGTTGAA	50
40	GAACGGTGAC	CAGGACTTGG	TCTTGAGGT	CGCCCAGCAC	TTGGGTGAGA	100
	ACACCGTCAG	AACCATTGCC	ATGGACGGTA	CCGATGGTTT	GGTCAGAGGC	150
	GAGGCTGTCA	CTGACACTGG	TGCTCCAATC	TCCGTGCCTG	TTGGTCGTGA	200
	GACTTTGGGT	CGTATCATCA	ACGTTATTGG	TGAGCCAATT	GACGAGAGAG	250
	GACCAATCAA	GTCCAAGAAG	AGAAACCCAA	TCCACACTGA	CCCACCAACC	300
45	TTCGTTGAGC	AGTCTACTTC	TGCTGAGGTT	TTGGAGACTG	GTATTAAGGT	350
	TGTCGACTTG	TTGGCCCCTT	ACGCCAGAGG	TGGTAAGATT	GGTTTGTTCG	400
	GTGGTGCCCG	TGTCGGTAAG	ACCGTCTTTA	TCCAAGAGTT	GATTAACAAC	450
	ATTGCCAAGG	CCCACGGTGG	TTTCTCTGTC	TTTACCGGTG	TCGGTGAGAG	500
	AACCAGAGAA	GGTAACGATT	TGTACCGTGA	AATGCAGGAG	ACCGGTGTCA	550
50	TCAACTTCGA	GGGTGACTCC	AAGGTCGCCT	TGGTCTTCGG	TCAGATGAAC	600
	GAGCCACCAG	GAGCTAGAGC	TAGAGTTGCT	TTGACCGGTT	TGACCATTCG	650
	CGAATACTTC	AGAGATGAAG	AAGGTCAGGA	TGTGTTGTTG	TTCGTTGACA	700
	ACATTTTCAG	ATTCACTCAG	GCTGGTTCCG	AGGTGTCCGC	CTTGTTGGGT	750
	CGTATTCCAT	CTGCTGTCTG	TTACCAGCCA	ACCTTGGCCA	CCGATATGGG	800
55	TACCTTGCAA	GAAAGAATTA	CCACCACCAA	GAAGGGTTCC	GTCACCTCTG	850
	TCCAGGCCCGT	TTACGTGCCA	GCTGATGATT	TGACCGATCC	TGCCCCAGCT	900
	ACCACTTTCG	CTCACTTGGA	TGCTACCACT	GTGTTGTCTA	GAGGTATTTC	950
	CGAGTTGGGT	ATCTACCCAG	CTGTCGACCC	ATTGGACTCC	AAGTCTAGAT	1000
	TGTTGGATGC	CTCTGTTGTC	GGTAAGGAGC	ACTACGATGT	TGCTACCAAC	1050
60	GTCCAGCAGA	CCTTGCAGGC	CTACAAGTCC	TTGCAGGATA	TCATTGCCAT	1100

TTTGGGTATG	GATGAATTGT	CCGAAGCCGA	CAAGTTGACT	GTCTGAGAGAG	1150
CTAGAAAGAT	TCAGAGATTG	TTGTCCCAGC	CATTCGCCGT	CGCCGAGGTT	1200
TTCCTGGTA	TCGAGGGTAA	GTTGGTCAGA	TTGGAGGAGA	CCGTCAAGTC	1250
TTTCAAGGAG	GTCTTGGATG	GTAAGTACGA	CCACTTGCCA	GAG	1293

5

2) INFORMATION FOR SEQ ID NO: 466

10 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1111 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

15

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Candida inconspicua*
 (B) STRAIN: ATCC 16783

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 466

AACGGTGGAT	CTAAGTTAGT	CTTAGAAGTT	GCTCAACATT	TGGGTGAAAA	50
25	CACTGTCAGA	ACCATTGCTA	TGGATGGTAC	TGAAGGTTTA	100
	AACCAGTTAA	TGATACTGGT	GCTCCAATCT	CTGTCCCAGT	150
	ACTTTAGGTA	GAATCTTAAA	CGTTATTGGT	GATCCAGTCG	200
	TCCAATTGAT	TGTAAGGAAA	GAAAACCAAT	TCATCAAGAT	250
	TCGTTGAACA	ATCTACTGAA	GCTGAAGTTT	TAGAAACCGG	300
30	GTTGATTTAT	TAGCTCCTTA	CGCTAGAGGT	GGTAAGATTG	350
	TGGTGCTGGT	GTCGGTAAAA	CCGTTTTTCAT	TCAAGAATTA	400
	TTGCAAAGGC	TCATGGTGGT	TTCTCAGTTT	TCCTGCTGTG	450
	ACCAGAGAAG	GTAATGATTT	ATACAGAGAA	ATGAAGGAAA	500
	TAACCTAGAA	GGTGAATCTA	AGGTCGCCTT	AGTTTTTCGGT	550
35	AACCACCAGG	AGCAAGAGCA	AGAGTTGCTT	TAACCGGTTT	600
	GAATACTTCA	GAGATGAAGA	AGGTCAAGAT	GTCTTGTTAT	650
	CATTTTTCAG	TTTACTCAAG	CAGGTTCTGA	AGTTTCTGCA	700
	GAATTCCATC	CGCTGTCGGT	TATCAACCAA	CTTTAGCAAC	750
	CTTTTACAAG	AAAGAATTAC	AACTACTAAG	AAAGGTTCCG	800
40	CCAAGCAGTT	TATGTCCCAG	CAGATGATTT	AACTGATCCT	850
	CTACTTTTCG	CCACTTAGAT	GCAACTACTG	TCTTATCTAG	900
	GAATTAGGTA	TTTACCCAGC	TGTCGATCCA	TTAGATTCTA	950
	ATTAGATGTT	GCTGTTGTTG	GTCAAGAACA	TTATGATGTT	1000
	TTCAAGAAAC	TTTACAAGCA	TACAAATCTT	TACAAGATAT	1050
45	TTAGGTATGG	ATGAATTATC	TGAACAAGAT	AAATTAACCG	1100
	AAGAAAGATT	C			1111

50 2) INFORMATION FOR SEQ ID NO: 467

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1283 bases
 (B) TYPE: Nucleic acid
 55 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

60 (vi) ORIGINAL SOURCE:

285

(A) ORGANISM: *Candida kefyr*

(B) STRAIN: ATCC 28838

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 467

5
 TCGAACAAGG TCAATTGCCA GAAATTTTGA ACGCTTTGGA GATTGAWACT 50
 CCTCAAGGTA AGTTGGTTTT GGAAGTTGCC CAACATTTGG GTGAAAACAC 100
 CGTCAGAACC ATTGCTATGG ACGGTACCGA AGGTTTGGTC CGTGGTGAGA 150
 AGGTTTTTGA CACTGGTGCT CCAATTTCCG TCCCAGTCGG TAGAGAAACT 200
 10 TTGGGTAGAA TCATCAACGT TATTGGTGAG CCAATTGACG AAAGAGGCCC 250
 AATCAAGTCC AAGATGAGAA AGCCAATTCA CGCTGACCCT CCATCCTTTG 300
 TTGAACAATC CACTGCTGCT GAAGTTTTGG AAACCGGTAT CAAGGTTGTC 350
 GACTTGTTGG CCCCATACGC CAGAGGTGGT AAGATTGGTT TGTTCCGGTGG 400
 TGCCGGTGTC GGTAAAGACCG TTTTCATCCA AGAGTTGATT AACAAATTG 450
 15 CCAAGGCCCA TGGTGGTTTC TCCGTCTTCA CCGGTGTCGG TGAAAGAACC 500
 AGAGAAGGTA ACGATTTGTA CCGTGAAATG AAGGAAACCG GTGTCATCAA 550
 CTTGGAAGGT GACTCCAAGG TCGCCTTGGT CTTCCGGTCAA ATGAACGAAC 600
 CACCTGGAGC TAGAGCCAGA GTTGCCCTTGA CCGGTTTGAC TATCGCTGAA 650
 TACTTCAGAG ATGAAGAAGG TCAAGATGTG TTGTTGTTTA TCGACAACAT 700
 20 TTTCAGATTC ACACAAGCCG GTTCCGAAGT GTCCGCTTTG TTGGGTCGTA 750
 TTCCATCCGC TGTCGGTTAC CAACCTACTT TGGCCACCGA TATGGGTTTG 800
 TTGCAAGAAA GAATTACCAC TACCAAGAAG GGTTCGGTTA CCTCCGTCCA 850
 AGCTGTCTAC GTCCCTGCTG ATGATTTGAC TGATCCTGCT CCAGCTACYA 900
 CTTTCGCCCA TTTGGACGCC ACCACCGTGT TGTCCAGAGG TATCTCCGAA 950
 25 TTGGGTATCT ACCCAGCTGT CGATCCATTG GATTCCAAGT CTAGATTGTT 1000
 GGACGCTGCC GTTGTGGTGC AAGAACATTA CGACGTCGCT ACTCAAGTTC 1050
 AACAACTTT GCAAGCTTAC AAGTCTTTGC AAGATATCAT TGCCATTTTG 1100
 GGTATGGATG AATTGTCTGA ACAAGACAAG TTGACTGTCG AAAGAGCCAG 1150
 AAAGATCCAA AGATTCTTGT CTCAACCATT CGCCGTCGCC GAAGTTTTC 1200
 30 CTGGTATCCC AGGTAGATTG GTCAGATTAA AGGACACCAT CGCTTCCTTC 1250
 AAGGCTGTTT TGGAAGGTAA GTACGATCAC TTG 1283

35 2) INFORMATION FOR SEQ ID NO: 468

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1287 bases
 (B) TYPE: Nucleic acid
 40 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

45 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Candida krusei*

(B) STRAIN: ATCC 34135

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 468

50
 CTTCGAACAA GGCCAATTAC CACAAATTTT AAACGCTTTA GTTATGGATA 50
 ATGGTGGTAA CAAGTTAGTT TTAGAAGTTG CTCAACATTT AGGTGAAAAC 100
 ACTGTCAGAA CCATTGCTAT GGATGGTACT GAAGGTTTAG TTAGAGGTCA 150
 AACCGTTAAC GATACCGGTG CTCCAATCTC TGTCCCAGTT GGTAGAGGTA 200
 55 CCTTAGGTAG AATCTTGAAC GTCATTGGTG ATCCAGTCGA TGAAAGAGGT 250
 CCAGTTGACT GTAAGGAAAG AAAGCCAATT CACGCTGATC CTCCAGCTTT 300
 CGTTGAACAA TCCACTGAAG CTGAAGTTTT GGAACTGGT ATTAAGGTTG 350
 TCGATTTATT AGCACCTTAC GCAAGAGGTG GTAAGATTGG TTTATTCGGT 400
 GGTGCTGGTG TTGGTAAGAC CGTTTTTATC CAAGAATTGA TCAACAATGT 450
 60 YGCAAAGGCT CATGGTGGTT TCTCCGTTTT CACTGGTGTT GGTGAAAGAA 500

	CCAGAGAAGG	TAACGATTTA	TACAGAGAAA	TGAAGGAAAC	TGGTGTATT	550
	AACTTGGAAG	GTGAATCCAA	GGTCGCCTTA	GTTTTCGGTC	AAATGAACGA	600
	ACCACCAGGA	GCTAGAGCAA	GAGTTGCTTT	AACTGGTTTG	ACCATTCGAG	650
	AATATTTTCA	AGATGAAGAA	GGTCAAGATG	TCTTGTTATT	CATTGATAAC	700
5	ATTTTCAGAT	TCACCCAAGC	AGGTTCTGAA	GTCTCTGCAT	TATTAGGTAG	750
	AATTCCATCT	GCTGTCGGTT	ATCAACCAAC	TTTAGCAACC	GATATGGGTC	800
	TTTTACAAGA	AAGAATTACC	ACCACCAAGA	AGGGTTCCGT	TACTTCTGTC	850
	CAAGCTGTTT	ATGTCCCAGC	CGATGATTTA	ACCGATCCTG	CTCCAGCTAC	900
	TACTTTTCGCC	CACCTGGATG	CAACCACTGT	CTTGTCYAGA	GGTATTTCCG	950
10	AATTAGGTAT	CTACCCAGCT	GTCGATCCAT	TAGATTCTAA	GTCTAGATTA	1000
	TTAGATGTTG	CAGTTGTTGG	TCAAGAACAT	TATGAAGTTG	CAACTCAAGT	1050
	CCAAGAAACT	TTACAAGCTT	ACAAGTCTTT	ACAAGATATT	ATTGCTATTT	1100
	TGGGTATGGA	TGAATTATCT	GAACAAGATA	AGTTAACYGT	TGAAAGAGCA	1150
	AGAAAGATCC	AAAGATTCTT	ATCTCAACCA	TTCTCTGTTG	CAGAAGTTTT	1200
15	CACTGGTATT	CCAGGTAAGT	TAGTCAGATT	AGAAGAAACC	ATCAAGTCTT	1250
	TCAGGGATGT	TCTTGCAGGT	AAGTACGATC	ACTTACC		1287

20 2) INFORMATION FOR SEQ ID NO: 469

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1283 bases
 (B) TYPE: Nucleic acid
 25 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

30 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Candida lambica*
 (B) STRAIN: ATCC 24750

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 469

35	TCGAACAAGG	TCAATTACCA	CCAATTCTTA	ACGCTTTGGT	CATGGAAAAC	50
	GATGGTCAAA	AGTTAGTTTT	GGAAGTTGCT	CAACATTTGG	GTGAAAACAC	100
	CGTCAGAAC	ATTGCTATGG	ACGGTACCGA	AGGTTTAGTT	AGAGGTCAAC	150
	CTGTTAACGA	CACCTGGTCT	CCAATCTCTG	TCCCAGTTGG	TAGAGGTACT	200
40	CTTGGTAGAA	TCTTGAACGT	CACTGGTGAC	CCAGTYGATG	AAAGAGGTCC	250
	TGTCGAMTGT	AAGGAGAGAA	GACCAATTCA	CCAAGACCCA	CCTGCTTTTCG	300
	TTGACCAATC	CACCTGAAGCT	GAAGTTTTGG	AAACCGGTAT	TAAGGTTGTC	350
	GATTTATTAG	CACCTTACGC	TAGAGGTGGT	AAGATTGGTT	TGTTCCGGTGG	400
	TGCTGGTGTC	GGTAAGACCG	TTTTTCATCCA	AGAATTGATT	AACAATGTTG	450
45	CTAAGGCCCA	CGGTGGTTTC	TCCGTTTTCA	CTGGTGTCGG	TGAAAGAACC	500
	AGAGAAGGTA	ACGATTTATA	CAGAGAAATG	AAGGAAACCG	GTGTTATTAA	550
	CCTTGAAGGT	GAATCTAAGG	TCGCCCTCGT	TTTCGGTCAA	ATGAACGAAC	600
	CACCAGGAGC	AAGAGCTAGA	GTTGCTCTTA	CTGGTTTGAC	CATTGCTGAA	650
	TACTTCAGAG	ATGAAGAAGG	TCAAGATGTC	TTGCTTTTCA	TTGACAACAT	700
50	TTTCAGATTC	ACCCAAGCAG	GTTCCGAAGT	GTCTGCTTTG	TTAGGTAGAA	750
	TTCCWTCTGC	CGTTGGTTAC	CAACCAACCT	TAGCAACCGA	TATGGGTTTG	800
	TTACAAGAAA	GAATTACCAC	CACCAAGAAG	GGTTCCTGCA	CCTCCGTCCA	850
	AGCTGTTTAC	GTCCAGCTG	ATGATTTRAC	TGACCCTGCA	CCAGCAACCA	900
	CTTTTCGCCCCA	CTTGGATGCT	ACCACCGTCT	TGTCTAGAGG	TATTTCCGAA	950
55	TTAGGTATTT	ACCCAGCTGT	CGATCCATTA	GATTCTAAGT	CTAGATTATT	1000
	GGATGTCGCT	GTTGTGCGTC	AAGAACATTA	TACCGTTGCA	ACYCAAGTCC	1050
	AAGAACTTTT	ACAAGCTTAC	AAGTCCTTAC	AAGATATCAT	TGCTATTTTG	1100
	GGTATGGACG	AATTATCTGA	ACAAGATAAG	CTTACTGTTG	AAAGAGCAAG	1150
	AAAGATCCAA	AGATTCCTTT	CCCAACCTTT	CTCCGTCGCA	GAAGTTTTCA	1200
60	CTGGTATCCC	AGGTAAGCTT	GTCAGATTAG	AAGAAACCAT	TATTTCTTTT	1250

5 2) INFORMATION FOR SEQ ID NO: 470

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1140 bases
(B) TYPE: Nucleic acid
10 (C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

15 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Candida lusitanae*
(B) STRAIN: ATCC 66035

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 470

20 AGGTGCCTCT GTCAGTGACA CTGGTTCTCC AATCTCTGTC CCTGTTGGTC 50
GTGAAACCTT GGGTAGAATT ATCAACGTTG TTGGTGAGCC AATTGACGAG 100
AGAGGCCCAA TCAACTCCAA GAAGAGAAAC CCAATTCACA CTGAGCCACC 150
ATCGTTTGTT GAACAATCCA CTTCTGCTGA AGTTTTGGAG ACTGGTATCA 200
25 AGGTTGTGCGA CTTGTTGGCC CCTTACGCCA GAGGTGGTAA GATTGGTTTG 250
TTCGGTGGTG CCGGTGTGCG TAAGACCGTT TTCATCCAAG AGTTGATTAA 300
CAACATTGCC AAGGCCACG GTGGTTTCTC TGTTTTCACT GGTGTCGGTG 350
AAAGAACCAG AGAAGGTAAC GATTTGTACC GTGAAATGCA AGAGACCGGT 400
GTCATCAACT TCGAGGGTGA CTCCAAGGTC GCCTTGGTCT TCGGTCAAAT 450
30 GAACGAACCA CCAGGAGCCA GAGCTAGAGT TGCTTTGACC GGTTTGACTA 500
TTGCCGAGTA CTTCAGAGAC GAAGAGGGCC AAGATGTCTT GTTGTTCGTT 550
GACAACATTT TCAGATTCAC CCAGGCCGGT TCTGAAGTGT CTGCTTTGTT 600
GGGTGCTATT CCATCCGCTG TCGGTTACCA ACCAACCTTG GCCACCGATA 650
TGGGTGCTTT GCAAGAGAGA ATTACCACCA CCAAGAAGGG TTCCGTCACC 700
35 TCTGTCCAAG CCGTTTATGT TCCAGCTGAT GACTTGACTG ACCCTGCTCC 750
AGCCACCACC TTCGCCCCACT TGGACGCCAC CACTGTGTTG TCCAGAGGTA 800
TCTCTGAATT GGGTATCTAC CCAGCTGTCG ACCCATGGA CTCCAAGTCT 850
AGATTGTTGG ACGCTTCTAT TGTGTTAAG GAGCACTACG AAGTTGCTTC 900
TAACGTTCAA CAACTTTGC AAGCTTACAA GTCTTTGCAA GATATCATTG 950
40 CCATTTGGG TATGGATGAA TTGTCTGAGG CTGACAAGTT GACCGTTGAG 1000
AGAGCCAGAA AGATCCAAAG ATTCTTGTCT CAACCATTCT CTGTTGCCGA 1050
GGTTTTCACT GGTATCCCAG GTAGATTGGT CAGATTGGAG GACACTGTCA 1100
GATCCTTCAA GGAAGTTTTG GACGGTAAGT ACGACCACTT 1140

45

2) INFORMATION FOR SEQ ID NO: 471

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1296 bases
(B) TYPE: Nucleic acid
50 (C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

55 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Candida norvegensis*
(B) STRAIN: ATCC 22977

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 471

	TCAATTCGAA	CAAGGTCAAT	TACCACCAAT	TTTAAACGCT	TTAGTCATGG	50
	ACAACGGTGG	AACTAAGTTA	GTTTTAGAAG	TTGCTCAACA	TTTAGGTGAA	100
5	AACACCGTCA	GAACCATTCG	TATGGATGGT	ACTGAAGGTT	TAGTTAGAGG	150
	TCAACCAGTT	AATGATACTG	GTGCTCCAAT	CTCTGTCCCA	GTCGGTAGAG	200
	GTACTIONTGG	TAGAATCTTA	AACGTTATTG	GTGATCCAGT	CGATGAAAGA	250
	GGTCCAATCG	ATTGTAAGGA	AAGAAAACCA	ATTCATCAAG	ATCCTCCTGC	300
	TTTCGTTGAA	CAATCAACTG	AAGCTGAACT	TTTAGAAACT	GGTATTAAAG	350
10	TTGTCGATTT	ATTAGCTCCT	TACGCTAGAG	GTGGTAAGAT	TGGTTTATTC	400
	GGTGGTGCAG	GTGTTGGTAA	AACCGTTTTT	ATTCAAGAAT	TAATTAACAA	450
	TGTTGCAAAA	GCTCATGGTG	GTTTCTCCGT	TTTCACTGGT	GTCGGTGAAA	500
	GAAC TAGAGA	AGGTAACGAT	TTATACAGAG	AAATGAAGGA	AACTGGTGTT	550
	ATTAATTTAG	AAGGTGATTC	TAAGGTCGCA	TTAGTTTTCG	GTCAAATGAA	600
15	CGAACCACCT	GGAGCAAGAG	CAAGAGTTGC	TTTAACTGGT	TTAACTATTG	650
	CTGAATATTT	CAGAGATGAA	GAAGGTCAAG	ATGTCTTGTT	ATTCATTGAT	700
	AACATTTTCA	GATTTACTCA	AGCAGGTTCT	GAAGTTTCCG	CTTTGTTAGG	750
	TAGAATTCCA	TCCGCTGTCG	GTTATCAACC	AACTTTAGCA	ACTGATATGG	800
	GTCTTTTACA	AGAAAGAATT	ACTACTACTA	AGAAAGGTTC	TGTTACTTCC	850
20	GTTCAAGCAG	TTTATGTCCC	AGCAGATGAT	TTAACTGATC	CTGCTCCAGC	900
	AACTACTTTC	GCCCACTTAG	ATGCAACTAC	TGTCTTATCT	AGAGGTATTT	950
	CCGAATTAGG	TATTTACCCA	GCTGTGATC	CATTAGATTC	TAAATCTAGA	1000
	TTATTAGATG	TTGCAGTTGT	TGGTCAAGAA	CATTATGATG	TTGCAACTCA	1050
	AGTTCAAGAA	ACTTTACAAG	CTTACAAATC	TTTACAAGAT	ATTATTGCTA	1100
25	TTT TAGGTAT	GGATGAATTA	TCTGAACAAG	ATAAATTAAC	CGTTGAAAGA	1150
	GCTAGAAAAA	TTCAAAGATT	CTTATCTCAA	CCTTTCTCTG	TCGCAGAAGT	1200
	TTTCACTGGT	ATCCCAGGTA	AGCTTGTTAG	ATTAGAAGAA	ACTATTTCTT	1250
	CATTCAGAGA	TGTCTTAGCA	GGTAAGTACG	ATCACTTACC	AGAAAA	1296
30						

2) INFORMATION FOR SEQ ID NO: 472

- (i) SEQUENCE CHARACTERISTICS:
- 35 (A) LENGTH: 1297 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear
- 40 (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Candida parapsilosis*
- (B) STRAIN: ATCC 90018
- 45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 472

	AACTTCGAA	GAAGGAAACT	TGCCAGCTAT	TTTGAACGCT	TTGACCTTGA	50
	AAAACGGTAA	ACAAGACTTG	GTCTTGGAAG	TTGCCCAACA	TTTGGGTGAA	100
50	AACACCGTCA	GAGCAATTGC	TATGGATGGT	ACTGAAGGTT	TAGTTAGAGG	150
	TACTTCTGTC	ACTGACACTG	GTGCCCCAAT	TTCTGTCCCA	GTTGGTAGAG	200
	GTACTIONTGG	TAGAATCATC	AATGTTACTG	GTGACCCAAT	TGATGAAAGA	250
	GGTCCAATTG	AATGTAAGAA	GAGAAACCCA	ATCCACGCTG	AACCACCTTC	300
	ATTCATTGAA	CAATCCACTG	CTGCTGAAGT	TTTGGAAACC	GGTATTAAAG	350
55	TTGTCGACTT	GTTGGCTCCA	TACGCTAGAG	GTGGTAAGAT	TGGTTTGTTT	400
	GGTGGTGCCG	GTGTCGGTAA	AACCGTGTTT	ATCCAAGAAT	TGATCAACAA	450
	CATTGCCAAG	GCACATGGTG	GTTTCTCGGT	TTTCACTGGT	GTTGGTGAAA	500
	GAACCAGAGA	AGGTAACGAT	TTGTACCGTG	AAATGAAGGA	AACTGGTGTT	550
	ATCAACTTGG	AAGGTGACTC	CAAGGTCGCT	TTGGTTTTCG	GTCAAATGAA	600
60	CGAACCACCT	GGAGCTAGAG	CTAGAGTTGC	TTTGACTGGT	TTGACCATTG	650

	CTGAATACTT	TAGAGATGAA	GAAGGTCAAG	ATGTCTTGTT	GTTTATTGAC	700
	AACATTTTCA	GATTCACCCA	AGCTGGTTCA	GAAGTGTCTG	CTTTGTTGGG	750
	TCGTATTCCA	TCCGCTGTCG	GTTATCAACC	AACCTTGGCC	ACCGATATGG	800
	GTCTTTTGCA	AGAACGTATT	ACCACTACCA	AAAAGGGTTC	AGTTACTTCA	850
5	GTCCAAGCCG	TTTACGTGCC	AGCTGATGAT	TTAACCGATC	CTGCTCCAGC	900
	TACCACTTTC	GCTCACTTGG	ATGCCACCAC	TGTGTTGTCT	AGAGGTATTT	950
	CGGAGTTGGG	TATTTACCCA	GCTGTCCGATC	CATTGGATTTC	CAAATCCAGA	1000
	TTGTTGGGATG	CTGCCGTTGT	TGGTCAAGAA	CATTACGACG	TTGCCACTGG	1050
	TGTTCAACAA	ACTTTACAAG	CTTACAAGTC	CTTGCAAGAT	ATCATTGCTA	1100
10	TCTTGGGTAT	GGATGAATTG	TCCGAACAAG	ATAAATTGAC	TGTCGAAAGA	1150
	GCTCGTAAGA	TTCAAAGATT	CTTGTCTCAA	CCATTTGCTG	TCGCTGAAGT	1200
	TTTCACTGGT	ATTCCAGGTA	AATTGGTTAG	ATTGTCTGAA	ACTGTCAAGT	1250
	CATTCAAGGA	AGTCTTGGA	GGTAAGTACG	ATAACTTGCC	AGAAAAT	1297

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2) INFORMATION FOR SEQ ID NO: 473

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 1285 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

25 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Candida rugosa*
 (B) STRAIN: ATCC 96275

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 473

	CCAGTTTGGC	AACGACCTCC	CTGCCATTTT	GAACGCCCTC	ACTCTTCAGC	50
	GTGAAGACGG	TAACAAGCTT	GTTCTTGAGG	TTGCCCAGCA	TCTCGGTGAG	100
35	AACACCGTCC	GTACCATTGC	TATGGACGGT	ACCGAGGGTT	TGGTGCGTGG	150
	CACTGGTGTG	CACGACACCG	GACACCCCAT	CATGACTCCC	GTCGGTGACG	200
	GTACCCTGGG	ACGTATTCTT	AACGTCACCG	GTGACCCTGT	AGACGAGCGT	250
	GGTCCCCTCA	AGACTGACAA	GTTCCGCCCC	ATCCACGCCG	AGGCCCTGTC	300
	CTTCGATGAG	CAGGCTACCA	GTGCCGAGGT	TCTTGAGACC	GGTATCAAGG	350
40	TTGTCGACTT	GCTCGCTCCT	TACGCCAAGG	GTGGTAAGAT	TGGTTTGTTT	400
	GGTGGTGCCG	GTGTCGGCAA	GACCGTCTTC	ATCCAGGAGC	TGATTAACAA	450
	CATCGCCAAG	GCCCACGGTG	GTTACTCCGT	GTTCACTGGT	GTCGGTGAGC	500
	GTA CTGCTGA	GGGTAACGAT	TTGTACAAGG	AAATGATCGA	GTCCGGTGTC	550
	ATCAACCTCG	ATGGTGAGTC	CAAGGTCGCC	TTGGTGTTTCG	GTCAGATGAA	600
45	CGAGCCCCCT	GGAGCCCGTG	CCCGTGTCGC	CCTTACCGGT	CTTACCATCG	650
	CTGAGTATTT	CCGTGATGAG	GAGGGTAAGG	ATGTCTTGTT	GTTTCGTTGAC	700
	AACATTTTCC	GCTTCACTCA	GGCCGGTTCT	GAGGTGTCCG	CCTTGCTTGG	750
	TCGTATTCTT	TCCGCTGTCG	GTTACCAGCC	TACCCTGGCC	ACCGATATGG	800
	GTGCCCTTCA	GGAGCGTATC	ACCACCACCA	AGAAGGGTTC	CGTTACATCC	850
50	GTCCAGGCCG	TCTACGTCCC	TGCCGATGAT	TTGACTGATC	CCGCCCCTGC	900
	CACCACCTTC	GCCCATTGTT	ATGCCACCAC	TGTCTTGTCT	CGTGCCATCT	950
	CTGAGTTGGG	TATCTACCCC	GCTGTGACCC	CTCTCGACTC	CAAGTCCCGT	1000
	CTTCTTGACG	CCGCTGTCTG	TGGTCAGGAG	CACTACGATA	CTGCCACCTC	1050
	CGTTCAGCAG	ACTTTGCAGG	CTTACAAGTC	TTTGCAGGAT	ATCATTGCCA	1100
55	TTCTTGGTAT	GGATGAGTTG	TCCGAGTCTG	ACAAGCTCAC	CGTCGAGCGT	1150
	GCTCGTAAGA	TCCAGCGTTT	CCTCTCCCAG	CCTTTCGCTG	TTGCTGAGGT	1200
	CTTCACTGGT	ATTCAAGGCC	GTCTTGTTCC	TCTCAAGGAC	ACTGTCCGCT	1250
	CCTTCAAGGA	GATTCTCGAA	GGTAAGTACG	ATGCT		1285

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2) INFORMATION FOR SEQ ID NO: 474

- (i) SEQUENCE CHARACTERISTICS:
- 5 (A) LENGTH: 1283 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

10 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Candida sphaerica*
- 15 (B) STRAIN: ATCC 2504

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 474

	TTGAACAAGG	TCAATTGCCA	GCTATTTTGA	ACGCTTTGGA	AATCGACACT	50
	CCAGAAGGAA	AGTTGGTTTT	GGAAGTCGCT	CAACATTGGA	GTGAAAACAC	100
20	TGTCAGAAC	ATTGCTATGG	ATGGTACTGA	AGGTTTAGTC	CGTGGTGAAA	150
	ACGTTTCTGA	CACTGGTGCT	CCAATTTCCG	TCCCAGTTGG	TAGAGAAACC	200
	TTGGGTAGAA	TTATCAACGT	TATTGGTGAG	CCAATTGACG	AAAGAGGTCC	250
	AATCAACTCC	AAGATGAGAA	AGCCAATTCA	TGCTGATCCT	CCATTATTCTG	300
	TTGAACAATC	CACTGCTGCT	GAAGTTTGG	AAACTGGTAT	CAAGGTTGTC	350
25	GACTTGTTGG	CCCCATACGC	CAGAGGTGGT	AAGATTGGTT	TGTTCCGGTGG	400
	TGCCGGTGTC	GGTAAGACCG	TTTTTCATCCA	AGAATTGATT	AACAACATTG	450
	CCAAGGCTCA	TGGTGGTTTC	TCTGTCTTCA	CTGGTGTCGG	TGAAAGAACC	500
	AGAGAAGGTA	ACGATTTGTA	CCGTGAAATG	AAGGAAACTG	GTGTTATCAA	550
	CTTGGAAGGT	GATTCTAAGG	TCGCGTTGGT	TTTCGGTCAA	ATGAACGAAC	600
30	CTCCTGGAGC	TAGAGCTAGA	GTCGCCTTGA	CTGGTTTGAC	CATCGCTGAA	650
	TACTTCAGAG	ATGAAGAAGG	TCAAGATGTC	TTGTTGTTTA	TCGACAACAT	700
	TTTCAGATTC	ACACAAGCCG	GTTCCGAAGT	GTCCGCTTGG	TTGGGTCGTA	750
	TTCCATCCGC	TGTCGGTTAT	CAACCAACTT	TGGCCACCGA	TATGGGTTTG	800
	TTGCAAGAAA	GAATTACTAC	CACCAAGAAG	GGTTCCGTC	CTTCTGTCCA	850
35	AGCCGTTTAC	GTGCCAGCTG	ATGATTTGAC	TGATCCTGCT	CCAGCTACCA	900
	CTTTCGCGCA	TTTGATGCC	ACCACTGTGT	TGTCCAGAGG	TATCTCTGAA	950
	TTGGGTATCT	ACCCAGCTGT	CGATCCTTTG	GATTCCAAAT	CTAGATTGTT	1000
	GGATGCTGCC	GTCGTTGGTC	AAGAACATTA	CGATGTCGCT	ACTCAAGTTC	1050
	AACAACTTT	GCAAGCTTAC	AAGTCTTTGC	AAGATATCAT	TGCCATTTTG	1100
40	GGTATGGATG	AATTGTCCGA	ACAAGATAAG	TTGACCGTCG	AAAGAGCTAG	1150
	AAAGATTCAA	AGATTCTTGT	CTCAACCTTT	CGCTGTCGCT	GAAGTCTTCA	1200
	CTGGTATCCC	AGGTAGATTG	GTCAGATTAA	AGGACACCAT	CTCTTCTTTC	1250
	AAGGCTGTCT	TGGACGGTAA	GTACGATCAC	TTG		1283

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2) INFORMATION FOR SEQ ID NO: 475

- (i) SEQUENCE CHARACTERISTICS:
- 50 (A) LENGTH: 1290 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

55 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Candida tropicalis*
- 60 (B) STRAIN: ATCC 13803

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 475

	CGACGAAGGT	AACCTGCCAG	CTATTTTGAA	TGCTTTGACT	TTGAAGAACG	50
	GTGACCAAGA	CTTGGTTTTG	GAAGTTGCTC	AACATTTGGG	TGAAAACACC	100
5	GTCAGGGCTA	TTGCTATGGA	TGGTACCGAA	GGTTTAGTCA	GAGGTACTGC	150
	TGTCACTGAT	ACCGGTGCTC	CAATTTCTGT	CCCAGTTGGT	AGAGGTACCT	200
	TGGGTAGAAT	TATCAACGTT	GTTGGTGAAC	CAATTGATGA	CAGAGGTCCA	250
	ATTGAATGTA	AGGAAAGAAA	GCCAATTCAC	GCTGAACCAC	CTTCATTCTG	300
	TGAACAATCT	ACTGCTGCCG	AAATTTTGGA	AACCGGTATT	AAGGTTGTCT	350
10	ATTTGTTGGC	TCCTTACGCT	AGAGGTGGTA	AGATTGGTTT	GTTCCGGTGGT	400
	GCTGGTGTCT	GTAAACCGT	CTTCATCCAA	GAATTGATTA	ACAACATTGC	450
	CAAAGCTCAT	GGTGGTTTCT	CTGTCTTTAC	CGGTGTCTGGT	GAAAGAAECA	500
	GAGAAGGTAA	CGATTTGTAC	CGTGAAATGA	AAGAAACTGG	TGTCATCAAC	550
	TTGGAAGGTG	ACTCCAAGGT	CGCCTTGGTC	TTCGGTCAAA	TGAACGAACC	600
15	ACCTGGTGCT	AGAGCTAGAG	TTGCTTTGAC	TGGTTTGACC	ATTGCTGAAT	650
	ACTTCAGAGA	TGAAGAAGGT	CAAGATGTCT	TGTTGTTCAT	TGACAACATT	700
	TTCAGATTCA	CCCAAGCTGG	TTCCGAAGTG	TCTGCTTTGT	TGGGTCGTAT	750
	TCCATCTGCT	GTCGGTTATC	AACCAACCTT	GGCCACTGAT	ATGGGTCTTT	800
	TGCAAGAACG	TATTACCACC	ACCAAGAAAG	GTTCTGTTC	TTCTGTCCAA	850
20	GCTGTTTATG	TCCCAGCCGA	TGATTTAACC	GATCCAGCTC	CAGCTACCAC	900
	CTTCGCTCAC	TTGGATGCCA	CTACTGTCTT	GTCTAGAGGT	ATTTCTGAAT	950
	TGGGTATTTA	CCCAGCTGTC	GATCCATTGG	ATTCTAAATC	CAGATTATTG	1000
	GATGCTACTG	TTGTTGGTCA	AGAACATTAT	GATGTTGCCA	CTGGTGTTCA	1050
	ACAAACTTTA	CAAGCTTACA	AGTCCTTGCA	AGATATCATT	GCTATTTTGG	1100
25	GTATGGATGA	ATTGTCCGAA	GCCGATAAAT	TGACTGTCTG	AAGAGCTCGT	1150
	AAGATTCAAA	GATTCTTGTC	CCAACCATTC	GCTGTTGCCG	AAGTTTTTCAC	1200
	TGGTATCCCA	GGTAGATTGG	TTAGATTACA	AGATACTGTT	AAATCTTTCA	1250
	AAGATGTCTT	GGAAGGTAAA	TACGATCACT	TGCCAGAAAA		1290

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2) INFORMATION FOR SEQ ID NO: 476

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 1267 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

40 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Candida utilis*
 (B) STRAIN: Csp 388

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 476

	TTTGAACGCC	CTTGAGATCA	AGAACCACGA	GTCTGGAAGA	TTGGTCCTCG	50
	AGGTTGCCCA	GCACTTGGGT	GAGAACACTG	TCAGAACTAT	TGCCATGGAT	100
50	GGTACCGAAG	GTCTCGTCCG	TGGTGAGTCT	GTTGTTGACA	CCGGTTCTCC	150
	AATTACTGTC	CCAGTTGGTC	GTGAGACCTT	GGGTCGTATC	ATCAACGTTA	200
	TTGGTGAGCC	AATTGATGAG	CGTGGTCCAA	TCAACACCAA	GCACAGAAAC	250
	CCAATTCACG	CTGAGCCACC	ATCCTTCGCT	GAGCAGTCTA	CTGCTGCTGA	300
	GGTTTTGGAG	ACTGGTATCA	AGGTTGTCTG	CCTTCTCGCC	CCATACGCCA	350
55	GAGGTGGTAA	GATTGGTCTC	TTTGGTGGTG	CCGGTGTCGG	TAAGACCGTT	400
	TTCATCCAGG	AGTTGATTAA	CAACATTGCC	AAGGCCACAG	GTGGTTTCTC	450
	TGTTTTTACC	GGTGTCTGGT	AGAGAACCAG	AGAGGGTAAC	GATTTGTACC	500
	GTGAGATGAA	GGAGACTGGT	GTCATCAATC	TCGAGGGTGA	GTCCAAGGTT	550
	GCTCTCGTCT	TCGGTCAGAT	GAACGAGCCA	CCAGGTGCCC	GTGCCCCTGT	600
60	CGCTTTGACC	GGTTTGACCA	TTGCTGAGTA	CTTCAGAGAT	GAGGAGGGTC	650

	AGGATGTCTT	GTTGTTTATT	GACAACATTT	TCAGATTCAC	CCAGGCCGGT	700
	TCCGAGGTGT	CTGCCTTGCT	TGGTCGTATT	CCATCCGCTG	TCGGTTACCA	750
	GCCAACTTTG	GCCACCGATA	TGGGTTTGT	GCAGGAGAGA	ATTACCACCA	800
	CCCAGAAGGG	TTCCGTCACT	TCTGTCCAGG	CCGTTTACGT	CCCAGCTGAT	850
5	GATTTGACTG	ATCCTGCTCC	AGCCACCACT	TTCGCCCCACT	TGGACGCCAC	900
	CACTGTGTTG	TCCCGTGGTA	TCTCTGAGTT	GGGTATTTAC	CCAGCTGTCTG	950
	ACCCATTGGA	CTCCAAGTCC	AGATTGTTGG	ACGCTGCCGT	TGTTGGTGAC	1000
	GAGCACTACA	ACACCGCCAC	CGATGTCCAG	CAGACCCTTC	AGGCTTACAA	1050
	GTCTCTCCAG	GATATCATTG	CTATTTTGGG	TATGGATGAG	TTGTCTGAGG	1100
10	CTGACAAGTT	GACTGTGCGAG	AGAGCCAGAA	AGATTTCAGCG	TTTCCTTTCC	1150
	CAGCCATTCTG	CTGTGCTGTA	GGTTTTTACC	GGTATCCCAG	GTAGATTGGT	1200
	TAGACTTCAG	GACACCATCA	AGTCCTTCAG	AGAGGTTTTG	GACGGTAAGT	1250
	ACGACCACTT	GCCAGAG				1267

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2) INFORMATION FOR SEQ ID NO: 477

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 1296 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

25 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Candida viswanathii*
 (B) STRAIN: ATCC 28269

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 477

	CCAATTCGAC	GAAGGTAGCT	TGCCAGCTAT	CTTGAACGCC	TTGACCTTGA	50
	AGAACGGTGA	CCAAGACTTG	GTCTTGGAAG	TTGCCCAACA	CTTGGGTGAA	100
35	AACACTGTCA	GAGCTATTGC	TATGGATGGT	ACCGAAGGTT	TGGTCAGAGG	150
	TACTGCTGTC	ACTGACACCG	GTGCTCCAAT	CTCCGTCCCA	GTCGGTAGAG	200
	GTACCTTGGG	TAGAATCATC	AACGTTGTTG	GTGAACCAAT	TGACGACAGA	250
	GGTCCAATTG	AATGTAAGGA	AAGAAAGCCA	ATTACGCTG	AACCACCTTC	300
	TTTCGTTGAA	CAATCCACTG	CTGCCGAAAT	TTTGGAACC	GGTATCAAGG	350
40	TTGTCGACTT	GTTGGCCCCA	TACGCCAGAG	GTGGTAAGAT	TGGTTTGTTC	400
	GGTGGTGCCG	GTGTCGGTAA	GACTGTCTTT	ATCCAAGAGT	TGATTAACAA	450
	CATTGCCAAG	GCCCATGGTG	GTTTCTCTGT	CTTCACTGGT	GTCGGTGAAA	500
	GAACCAGAGA	AGGTAACGAT	TTGTACCGTG	AAATGAAGGA	AACCGGTGTC	550
	ATCAACTTGG	AAGGTGACTC	CAAGGTCGCC	TTGGTTTTTCG	GTCAAATGAA	600
45	CGAACCACCT	GGTGCTAGAG	CTAGAGTTGC	TTTGAAGTGGT	TTGACCATTG	650
	CCGAATACTT	CAGAGACGAA	GAAGGTCAAG	ATGTCTTGTT	GTTTATTGAC	700
	AACATTTTCA	GATTCACCCA	AGCCGGTTCC	GAAGTGTCTG	CTTTGTTGGG	750
	TCGTATTCCA	TCTGCCGTCG	GTTATCAACC	AACCTTGGCC	ACCGATATGG	800
	GTCTTTTGCA	AGAACGTATT	ACCACCACCA	AGAAGGGTTC	CGTCACCTCT	850
50	GTCCAAGCTG	TCTATGTCCC	AGCCGATGAT	TTGACCGATC	CTGCTCCAGC	900
	CACCACCTTC	GCTCACTTGG	ATGCCACTAC	TGTCTTGTCT	AGAGGTATTT	950
	CCGAATTGGG	TATCTACCCA	GCTGTGATC	CATTGGACTC	CAAGTCCAGA	1000
	TTGTTGGATG	CTGCTGTTGT	TGGTCAAGAA	CATTACGATG	TTGCCACTGG	1050
	TGTCCAACAA	ACCTTGCAAG	CTTACAAGTC	TTTGCAAGAT	ATCATTGCCA	1100
55	TTTTGGGTAT	GGATGAATTG	TCTGAATCCG	ATAAGTTGAC	TGTCGAAAGA	1150
	GCTCGTAAGA	TCCAAAGATT	CTTGTCGCAA	CCATTTGCTG	TTGCCGAAGT	1200
	TTTCACTGGT	ATCCCAGGTA	GATTAGTTAG	ATTGCTGGAA	ACCGTCCAAT	1250
	CTTTCAAAGA	CGTCTTGGCT	GGTAAATACG	ATCACTTGCC	AGAAAA	1296

60

2) INFORMATION FOR SEQ ID NO: 478

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 1295 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

10 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Candida zeylanoides*
 (B) STRAIN: ATCC 7351

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 478

	TCAATTCGAG	CAAGGCAACC	TCCCTGCCAT	CTTGAACGCT	CTCACCTTGA	50
	AGAATGGTGA	CAACGACTTG	GTTTTTGAAG	TTGCCCAGCA	CTTGGGTGAG	100
20	AACACCGTCA	GAGCCATTGC	CATGGATGGT	ACCGAGGGTT	TGGTTAGAGG	150
	TGCGTCCGTC	AAGGACACTG	GCGCCCCCTAT	CTCGGTCCCC	GTTGGCCGCG	200
	GGACTTTGGG	TCGTATCATC	AACGTCACCG	GTGACCCCAT	TGACGAGAGA	250
	GGTCCCATCG	AGCTGACCCA	GAGAAACCCT	ATCCACGCCG	ACCCCCCCTC	300
	GTTCGTTGAG	CAGTCCACCA	ACGCTGAGGT	TTTGAGAGCT	GGTATCAAGG	350
25	TTGTCGATTT	GTTGGCTCCC	TACGCCAGAG	GTGGTAAGAT	TGGTTTGTTT	400
	GGTGGTGCCG	GTGTCGGTAA	GACCGTCTTC	ATTGAGGAGT	TGATCAACAA	450
	CATCGCCAAG	GCCCACGGTG	GGTTCTCGGT	CTTCACTGGT	GTCGGTGAGA	500
	GAAC TAGAGA	GGGTAACGAC	TTGTACCGTG	AGATGAAGGA	GACCGGTGTC	550
	ATCAACTTGG	AGGGTGACTC	CAAGGTGGCC	TTGGTGTTTC	GTCAGATGAA	600
30	CGAGCCCCCT	GGAGCCAGAG	CCAGAGTCGC	CTTGACCGGG	TTGACCATTTG	650
	CCGAATACTT	TAGAGACGAG	GAGGGTCAGG	ATGTGTTGTT	GTTTCGTCGAC	700
	AACATCTTCA	GATTCACCCA	AGCTGGTTCG	GAGGTGTCGG	CCTTGTTGGG	750
	TCGTATTCCC	TCTGCCGTCG	GTTACCAGCC	CACCTTGCCA	ACTGATATGG	800
	GATTGTTGCA	GGAGCGTATC	ACCACGACCA	AGAAGGGTTC	CGTCACCTCA	850
35	GTGCAGGCCG	TCTACGTCCC	CGTGATGAC	TTGACTGACC	CTGCTCCC GC	900
	CACCACCTTT	GCCCCACTTG	ACGCCACCAC	CGTGTTGTCC	AGAGGTATCT	950
	CTGAGTTGGG	TATCTACCCC	GCCGTCGACC	CCTTGGA CTC	CAAATCGAGA	1000
	TTGTTGGACG	CTGCCGTGGT	CGGTCAGGAG	CACTACGATG	TTGCCTCGAA	1050
	CGTCCAGCAG	ACCTTG CAGG	CCTACAAGTC	CCTG CAGGAT	ATCATTGCCA	1100
40	TTTTGGGTAT	GGATGAGTTG	TCCGAGGCTG	ACAAGTTGAC	CGTTGAGAGA	1150
	GCCAGAAAGA	TCCAGAGATT	CTTGTCGCAG	CCCTTCGCTG	TTGCCGAGGT	1200
	TTTCACTGGT	ATCAAGGGTA	GATTGGTCAG	ATTGGAGGAC	ACCGTCAGAT	1250
	CTTTC AAGGA	GGTTTTGGAG	GGTAAGTACG	ACCACTTGCC	CGAGA	1295

45

2) INFORMATION FOR SEQ ID NO: 479

(i) SEQUENCE CHARACTERISTICS:

- 50 (A) LENGTH: 534 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

55 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Coccidioides immitis*
 (B) STRAIN: Silveira

60

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 479

	TTCAGGAATT	GATTGTAAGT	TCTGTTATCA	ACTAAAGCCG	ACAGCGGTTG	50
	CTGATATGCT	CTAGAACAAC	ATTGCTAAGG	CTCACGGTGG	TTACTCCGTG	100
5	TTCACTGGTG	TCGGTGAGCG	TACCCGTGAG	GGTAACGATT	TGTACCATGA	150
	AATGCAAGAG	ACCCGTGTCA	TTCAACTCGA	CGGAGAGTCC	AAGGTCGCTC	200
	TTGTCTTCGG	TCAAATGAAC	GAGCCCCCTG	GTGCCCCGTG	CCGTGTTGCC	250
	CTTACCGGTT	TGACCATTGC	TGAATACTTC	CGTGACGAGG	AAGGCCAAGA	300
	CGGTAGGCTT	CATGCTTCTA	TCGCTAGGGG	CGTGTGATAC	AGGAGGCTAA	350
10	TCGCTTTTCT	AGTGCTTCTC	TTTATTGACA	ACATTTTCCG	TTTCACTCAA	400
	GCTGGTTCTG	AAGTGTCTGC	CTTGCTCGGT	CGTATTCCTT	CCGCTGTCGG	450
	TTACCAACCT	ACTCTCGCCG	TCGACATGGG	TGTTATGCAG	GAACGTATCA	500
	CCACCACCAC	CAAGGGATCC	ATTACTTCAG	TGCA		534

15

2) INFORMATION FOR SEQ ID NO: 480

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 494 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

25 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Cryptococcus albidus*

(B) STRAIN: ATCC 66030

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 480

	CGTCTTGATT	CAAGAATTGA	TCAACAACAT	CGCCAAGGCC	CACGGTGGTT	50
	ACTCGGTCTT	CACCGGTGTC	GGTGAGCGAA	CTCGAGAGGG	TAACGATCTG	100
35	TACCACGAAG	TGAGTTGCGC	CGTCCGAGTG	TTTCCCGGGG	AATCGCAAGA	150
	CTGATGTTGT	CCTTTCTTCT	CAGATGAGGG	AAACCGGTGT	CATCAACCTC	200
	GAGGGTGACT	CCAAGGTCGC	CTTGGTCTTC	GGTCAGATGA	ACGAGCCCCC	250
	TGGAGCCCGA	GCCCGAGTCG	CCTTGACCGG	TTTGACCATT	GCCGAATACT	300
	TCCGAGACGA	GGAGGGTCAG	GATGTCTTGT	TGTTCAATTGA	CAACATTTTC	350
40	CGATTACCC	AAGCCGGTTC	GGAAGTGTC	GCCTTGTTGG	GTCGTATCCC	400
	CTCCGCCGTC	GGTTACCAGC	CCACTCTGTC	CACCGACATG	GGTACCATGC	450
	AGGAGCGAAT	TACCACCACC	AAGAAGGGTT	CCATCACTTC	CGTC	494

45

2) INFORMATION FOR SEQ ID NO: 481

(i) SEQUENCE CHARACTERISTICS:

50 (A) LENGTH: 415 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

55

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Fusarium oxysporum*

(B) STRAIN: WSA-212

60 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 481

	TTCAGGAGCT	TATCAACAAC	ATCGCCAAGG	CCCACGGTGG	TTACTCCGTC	50
	TTCACTGGTG	TCGGTGAGCG	AACTCGTGAG	GGTAACGATC	TGTACCACGA	100
	AATGCAGGAG	ACTTCCGTCA	TTCAGCTTGA	TGGCGAGTCC	AAGGTCGCCC	150
5	TGGTCTTCGG	TCAGATGAAC	GAGCCCCCTG	GAGCTCGTGC	CCGTGTCGCC	200
	CTTACCGGTC	TTACTGTAGC	TGAATACTTC	AGAGATGAGG	AGGGTCAGGA	250
	CGTGCTGCTC	TTCATTGACA	ACATTTTCCG	ATTCACCTCAG	GCCGGTTCCG	300
	AGGTGTCTGC	CCTTCTCGGT	CGTATCCCCT	CTGCCGTCGG	TTACCAGCCC	350
	ACCCTCGCCG	TCGACATGGG	TGGTATGCAA	GAGCGTATTA	CCACCACCAC	400
10	CAAGGGTTCC	ATTAC				415

2) INFORMATION FOR SEQ ID NO: 482

15

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1281 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

25

- (A) ORGANISM: *Geotrichum* spp.
 (B) STRAIN: Lev-4

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 482

30	AGGACAACCT	CCCCGCTATT	CTTAACGCTC	TTGAGCTTAA	GAGAGATAAC	50
	GGTGAGAAGC	TCGTCTCTCG	GGTTGCCCCAG	CATCTGGGTG	AGAACACTGT	100
	CCGTACTATT	GCTATGGACG	GTACTGAGGG	TCTCGTCCGT	GGTCAGCCCCG	150
	TTGTTGACAC	CGGTGCCCCC	ATTACCATTTC	CCGTTGGTCCG	TGGTACTCCTT	200
	GGTGAATTA	TCAACGTCAT	TGGTGAGCCC	ATCGATGAGC	GTGGACCCAT	250
35	TGAGGCTACC	AAGTACCTCC	CCATCCACAC	CGAGCCCCCC	ACCTTCGCTG	300
	AGCAGTCTAC	CTCCGCTGAG	GTTCTTGAGA	CTGGTATCAA	GGTTGTTCGAT	350
	CTCCTTGCCC	CCTACGCCCCG	TGGTGGAAG	ATTGGTCTCT	TCGGTGGTGC	400
	CGGTGTCGGT	AAGACCGTTT	TCATTACAGGA	GCTGATTAA	AACATTGCCA	450
	AGGCCCATGG	TGGTTTCTCC	GTTTTCACCG	GTGTCGGTGA	GAGAACCCGT	500
40	GAGGGTAACG	ATTTGTACCG	TGAGATGAAG	GAGACCGGTG	TCATCAACCT	550
	CGAGGGTGAG	TCTAAGGTCG	CTCTCGTTTT	CGGTCAGATG	AACGAGCCCC	600
	CTGGAGCCCCG	TGCCCGTGTT	GCTCTTACTG	GTCTTACCAT	TGCTGAGTAC	650
	TTCCGTGATG	AGGAGGGTCA	GGATGTGTTG	CTCTTCGTTG	ACAACATTTT	700
	CCGTTTCACT	CAGGCCGGTT	CCGAGGTGTC	TGCCCTTTTG	GGTCGTATTC	750
45	CCTCCGCTGT	CGGTACCAG	CCCACCCTTG	CCACTGATAT	GGGTGCCCTG	800
	CAAGAGCGTA	TTACCACCAC	CCAGAAGGGT	TCCGTCACTT	CCGTCCAGGC	850
	CGTCTACGTC	CCTGCCGATG	ATTTGACCGA	TCCTGCCCCCT	GCTACCACCT	900
	TCGCCCATTT	GGATGCCACC	ACCGTCTTGT	CGCGTTCCAT	TTCTGAGTTG	950
	GGTATCTACC	CCGCTGTCTGA	TCCCCTTGAT	TCCAAGTCTC	GTCTTTTGGA	1000
50	TATCACCGTC	GTTGGCCAGG	AGCACTACGA	TGTTGCTACC	CAGGTCCAGC	1050
	AGACCTCCA	GTCCTACAAG	TCTCTTCAGG	ATATCATTGC	CATTTTGGGT	1100
	ATGGATGAGT	TGTCTGAGGC	TGATAAGCTT	ACTGTCGAGC	GTGCCCCGTA	1150
	GATCCAGAGA	TTCCTTTCCC	AGCCCTTCAC	TGTCGCTGAG	GTTTTCACTG	1200
	GTATCGAGGG	CCGTCTCGTT	CCTTTGAAGG	ACACTGTTTCG	CTCTTTCAAG	1250
55	GAGATCCTTG	AGGGCAAGTA	CGACCACCTC	C		1281

2) INFORMATION FOR SEQ ID NO: 483

60

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 586 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Histoplasma capsulatum*
 (B) STRAIN: G185A5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 483

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15  ATTCAAGAAT TGATCGTACG TTCCTCCGCC CCACACACGA TCAATGGAGA      50
    AAGAAACAAA TTTTGGGGA GTGGTCATTT TTTCTAATAA TTCGAATAGA      100
    ACAACATTGC CAAAGCCCAC GGTGGTTACT CCGTGTTTAC TGGTGTTCGGC      150
    GAGCGGACCC GTGAAGGAAA TGAAGTTGAC CACGAAATGC AGGAAACCCG      200
    TGTTATCCAG CTCGATGGAG AGTCCAAGGT CGCCCTCGTT TTCGGTCAGA      250
20  TGAACGAGCC TCCCGGAGCC CGTGCCCGTG TTGCCCTCAC TGGTCTGACC      300
    GTTGCCGAGT ACTTCCGTGA CGAGGAAGGC CAAGACGGTA TGTATAAGTA      350
    TACACCGTAG CAAATCAACA CAGAGCTTCA CTCACGCTCG GATTTAGTGC      400
    TTCTCTTCAT CGACAACATT TTCCGCTTCA CTCAGGCCGG TTCCGAAGTG      450
    TCTGCCCTGC TCGGCCGTAT TCCCTCCGCC GTCGGTTACC AACCACCCCT      500
25  CGCCGTGGAC ATGGGTGGTA TGCAGGAACG TATCACC ACT ACCACCAAGG      550
    GCTCCATCAC CTCTGTGCAR GCCGTCTACG TCCCCG      586
  
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2) INFORMATION FOR SEQ ID NO: 484

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1145 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Malassezia furfur*
 (B) STRAIN: ATCC 42132

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 484

```

45  GCGTGGCCAG AAGGTCATTG AACTGGTGC TCCCATCACC ATCCCCGTCG      50
    GTGGTGCCAC ACTGGGTCGT ATTCTGAACG TCACGGGTGA CCCTATTGAC      100
    GAGCGTGGCC CCGTTAAGAC TGACGTTTTC CGCCCCATTC ACCGTGACCC      150
    CCCTGCCTTT GTCGAGCAGT CGACTGATGC CGAGATTCTC GAGACTGGTA      200
50  TCAAAGTCGT TGACCTGATT GCCCCTTACG CCCGTGGTGG TAAGATTGGT      250
    CTGTTCCGTG GTGCCGGTGT CGGTAAGACC GTGCTTATCC AGGAGCTCAT      300
    CAACAACATC GCCAAGGCCC ACGGTGGTTT CTCCGTGTTC ACTGGTGTGC      350
    GTGAGCGTAC TCGTGAGGGT AACGATTTGT ACCACGAGAT GATTGAAACC      400
    GGTGTCATTA ACCTCGAGGG TGAAGCAAG GTGGCTCTGG TGTTCCGGTCA      450
55  GATGAACGAG CCCCCGGGTG CCCGTGCGCG TGTCGCTCTT ACTGGTCTGA      500
    CTGTGGCCGA GTAATTCCTG GACGACGAGG GCCAGGATGT GCTGCTGTTC      550
    ATTGACAACA TTTTCCGTTT CACCCAGGCC GGTTCGGAGA CTTCGGCTCT      600
    GCTGGGTCGT ATCCCTTCGT CGGTCGGTTA CCAGCCCACT TTGTCGACCG      650
    ATATGGGTGC CATGCAGGAG CGTATACCA CCACCAAGAA GGGTTTCGATT      700
60  ACGTCGGTGC AGGCCGTCTA CGTGCCCGCC GATGATGTCA CTGACCCTGC      750
  
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	CCCTGCCACT	ACCTTCGCCC	ACCTTGACGC	TACCACTGTG	CTTGACCGTT	800
	CGATCGCTGA	GCTGGGTATC	TACCCCGCTG	TTGACCCGTT	GAACCTCGAAC	850
	TCGCGTATGC	TTGACCCCGC	TATTGTGGGT	CAGGAGCACT	ACGACGTGGC	900
	CTCTGGCGTG	CAGAAGCTGC	TCCAGGACTA	CAAGTCGCTT	CAAGATATCA	950
5	TTGCCATTCT	GGGTATGGAT	GAGCTTTCTG	AGGAGGACAA	GCTCACTGTC	1000
	GAGCGTGCCC	GTAAGATGCA	GCGTTTCATG	TCGCAGCCTT	TCGCTGTGCG	1050
	CCAGGTCTTT	ACTGGTATCG	AAGGTCGTCT	TGTTGCCCTG	AAGGACACGA	1100
	TCAAGGCCTG	CAAGGAGATC	CTGTCGGGCA	AGCACGACAA	CCTCC	1145

10

2) INFORMATION FOR SEQ ID NO: 485

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 1261 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

20 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Malassezia pachydermatis*
 (B) STRAIN: ATCC 42756

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 485

	TCCCGCCATC	TTCAACGCCC	TGGAGGTCCA	GGACATGAAG	AACGGTGGCC	50
	GCCTTGTTCT	GGAGGTTGCC	CAGCACCTTG	GTGAGAACAC	TGTTCTGTTGC	100
30	ATTGCTATGG	ACGGTACCGA	GGGTCTTGTC	CGTGGTCAGA	AGGTCCTTGA	150
	CACTGGTGCC	CCGATCACTA	TCCCTGTCGG	TAACGGTACC	TTGGGCCGYA	200
	TCCTGAACGT	CACTGGTGAG	CCTGTGGATG	AGCGTGGTCC	GGTTAAGACT	250
	GACGTCTACC	GTCCAATCCA	CCGTGAGCCC	CCGGCGTTCG	TTGAGCAGTC	300
	GACTGATGCT	GAGATTCTTG	AGACTGGTAT	CAAGGTGGTC	GACCTGCTCG	350
35	CCCCATACGC	TCGTGGTGGT	AAGATTGGTC	TWTTCCGGTGG	TGCYGGTGTY	400
	GGTAAGACCG	TGCTGATTCA	GGAGCTTATC	AACAACATTG	CCAAGGCCCA	450
	CGGTGGTTTC	TCGGTGTTCA	CTGGTGTCCG	TGAGCGTACT	CGTGAGGGTA	500
	ACGATCTGTA	CCATGAAATG	ATTGAGACTG	GTGTCATCAA	CGTTGACGGT	550
	GACTCGAAGG	TCGCTCTCGT	GTTCCGGTCAG	ATGAACGAGC	CCCCGGGTGC	600
40	CCGTGCCCGT	GTCCGCCCTGA	CYGGTCTGAC	CATCGCCGAG	TACTTCCGTG	650
	ACGACGAGGG	TCAGGATGTG	CTGCTCTTCA	TTGACAACAT	TTTCCGTTTC	700
	ACTCAGGCTG	GTTCCGAGAC	TTCGGCTCTG	CTGGGTCGTA	TCCCGTCGGC	750
	TGTCGGTTAC	CAGCCKACCC	TTGCCACGGA	TATGGGTGCC	ATGCAGGARC	800
	GTATYACCAC	CACCAAGAAG	GGTTCGATTA	CCTCGGTGCA	GGCYGTTTAC	850
45	GTTCCGGCCG	ACGATGTGAC	TGACCCTGCC	CCGGCCACGA	CCTTCGCCCCA	900
	CTTGACGCC	ACCACGGTGT	TGGACCGTTC	GATTGCGYAG	CTGGGTATCT	950
	ACCCGGCCGT	CGACCCGCTG	AACTCGAAGT	CGCGTATGCT	TGACCCGTCA	1000
	ATTGTCGGTG	TGGAGCACTA	CAACGTTGCT	TCGGGTGTCC	AGAAGCTTCT	1050
	YCAGGACTAC	AAGTCGCTCC	AAGATATCAT	TGCCATTCTG	GGTATGGATG	1100
50	AGTTGTCGGA	GGAGGACAAG	CTCACTGTG	AGCGTGCCCG	TAAGATGCAG	1150
	CGTTTCCTGT	CGCAGCCTTT	CGCTGTGGCC	CAGGTCTTCA	CTGGTATCGA	1200
	GGGTCGTCTT	GTGTCGCTCA	AGGACACCAT	CAACGCCTGC	AAGGAGATTC	1250
	TGTCCGGTAA	G				1261

55

2) INFORMATION FOR SEQ ID NO: 486

(i) SEQUENCE CHARACTERISTICS:

- 60 (A) LENGTH: 1282 bases

- (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

5 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Metschnikowia pulcherrima*
 (B) STRAIN: DSM 70336

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 486

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AGGAGGGCAA CTTGCCAGCT ATCTTCAACG CTTTGACGTT GAAGAACGGC      50
GACCAGAAAGT TGGTCTTGGA GGTGGCCAG CACTTGGGTG AGAACACCGT      100
15 CAGAACCATT GCCATGGACG GTACCGAGGG TTTGGTCAGA GGCGCCTCTG      150
TCACCGACAC YGGTGCCCTT ATCTCCGTGC CTGTCGGCCG TGAGACCTTG      200
GGTCGTATTA TCAATGTTGT TGGTGAGCCA ATCGACGAGA GAGGCCCAAT      250
CAACACCAAG AAGAGAAACC CTATTCACAC CGACCCACCT TCGTTTGTCC      300
AGCAATCCAC TTCCGCCGAG GTCTTGGAGA CTGGTATCAA GGTGTGCGAC      350
20 TTGTTGGCCC CTTACGCCAG AGGTGGTAAG ATTGGTTTGT TCGGTGGTGC      400
CGGTGTGCGT AAGACCGTGT TCATCCAGGA GTTGATTAAC AACATTGCCA      450
AGGCCCACGG TGGTTTCTCC GTTTTCACCG GTGTCGGTGA GAGAACCAGA      500
GAGGGTAACG ATTTGTACCG TGAAATGCAG GAGACTGGTG TCATCAACTT      550
CGAGGGTGAC TCCAAGGTCG CCTTGGTTTT CGGTCAGATG AACGAGCCTC      600
25 CAGGAGCTAG AGCYAGAGTT GCCTTGACCG GTTTGACCAT CGCCGAGTAC      650
TTCAGAGACG AGGAGGGTCA GGATGTGTTG TTGTTTCGTCG ACAACATTTT      700
CAGATTCACC CAAGCCGGTT CTGAGGTGTC TGCCCTTGTTG GGTTCGTATTC      750
CATCCGCTGT CGGATACCAG CCAACCTTGG CCACCGATAT GGGTGCCTTG      800
CAGGAGAGAA TTACCACCAC CAAGAAGGGT TCCGTCACCT CCGTCCAGGC      850
30 CGTCTACGTG CCAGCCGATG ACTTGACTGA CCCTGCGCCA GCCACCACTT      900
TCGCCCCTT GGACGCCACC ACTGTGTTGT CCAGAGGTAT CTCTGAGTTG      950
GGTATCTACC CCGCTGTCGA CCCCTTGGAC TCCAACCTCA GATTGTTGGA     1000
CGCCACCGTT GTTGCCAGG AGCACTACGA CGTCGCCACC AACGTCCAGC     1050
AAACTTTACA AGCTTACAAG TCCTTGCAAG ATATCATTCG CATTTTGGGT     1100
35 ATGGATGAGT TGTCCGAGAC CCGACAAGTT GACCCGTCGA GAGAGCCAGA     1150
AAGATCCAGA AGTTCTTGTC CCAGCCATTT GCCGTCGCCG AGGTTTTCAC     1200
CGGTATTGAG GGTAGATTGG TTAGATTGGA GGACACCGTT AGATCCTTTA     1250
AGGAGGTTTT GGAAGGTAAG TACGACCACT TG                                1282

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2) INFORMATION FOR SEQ ID NO: 487

(i) SEQUENCE CHARACTERISTICS:

- 45 (A) LENGTH: 482 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

50 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Penicillium marneffe*
 (B) STRAIN: WSA-214

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 487

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TGTCTTTATC CAGGAGTTGA TTGTACGTCT TTACCTTTCT GCCTGACTGT      50
TTACGACAAC TAACGAAAGC GTAGAACAAC ATTGCCAAGG CTCACGGTGG      100
60 TTA CTCTGTC TTA CTGGTG TCGGTGAACG TACTCGTGAG GGTAACGATT      150

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	TGTACCACGA	AATGCAGGAA	ACTGGTGTCA	TTCAGCTCGA	GGGTGAATCC	200
	AAGGTCGCCC	TCGTGTTCGG	TCAGATGAAC	GAGCCCCCGG	GTGCCCCGTGC	250
	CCGTGTGCGT	CTTACTGGTT	TGACCATTGC	CGAGTACTTC	CGTGACGAGG	300
	AAGGTCAGGA	CGTGCTTCTC	TTCATTGACA	ACATTTTCCG	TTTCACTCAG	350
5	GCCGGTTCTG	AGGTGTCTGC	CCTTCTGGGT	CGTATCCCCT	CTGCCGTCGG	400
	TTACCAGCCC	ACCCTTGCCG	TCGACATGGG	TATCATGCAG	GAGCGTATTA	450
	CCACCACCAC	CAAGGGTTCC	ATCACCTCCG	TC		482

10

2) INFORMATION FOR SEQ ID NO: 488

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1290 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Pichia anomala*
 (B) STRAIN: ATCC 18205

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 488

	TCGAACAAGG	TAACCTACCA	GCTATCTTGA	ATGCTTTAGA	AATCAAAACC	50
	CCAAGTGGTA	CTCCATTAGT	TTTAGAAGTT	GCTCAACATT	TAGGTGAAAA	100
	CACTGTCAGA	ACTATTGCTA	TGGATGGTAC	TGAAGGTTTA	GTTCGTGGTG	150
30	AACAAGTTAC	TGATACTGGT	TCTCCAATCA	CTGTCCCAGT	TGGTCGTGAA	200
	ACTTTAGGTC	GTATTATCAA	CGTTGTTGGT	GAACCAATTG	ATGAACGTGG	250
	TCCAATTAAC	ACCAAACAAA	GAAACCCAAT	TCACGCTGAA	CCACCTTCAT	300
	TCAGTGAACA	ATCAACTGCT	GCTGAAGTTT	TAGAAACTGG	TATCAAAGTT	350
	GTYGATTAT	TAGCTCCATA	CGCTAGAGGT	GGTAAAATTG	GTTTATTTCGG	400
35	TGGTGCCGGT	GTCGGTAAAA	CTGTCTTTAT	CCAAGAATTG	ATTAACAACA	450
	TTGCTAAAG	TCATGGTGGT	TTCTCAGTTT	TCACCGGTGT	TGGTGAAAGA	500
	ACCAGAGAAG	GTAACGATTT	ATACCGTGAA	ATGAAAGAAA	CTGGTGTTAT	550
	TAACCTGGAA	GGTGATTCTA	AGGTCGCTTT	AGTTTTCGGT	CAAATGAATG	600
	AACCACCAGG	TGCTAGAGCT	CGTGTTGCTT	TAACTGGTTT	GACCATTGCT	650
40	GAATACTTCA	GAGATGAAGA	AGGTCAAGAT	GTCTTGTTAT	TCGTTGATAA	700
	CATTTTCAGA	TTCACCCAAG	CCGGTTCAGA	AGTTTCTGCC	TTATTAGGTC	750
	GTATTCCATC	TGCTGTCGGT	TATCAACCAA	CTTTAGCAAC	TGATATGGGT	800
	TTGTTACAAG	AACGTATTAC	CACCACACAA	AAAGGTTTCA	TTACTTCTGT	850
	CCAAGCTGTT	TATGTCCCAG	CTGATGATTT	AACAGATCCT	GCTCCAGCTA	900
45	CCACTTTCGC	CCATTGATG	GCTACTACTG	TCTTGTCTCG	TGGTATTTCA	950
	GAATTAGGTA	TTTACCCAGC	TGTCGATCCA	TTAGATTCTA	AATCAAGATT	1000
	ATTAGATGCT	TCAGTTGTTG	GTCAAGAACA	TTATGATGTT	GCTACCAACG	1050
	TTCAACAAAC	TTTACAAGCT	TACAAATCTT	TACAAGATAT	TATTGCTATT	1100
	TTAGGTATGG	ATGAATTGTC	TGAACAAGAT	AAATTGACTG	TCGAAAGAGC	1150
50	AAGAAAAATC	CAAAGATTCT	TATCTCAACC	ATTTGCTGTT	GCCGAAGTTT	1200
	TCACTGGTAT	YCCAGGTAGA	TTGGTTAGAT	TAAAAGACAC	TATCAAATCA	1250
	TTCAAAGATG	TTTTGGAAGG	TAAATATGAT	CACTTACCAG		1290

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2) INFORMATION FOR SEQ ID NO: 489

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1291 bases
 (B) TYPE: Nucleic acid

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(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

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(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Pichia anomala*

(B) STRAIN: ATCC 2149

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 489

	CCAATTCGAA	CAAGGTA	ACT	TACCAGCTAT	CTTGAATGCT	TTAGAAATCA	50
	AAACCCCAAG	TGGTACTCCA	TTAGTTT	TTAG	AAGTTGCTCA	ACATTTAGGT	100
	GAAAACACTG	TCAGAACTAT	TGCTATGGAT	GGTACTGAAG	GTTTAGTCCG		150
15	TGGTGAACAA	GTTACTGATA	CTGGTTCTCC	AATCACTGTC	CCAGTTGGTC		200
	GTGAAACTTT	AGGTCGTATT	ATCAACGTTG	TTGGTGAACC	AATTGATGAA		250
	CGTGGTCCAA	TTAACACCAA	ACAAAGAAAC	CCAATTCACG	CTGAACCACC		300
	TTCATTCACT	GAACAATCAA	CTGCTGCTGA	AGTTTTAGAA	ACTGGAATCA		350
	AAGTTGTTGA	TTTATTAGCT	CCATACGCTA	GAGGTGGTAA	AATTGGTTTA		400
20	TTCGGTGGTG	CCGGTGTCTG	TAAAACTGTC	TTTATCCAAG	AATTGATTAA		450
	CAACATTGCT	AAAGCTCATG	GTGGTTTCTC	AGTTTTCACC	GGTGTGGTG		500
	AAAGAACCAG	AGAAGGTAAC	GATTTATACC	GTGAAATGAA	AGAAACTGGT		550
	GTTATTA	ACT	TGGAAGGTGA	TTCTAAGGTC	GCTTTAGTTT	TCGGTCAAAT	600
	GAATGAACCA	CCAGGTGCTA	GAGCTCGTGT	TGCTTTAACT	GGTTTGACCA		650
25	TTGCTGAATA	CTTCAGAGAT	GAAGAAGGTC	AAGATGTCTT	GTTATTCGTT		700
	GATAACATTT	TCAGATTCAC	CCAAGCCGGT	TCAGAAGTTT	CTGCCTTATT		750
	AGGTCGTATT	CCATCTGCTG	TCGGTTATCA	ACCAACTTTA	GCAACTGATA		800
	TGGGTTTGTT	ACAAGAACGT	ATTACCACCA	CACAAAAAGG	TTCACTTACT		850
	TCTGTCCAAG	CTGTTTATGT	CCCAGCTGAT	GATTTAACAG	ATCCTGCTCC		900
30	AGCTACCACT	TTCGCCCATT	TGGATGCTAC	TACTGTCTTG	TCTCGTGGTA		950
	TTTCAGAATT	AGGTATTTAC	CCAGCTGTCTG	ATCCATTAGA	TTCTAAATCA		1000
	AGATTATTAG	ATGCTTCAGT	TGTTGGTCAA	GAACATTATG	ATGTTGCTAC		1050
	CAACGTTCAA	CAAACCTTAC	AAGCTTACAA	ATCTTTACAA	GATATTATTG		1100
	CTATTTTAGG	TATGGATGAA	TTGTCTGAAC	AAGATAAATT	GACTGTCGAA		1150
35	AGAGCAAGAA	AAATCCAAAG	ATTCTTATCT	CAACCATTG	CTGTTGCCGA		1200
	AGTTTTCACT	GGTATCCCAG	GTAGATTGGT	TAGATTAAAA	GACACTATCA		1250
	AATCATTCAA	AGATGTTTTG	GAAGGTAAAT	ATGATCACTT	A		1291

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2) INFORMATION FOR SEQ ID NO: 490

(i) SEQUENCE CHARACTERISTICS:

45 (A) LENGTH: 508 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

50

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Rhodotorula minuta*

(B) STRAIN: ATCC 10658

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 490

	CGTATTGATT	CGTGAGTGGC	CGTTCCTTA	CAGCAAGCTT	ATAAAGGAGC	50
	GAAAAAGATC	TGACATTCCG	CTTATGTGCT	ATACAGAGGA	ACTCATCAAC	100
	AACGTCGCCA	AGGCTCATGG	TGGTTACTCT	GTCTTCACCG	GTGTCGGAGA	150
60	GCGAACACGT	GAAGGTAACG	ATCTCTACCA	CGAAATGATT	GAAACCGGTG	200

	TCATTACGCT	CAAGAACGAC	AAGTCCAAGG	CCGCTCTGGT	CTTCGGACAG	250
	ATGAACGAGC	CCCCCGGAGC	TCGTGCCCCG	GTCGCTCTGA	CCGGTCTCAC	300
	CATCGCCGAG	TACTTCCGTG	ACGTCGAAGG	ACAGGATGTG	CTACTCTTCA	350
	TCGACAACAT	TTTCCGATTC	ACCCAGGCCG	GTTCAGAGGT	ATCTGCCCTG	400
5	CTCGGACGTA	TCCCATCTGC	TGTCGGATAC	CAGCCCACAC	TCTCAACCGA	450
	TATGGGTGGT	ATGCAAGAGC	GAATCACAAC	CACCAAGAAG	GGTTCGATTA	500
	CCTCCGTC					508

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2) INFORMATION FOR SEQ ID NO: 491

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 686 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Rhodotorula mucilaginosa*
 (B) STRAIN: ATCC 66034

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 491

	TGTCCTCATT	CAGGAGCTCA	TCAACAACAT	CGCCAAGGCC	CACGGTGGTT	50
	ACTCGGTCTT	CACCGGTGTC	GGCGAGCGTA	CCCGTGAGGG	TAACGGTGAG	100
	TCTCCCCCTT	CAAACCTTTG	GCCGGCTAGT	TGGCGCAGCG	CAAACCTGACG	150
30	CGCGCGCCCT	GTCCAGACTT	GTACCACGAG	ATGATCGAGA	CTGGTGTCAT	200
	CCAGCTCGAG	AACGACAAC	CGAAGTGCGC	TCTCGTGTTT	GGCCAGATGA	250
	ACGAGCCCCC	TGGTGCCCCG	GCCCCGTGTC	CTCTCACTGG	GTTCTGTCCTT	300
	TCTCTCTCTC	GAGCGTCCTG	GCTTGATACG	GAACGCTGAC	ACGTCACGCA	350
	GTCTCACTAT	TGCTGAGTAC	TTCCGTGACG	AGGAGGGCCA	GGACGTGCTC	400
35	CTCTTCATCG	ACAACATCTT	CCGTTTCACC	CAGGGTGAGC	CGCCTCCGCG	450
	GGCATTCTCC	CGTTTCTTTC	GCGCTGACGT	CTGTCCCGTA	TAGCCGGTTC	500
	GGAGGTGTCT	GCCCTTCTCG	GACGTATCCC	GTCCGCTGTC	GGATACCAGC	550
	CGACTCTCTC	GACCGACATG	GGTCAGATGC	AGGAGCGTAT	CACGTAAGTT	600
	TGGCCGCGAG	TCCGTCCGCG	GCGCCCTTTG	TGTCTGACCG	TGTTCCACCG	650
40	CTCAGCACCA	CCAAGAAGGG	CTCGATCACC	TGTGTC		686

2) INFORMATION FOR SEQ ID NO: 492

45

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 625 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Sporobolomyces salmonicolor*
 (B) STRAIN: ATCC 32311

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 492

60	TGTCTTGATT	CAGGAGCTCA	TCAACAACGT	CGCCAAGGCG	CACGGTGGTT	50
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	ACTCCGTTTT	CACCGGTGTC	GGTGAGCGTA	CCCGTGAGGG	TAACGGTGAG	100
	CACACTTTTCG	CCGACCTGGC	CATTCCGGAA	CGTGCGGACT	GACGAGGACC	150
	ACCTCGAACA	GATCTCTACC	ACGAGATGAT	CGAGACCGGT	GTCATTTCAGC	200
	TCGACAACGA	CAAGTCGAAG	ACTGCTCTCG	TCTTCGGCCA	GATGAACGAG	250
5	CCCCCTGGCG	CCCGTGCCCG	TGTCGCTCTT	ACTGGTCTCA	CCATCGCGGA	300
	GTACTTCCGT	GACGACGAGG	GCCAGGACGT	GCTTCTCTTC	ATCGACAACA	350
	TCTTCCGTTT	CACCCAGGGT	ACGTTTCGATC	CCGCCCCGTCC	AACACGAATG	400
	TCGTGGTGAC	TGACAACCTG	TTGCGCGTGC	AGCCGGTTCG	GAGGTGTCTG	450
	CCTTTCTCGG	TCGTATCCCG	TCCGCTGTGC	GATACCAGCC	CACTCTCTCG	500
10	ACCGACATGG	GTGGCATGCA	GGAGCGTATC	ACGTACGCCC	TCTTCTGCTT	550
	TCTCTCGTTT	CGCTCTGCAT	CGCTCACGCA	TGTTTCGCCCC	ACAGCACCAC	600
	CAAGAAGGGT	TCGATCACCT	GTGTC			625

15

2) INFORMATION FOR SEQ ID NO: 493

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 1211 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

25 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Sporothrix schenckii*
 (B) STRAIN: WSA-148

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 493

	TCTCGTCCGT	GGTGCTAAGG	CCACTGACAC	TGGTTCCCCC	ATTACCATCC	50
	CCGTCGGCCC	CGGTACCCCTC	GGTCGCATCA	TGAACGTCAC	CGGTGACCCG	100
35	ATCGACGAGC	GCGGTCCCAT	CAAGACCGAC	AAGTTCCGTC	CCATCCACGC	150
	TGAGGCTCCC	GAGTTCGTTG	ACCAGTCGAC	CACCGCTGAG	GTTCTCGTGA	200
	CTGGTATCAA	GGTCGTCGAT	CTGCTTGCTC	CCTACGCCCC	TGGTGGAAG	250
	ATTGGTCTGT	TTGGCGGTGC	CGGTGTTGGC	AAGACCGTGT	TCATCCAGGA	300
	GCTCATCAAC	AACATCGCCA	AGGCCCCACG	TGGTTACTCC	GTCTTCACCG	350
40	GTGTCGGCGA	GCGTACCCGT	GAGGGTAACG	ATCTGTACCA	CGAAATGCAG	400
	GAGACCTCTG	TCATTACAGCT	TGACGGTGAC	TCCAAGGTTCG	CCCTGGTGTT	450
	CGGTGAGATG	AACGAGCCCC	CTGGTGCTCG	TGCCCCGTGTC	GCCTTGACCG	500
	GTTTGACTGT	CGCTGAGTAC	TTCCGTGACG	AGGAGGGCCA	GGATGGTATG	550
	TTTTGAATTA	TTTCCTTGTC	GTACAGTTCC	AAATCGAAGA	ATTACTAACT	600
45	TGTCAGTGCT	TCTCTTCATC	GACAACATTT	TCCGCTTCAC	CCAGGCCCGT	650
	TCTGAGGTGT	CTGCCCTTCT	GGGTCGTATT	CCCTCCGCTG	TCGGTTACCA	700
	GCCCCACGCTC	GCCGTGGACA	TGGGTCTGAT	GCAGGAGCGT	ATTACCACCA	750
	CCCGCAAGGG	CTCAATTACC	TCCGTCCAGG	CCGTCTACGT	GCCCCGCTGAC	800
	GATCTGACGG	ATCCCGCCCC	CGCCACCACC	TTCGCCCATC	TGGACGCCAC	850
50	CACTGTGCTG	TCCCGAGGTA	TCTCTGAGCT	GGGTATCTAC	CCCGCTGTCTG	900
	ACCCCTCGA	CTCCAAGTCG	CGTATGCTGG	ACCCCGTAT	TGTCGGTGAC	950
	GACCACTACG	AGACCGCCAC	TCGCGTCCAG	CAGATCCTCC	AAGAGTACAA	1000
	GTCGCTGCAG	GACATCATCG	CCATTCTGGG	TATGGACGAG	CTGTCTGAGG	1050
	CCGACAAGCT	TACAGTCGAG	CGTGCTCGTA	AGATCCAGCG	TTTCCTGAGC	1100
55	CAGCCGTTCA	CGGTGCGGCA	GGTCTTCACT	GGTATCGAAG	GCCAGCTGGT	1150
	CGATCTGAAG	GACACTATCG	CTTCGTTCAA	GGCTATCCTG	AGCGGTGAGG	1200
	GTGACAGCCT	T				1211

60

2) INFORMATION FOR SEQ ID NO: 494

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 1133 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

10 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Stephanoascus ciferrii*
(B) STRAIN: ATCC 52550

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 494

TCTTGTTAGA GGCACCCAG TCAAGGACAC TGGTGCTCCA ATTACCATT 50
CAGTTGGTAA CGGCACTTTG GGCCGTATCG TCAACGTTCT CGGTGAGCCA 100
ATTGATGAGC GTGGACCACT CAAGGCTGAC AAGTTCAGAC CTATTCACGC 150
20 TGAGCCACCA ACCTTCGCTG ACCAGTCCAC CTCTGCCGAG GTTCTTGAGA 200
CCGGTATTAA GGTGTGCGAC TTGCTTGCCC CTTATGCCAG AGGTGGTAAG 250
ATTGGTCTTT TCGGTGGTGC CGGTGTGCGT AAGACTGTGT TCATTGAGGA 300
GCTTATTAAC AACATTGCTA AGGCCACCG TGGTACTCT GTCTTCACTG 350
GTGTCGGTGA GCGAACTCGT GAAGGTAACG ATTTGTACCA CGAAATGATG 400
25 GAGACCGGTG TCATCAACCT TGAGGGTGAC TCCAAGGTGT CTCTTGTGTT 450
CGGTCAGATG AACGAGCCTC CAGGAGCCCG TGCCCGTGTT GCCTTGACCG 500
GTTTGACCAT TGCCGAGTAC TTCAGAGATG AGGAGGGCCA GGATGTCTTG 550
TTGTTTCATTG ACAACATTTT CCGATTCACC CAGGCCGGTT CTGAGGTCTC 600
TGCCTTGTTG GGTCGTATCC CATCTGCCGT CGGTTACCAA CCAACCTTGG 650
30 CTA CTGATAT GGGTGGTCTT CAAGAACGTA TTACCACCAC TCAAAAGGGT 700
TCCGTACACT CTGTCCAGGC TGTCTACGTC CCAGCTGACG ATTTGACTGA 750
TCCTGCCCCA GCTACCACCT TCGCCCATTT GGACGCCACC ACCGAATTGT 800
CCCGATCTAT CTCTGAGTTG GGTATCTACC CAGCTGTCGA CCTCTTGGT 850
TCCAAGTCCC GTCTTTTGA TGCCTCCGTC GTCGGCCAAG AGCACTACGA 900
35 CGTTGCCGCC AACGTCCAAC AGACCTTGCA GGCTACAAG TCTCTCCAGG 950
ATATCATTGC CATTTTGGGT ATGGACGAAT TGTCTGAGGC TGATAAGCTC 1000
ACTGTCGAGC GTGCTCGTAA GATGCAGAGA TTCCTTTCTC AGCCATTAC 1050
CGTCGCTGAG GTCTTCACTG GTCTCGAGGG TAGACTCGTT TCTTTGAAGG 1100
ACACCATCCG ATCCTTCAAG GAGATCCTTG ACG 1133
40

2) INFORMATION FOR SEQ ID NO: 495

(i) SEQUENCE CHARACTERISTICS:

- 45 (A) LENGTH: 608 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

50 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 55 (A) ORGANISM: *Trichophyton mentagrophytes*
(B) STRAIN: WSA-225

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 495

GGAGTTGATT GTAAGTCATT TGAAACCCAG CCCCAAGAAA CAGAAGCTAG 50
60 GCGAAAATTG GACAATTGAG CAATTTAGCC ATTGGAGAAA AGAAATTTCC 100

	AGTATTAATT	GTTTTTATAG	AACAACATTG	CCAAGGCTCA	CGGTGGTTAC	150
	TCTGTCTTCA	CTGGTGTCCG	AGAGCGTACC	CGTGAAGGAA	ACGATCTCTA	200
	CCATGAAATG	CAGGAGACCC	GTGTCAATTCA	GCTTGATGGC	GAGTCCAAGG	250
	TCGCCCTGGT	CTTCGGCCAG	ATGAACGAGC	CCCCAGGTGC	CCGTGCCCCG	300
5	GTTGCTCTTA	CTGGTTTGAC	CATTGCTGAG	TACTTCCGTG	ATGAGGAAGG	350
	TCAAGACGGT	GAGTTTCTTA	TGGATAAAAA	AAAATTTTTT	TTTTTTTTTT	400
	TTTTTTTCAA	GAAATTCATG	TTCTAACAAA	GTGTATTCTA	GTGCTTCTCT	450
	TCATCGACAA	CATTTTCCGT	TTCACCTCAGG	CTGGTTCCGA	AGTGTCTGCC	500
	CTGCTTGGTC	GTATCCCATC	TGCCGTCGGT	TACCAACCCA	CTCTTGCCGT	550
10	CGACATGGGT	GGTATGCAGG	AACGTATTAC	CACCACCAAG	AAGGGATCCA	600
	TTACCTCC					608

15 2) INFORMATION FOR SEQ ID NO: 496.

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 794 bases
 (B) TYPE: Nucleic acid
 20 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

25 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Wangiella dermatitidis*
 (B) STRAIN: WSA-229

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 496

30	GTTTATTCAA	GAATCATTG	TGGGTGGCAT	TCTCATAATG	TTTCGGCCAC	50
	AATTACTGAT	TGAAAATAGA	ACAACATTGC	AAAGGCTCAT	GGTGGTTACT	100
	CCGTGTTTAC	TGGTGTCCGC	GAGCGAACTC	GTGAGGGTAA	CGACTTGTAC	150
	CACGAAATGC	AGGAGACCTC	TGTCATTGAG	CTCGATGGCG	AGTCCAAGGT	200
35	CGCGCTGGTG	TTTGGTCAAA	TGAACGAACC	TCCTGGTGCT	CGTGCTCGTG	250
	TTGCTCTGAC	TGGGTAAGTT	GTTCTTTCGC	TTCTTGCGCG	TATCCACATC	300
	CCCATCTTGA	GAATACGTCT	GCCACCATGT	CATGTGATGT	TGGGCTGGTT	350
	CTGGTTTTTTG	GGAGGCCCTC	AAGTTCAATT	TTTGGATGAC	AGCACCAGCT	400
	TTACAAGATT	ATGCTAACTT	AATGGAGTCT	TACGGTGGCT	GAGTTCCTCA	450
40	GGGATGAGGA	GGGACAGGAT	GGTAAGTTTG	ATAACAATCT	CGTCGGTGTC	500
	AATATCGACG	GCGTACTCTT	CGCATCAAAA	AACCAAAGAG	GTGGTTTGGT	550
	GTGAGAAGTG	CGCCGGAAT	AATGGCAACC	ACGTGACAAT	GACCACGTGT	600
	GGGGCTCCCG	TGCTAACACG	TGACAGTCTT	GCTCTTCATC	GACAACATTT	650
	TCCGATTAC	TCAASCCGGT	TCTGARGTGT	CTGCCTTGCT	TGGTCGTATT	700
45	CCATCTGCCG	TCGGTTACCA	ACCCACACTC	GCCGTCGACA	TGGGTCTCAT	750
	GCAGGAACGT	ATCACCACCA	CCCGGAAGGG	ATCCATCACA	TCTG	794

50 2) INFORMATION FOR SEQ ID NO: 497

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1148 bases
 (B) TYPE: Nucleic acid
 55 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

60 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Yarrowia lipolytica*
 (B) STRAIN: ATCC 38295

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 497

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5      TCTTGTCCGA GGCACCGCCG TCGCTGACAC CGGTGCTCCC ATCACTATCC      50
      CCGTCGGCCG AGGTACCCTT GGTCGAATCA TCAACGTCTG TGGTGAGCCC      100
      ATTGACGAGC GAGGACCCAT CGAGGCTTCC AAGTACCTCC CCATCCACGC      150
      TGACCCCCCT ACCTTCGCTG AGCAGTCTAC CTCCGCTGAG GTTCTCGAGA      200
10     CCGGTATTAA GGTCGTCGAC CTCCTCGCCC CTTACGCCCC AGGTGGTAAG      250
      ATTGGTCTCT TCGGTGGTGC CGGTGTCGGT AAGACTGTCT TCATCCAGGA      300
      GCTGATTAAAC AACATTGCCA AGGCCCATGG TGGTTTCTCC GTTTTCTGCG      350
      GTGTCGGTGA GCGAACCCGA GAGGGTAACG ATCTTTACCG AGAGATGAAG      400
      GAGACTGGTG TCATCAACCT CGAGGGTGAG TCTAAGGTCA CCCTCGTCTT      450
15     CGGTCAGATG AACGAGCCTC CCGGAGCCCG TGCCCGAGTC GCCCTTACTG      500
      GTCTGACCAT TGCCGAGTAC TTCCGAGACG AGGAGGGTCA GGATGTGTTG      550
      CTCTTCGTTG ACAACATTTT CCGATTACCC CAGGCCGGTT CCGAGGTGTC      600
      CGCTCTGCTT GGTCTGAATTC CCTCCGCTGT CGGTTACCAG CCCACTCTGG      650
      CCACCGATAT GGGTGCCCTC CAGGAGCGAA TTACCACCAC CCAGAAGGGT      700
20     TCCGTCACCT CCGTCCAGGC CGTCTACGTG CCTGCCGATG ATTTGACCGA      750
      TCCTGCTCCC GCCACCACCT TCGCCCATCT TGACGCCACC ACCGTCTCTG      800
      CCCGAGGTAT TTCCGAGCTG GGTATCTACC CCGCTGTCGA TCCCCTTGAT      850
      TCCAAGTCTC GACTTCTGGA TATCGATGTT GTCGGAAAGG AGCACTACGA      900
      TGTTGCTTCC AACGTCCAGC AGACCCCTCA GGCTTACAAG TCTCTCCAGG      950
25     ATATCATTGC CATTCTTGGT ATGGATGAGC TGTCCGAGCA GGACAAGCTG      1000
      ACCGTCGAGC GAGCTCGAAA GATCCAGCGA TTCTGTCTC AGCCCTTCAC      1050
      CGTCGCCGAG GTTTTCACCG GTATTGAGGG ACGACTTGTC TCTCTCAAGG      1100
      AACTGTCCG ATCCTTCAAG GAGATCCTTG ACGGTAAGCA CGATGCTC      1148
  
```

30

2) INFORMATION FOR SEQ ID NO: 498

(i) SEQUENCE CHARACTERISTICS:

```

35     (A) LENGTH: 966 bases
      (B) TYPE: Nucleic acid
      (C) STRANDEDNESS: Double
      (D) TOPOLOGY: Linear
  
```

40 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Aspergillus fumigatus*
 (B) STRAIN: WSA-172

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 498

```

      GCGCTATTGT CGTTGTTGCT GCCTCCGACG GTCAGATGTA GGTGGAACAT      50
      CTTGGGAAAT ACGTCGTAAA ACACGTCGCT TACGTTTTCG CGAATAGGCC      100
50     CCAGACTCGT GAGCATTGTC TGCTCGCCCG CCAGGTGGT GTCCAGAAGA      150
      TCGTTGTCTT CGTCAACAAA ATCGATGCTA TTGATGATCC GGAGATGCTG      200
      GAACTGGTCG AACTCGAGAT GCGTGAGCTG CTGAACAGCT ACGGTTTCGA      250
      GGGTGAAGAG ACTCCGATCA TTTTCGGTTC CGCTCTCTGT GCTCTCGAAG      300
      GACGCCGTGA CGACATCGGT AAAGACAGAA TTGAGCAGCT TATGAACGCT      350
55     GTCGACACCT GGATCCCCAC TCCTCAGCGT GACCTCGACA AACCTTTCTT      400
      GATGTCTGTC GAGGAAGTGT TCTCTATCGC CGGCCGTGGT ACCGTGGCTT      450
      CTGGTCGTGT CGAGCGTGGT ATCTTGAAGA AGGACTCTGA GGTGAGATT      500
      GTTGGAGGCT CCTTCGAACC CAAGAAGACC AAAGTCACCG ACATTGAAAC      550
      CTTCAGAAG AGCTGTGATG AATCGCGTGC TGGTGACAAC TCTGGTCTCC      600
60     TCCTGCGTGG TATCCGACGT GAAGACGTCA AGCGTGGTAT GGTCAATTGCT      650
  
```

	GTTCCCGGCA	GCACCAAGGC	TCACGACAAG	TTCCTCGTCT	CCATGTACGT	700
	CCTGACCGAG	GCGGAGGGTG	GTCGTCGTAC	TGGCTTCGGT	GCCAACTACC	750
	GTCCCCAAGT	CTTCATCCGT	ACTGCAGGTA	AGTTCCCGCA	CACCGTGTCC	800
	AGATCTTCCG	AGAGATTAGC	GATATATGCT	AATGATTCAT	CAGACGAGGC	850
5	TGCTGACCTC	AGCTTCCCTG	ACGGCGACCA	ATCTCGCAGA	GTTATGCCTG	900
	GTGACAACGT	CGAGATGATC	CTGAAGACCC	ACCACCCTGT	TGCTGCTGAG	950
	GCTGGTCAAC	GCTTCA				966

10

2) INFORMATION FOR SEQ ID NO: 499

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 846 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

20

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Blastoschizomyces capitatus*
 (B) STRAIN: ATCC 10663

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 499

	TGGTGCTATT	ATTGTTGTTG	CTGCTTCTGA	TGGTCAAATG	CCCCAAACCC	50
	GTGAGCACTT	GCTTCTTGCT	CGTCAAGTTG	GTGTTAAGCA	CATTGTTGTT	100
	TTCGTTAACA	AGATTGATAC	TATTGATGAT	CCTGAAATGT	TGGAACCTGT	150
30	CGAAATGGAA	ATGAGAGAAC	TTCTTTCTTC	TTACGGTTTT	GATGGCGATA	200
	ACACCCCTGT	CATTATGGGT	TCTGCTCTCT	GTGCTCTTGA	AGGTCGTGAA	250
	CCAGAAATTG	GTGAACAAAG	AATCAACCAA	CTCCTTGATG	CTATCGATGA	300
	ATACATTCTT	ACCCAGTTC	GTGATATGGA	CCAACCTTTC	TTGATGCCAC	350
	TTGAAGGTGT	TTTCTCTATT	CCAGGTCGTG	GTACTGTTGC	CACTGGACGT	400
35	GTCTATCGTG	GTACTTTGAA	GAGAGGTGAA	GAAGTTGAAG	TTGTTGGCTA	450
	CAATGATGCT	CCAATCAAGA	CCACCGTTAC	TGGTATTGAA	ATGTTCAAGA	500
	AGGAAGTTGA	TCAAGCTCAA	GCTGGTGACA	ACGCTGGTAT	TCTTTTGAGA	550
	GGTGTTAAGC	GTGAAGACCT	TAAGCGTGCT	ATGGTTGTTG	CTAAACCAGG	600
	TACCGTTAAG	CCACACACCA	AGTTCCCTTG	CTCCATCTAT	GTTTTGACTA	650
40	AGGAAGAAGG	TGGCAGACAC	TCTGGCTTTG	GTCTTAACTA	CAGACCTCAA	700
	CTTTTCCTTG	GTTCTGCTGA	TGTTACCACT	GTCTTGACCT	TCCCAGAGGG	750
	TGTTGACCAA	AGCACTCAAG	TCATGCCAGG	TGACAACACT	GAAATGGTTT	800
	GCGAACTTGT	TCACCCAGTT	GCTGTGGAAC	AAGGCCAACG	TTTCAA	846

45

2) INFORMATION FOR SEQ ID NO: 500

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 846 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

55

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Candida rugosa*
 (B) STRAIN: ATCC 96275

60

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 500

	GGTGCCATTA	TTGTTGTTGC	TGCCTCTGAT	GGACAGATGC	CCCAGACCCG	50
	TGAGCATCTT	TTGCTTGCCC	GCCAAGTCGG	TATGCAAAAG	GTCGTTGTGT	100
5	TTGTTAACAA	GATTGATACC	ATTGATGACC	CTGAAATGCT	TGATCTTGTC	150
	GAGATGGAGA	TGCGTGAACT	GTTGAATGAA	TATGACTTCG	ATGGAGATAA	200
	CTCTCCTGTC	ATTATGGGCT	CTGCTCTTGC	TGCTCTTGAG	GACAAGAACC	250
	CCGAGATTGG	TAAGGACCGT	ATCATGCAGC	TCTTGGACGC	TGTTGATGAA	300
	TGGATCCCTA	CCCCCGAGCG	TGACCTTGAC	AAGCCTTTCA	TGATGCCTAT	350
10	TGAGGCCTCT	TTCTCCATTT	CTGGTCGTGG	TACTGTTGCC	ACTGGCCGTG	400
	TCGAGCGTGG	TATTCTCAAG	AAGGGTGAGG	AAGTCGAGAT	CGTTGGTTTC	450
	AACAAGCAGC	CCCTGAAATC	TGTTGTTACT	GGTATTGAAA	TGTTCAAGAA	500
	GGAACCTTGAT	CAGGCCCAGG	GCGGTGATAA	TGCTGGTATC	TTGCTTCGTG	550
	GTATTTCGTC	TGAGGACTTG	CAGCGTGTA	TGGTTTTGGC	CAAGCCTGGA	600
15	ACTGTTAAGG	CTCACACCAA	GTTCCCTTCC	TCCATCTACG	TTCTCTCCAA	650
	GGAAGAGGGC	GGCCGTCACT	CTCCTTTCGG	TATGAACTAT	CGTCCCCAGA	700
	TGTTTCGTTT	TGCAGCTGAT	GTCACCGTTA	CTCTTACTTT	CCCTGAGGGT	750
	GTTGAACAGC	ACACTCAGGT	CTTCCCTGGT	GAGAACACCG	AGATGGTTGG	800
	CGAGCTCGTT	CACCCTACTG	CTATTGAGGT	TGGTCAACGC	TTCAAC	846

2) INFORMATION FOR SEQ ID NO: 501

25 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 944 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

30

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Coccidioides immitis*
 (B) STRAIN: Silveira

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 501

	AGTTGTCGTC	GTTGCTGCTT	CAGACGGTCA	AATGTATGCA	ACCGAGAGCA	50
40	CTCCCGGATC	TTGGTTTAAA	TGGCACTAAT	ATAAGACAGG	CCTCAAACCTC	100
	GAGAGCATTT	ACTTCTCGCC	CGTCAGATCG	GTATCCAAAA	AATCGTCGTC	150
	TTCGTGAACA	AGGTTGATGC	CATCGAGGAC	AAAGAGATGT	TGGAGCTTGT	200
	TGAATTGGAG	ATGCGTGAAC	TCCTAACCAG	CTACGGTTTC	GAGGGTGAAG	250
	AAACTCCCAT	CATTTTTTGGC	TCTGCTCTCT	GTGCCCTCGA	AGGAAGACAA	300
45	CCCGAGATCG	GTGTTACCAA	GATTGATGAG	CTCTTGACAG	CCGTCGACAC	350
	CTGGATTCCC	ACTCCTCAGC	GTGAGACTGA	CAAGCCCTTC	TTGATGTCCA	400
	TTGAGGAAGT	GTTCTCTATT	TCCGGACGAG	GAACCGTTGT	CTCCGGCCGT	450
	GTGGAGCGTG	GTATCCTCAA	GAAGGACTCC	GAAGTTGAAA	TTGTCGGCGG	500
	TTCGCCCCGAG	CCAATCAAAA	CCAAGGTTAC	CGATATCGAA	ACCTTTAAGA	550
50	AGTCTTGCGA	CGAGTCTCGC	GCTGGTGATA	ACTCCGGCTT	GCTCCTACGA	600
	GGCGTTAAGC	GTGAAGATAT	TAGCCGTGGC	ATGGTCGTCG	CTGTACCAGG	650
	AAGTGTC AAG	GCCCATACTG	AATTCTTAGT	TTCGCTTTAC	GTCCTCACCG	700
	AAGCTGAGGG	TGGGCGCAAA	TCTGGATTCA	GCAGCAAGTA	CCGCCCACAG	750
	ATGTTTCATTC	GCACTGCCCG	TATGTAATAC	TGTGATAATT	TCGTTGACAT	800
55	GGTACTGATT	GAATTCTATA	GACGAAGCGG	CTCAGCTCAG	CTGGCCCGGA	850
	GAAGATCAAG	ACAAGATGGC	TATGCCAGGA	GACAATATCG	AAATGATTTG	900
	CACCACCTTG	CACCCAGTTG	CCGCCGAGGC	TGGCCAGCGA	TTCA	944

60

2) INFORMATION FOR SEQ ID NO: 502

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 849 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Fusarium oxysporum*
 (B) STRAIN: WSA-212

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 502

```

GCTATCATCG TCGTTGCTGC CTCCGATGGA CAGATGCCCC AGACCCGTGA      50
ACACTTGCTC CTCGCTCGTC AGGTCGGTGT CCAGCGAATT GTCGTCTTCG      100
TCAACAAGGT CGATGCCATT GATGACCCCG AGATGCTTGA GCTCGTCGAG      150
20 ATGGAGATGC GCGAGCTTCT TAACACCTAC GGCTTCGAAG GCGACGACAC      200
TCCCGTCATC ATGGGCTCTG CTCTTATGTC TCTCCAGAAC CAGCGCCCCG      250
AGATTGGCAC CGAGAAGATC GATGAGCTCC TTGCTGCCGT CGACGAGTGG      300
ATCCCAACCC CCGAGCGTGA CCTTGACAAG CCCTTCCTTA TGTCCGTCGA      350
GGATGTCTTC TCCATTGCCG GCCGTGGTAC CGTCGTGTCT GGCCGTGTGG      400
25 AGCGTGGTAT TCTGAAGCGT GATCAGGAGA TCGAGCTTGT CGGAAAGGGG      450
CAGGAGGTTA TCAAGACCAA GGTTACCGAC ATTGAGACCT TCAAGAAGTC      500
TTGTGAGCAG TCCCAGGCTG GTGACAAC TC TGGTCTCCTC ATCCGAGGTG      550
TTCGCCGTGA GGATGTCCGC CGTGGTATGG TTGTCTGCGC TCCTGGCACC      600
GTCAAGTCTC ATACCCAGTT TCTCGCTTCC CTCTACGTCC TCACCAAGGA      650
30 GGAGGGTGGC CGACACACCG GTTTCCAGGA GCACTACCGA CCCCAGCTCT      700
ATCTCCGAAC TGCAGATGAG TCCATTGACC TGACTTTCCC CGAGGGTACT      750
GAGGATGCCT CCAGTAAGAT GGTGCATGCCT GGTGACAACA CCGAGATGGT      800
TGTCACCATG GGTCAACCCA ATGCCATCGA GGTGGTGCAG CGATTCAAC      849

```

35

2) INFORMATION FOR SEQ ID NO: 503

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1064 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

45 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Histoplasma capsulatum*
 (B) STRAIN: G186A5

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 503

```

TGGTGCTATT GTCGTTGTTG CTGCTGCTGA CGGCCAAATG TAAGACGCCG      50
CGAGGGACTG CTGAGGGTTT TATGCTTTT AGGCCCCCTT GTTTCTGAGA      100
55 GCATGATGAT ACTAATATTC GGAAACGTAT CTATTAGGCC TCAAACACGT      150
GAGCATTTCG TCCTTGCCCG ACAGGTCGGT GTCCAAAAGA TCGTCGTTTT      200
CGTGAACAAA GTCGACGCCC TTGAGGACAA GGAGATGTTG GAGCTTGTCG      250
AGTTAGAAAT GAGAGAGCTC TTAAACACCT ACGGCTTCGA GGGTGAAGAG      300
ACACCCATCA TCTTTGGTTC TGCCCTTTGC GCCATGGAAG GCCGTGAGCC      350
60 TGAGTTGGGA GAAAAGAAAA TTGATGAATT GCTGGAGGCT GTTGATACTT      400

```

	GGATCCCCAC	ACCACAACGT	GATACCGAAA	AACCTTTCTT	GATGTCCGTT	450
	GAGGAAGTAT	TCTCTATCTC	CGGCCGTGGA	ACCGTTGCCT	CCGGTCGTGT	500
	TGAGCGCGGT	GTCCTCAAGA	AGGATTGAGA	AGTCGAGCTA	ATTGGGGGCG	550
	GCTCCACCCC	CATCAGGACG	AAGGTAAGTG	ATATCGAAAC	TTTCAAGAAA	600
5	TCCTGTGACG	AGTCTAGAGC	TGGGGACAAC	TCCGGTCTTT	TATTGCGTGG	650
	TATCAAGCGT	GAAGATATCC	GCCGTGGTAT	GGTAGTTGCC	GTTCCTGGCA	700
	GCGTCAAGGC	CCACGACAAG	TTCTTGGTGT	CGATGTATGT	CCTGACCGAA	750
	GCTGAGGGTG	GTCGCCGAAC	CGGATTGCGC	CAGAACTATC	GTCCTCAAAT	800
	GTTTCATCCGC	ACAGCTGGTA	TGTCAAAATG	GGACCCCTTT	TCATAATCCT	850
10	TTCTTTTTTT	CCTTTTCCTC	TCTATCTCTC	TTTCTGTTTC	CTTTCAACTC	900
	GCCTGATTCA	CGAAATTAAC	TAACCCGTTT	GATTATAGAC	GAAGCCGCCC	950
	ATCTCAGCTT	CCCTAGTGGA	GCAGATGAAA	GCAAACCTCGT	TATGCCTGGT	1000
	GACAACGTCG	AGATGATCCT	CCAGACACAC	CGCCCCGTGG	CTGCTGAGGC	1050
	CGGCCAGCGA	TTCA				1064

15

2) INFORMATION FOR SEQ ID NO: 504

20 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 982 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

25

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Paracoccidioides brasiliensis*
- (B) STRAIN: ATCC 32071

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 504

	TGGTGCTATC	GTCGTTGTTG	CTGCCTCTGA	CGGCCAAATG	TAGGGATTTT	50
35	GCAAGACTGG	TGAAAAAATC	TAAAGAAAAT	AGAAAAGATT	GTGCTGATGT	100
	TTGGTATCAG	GCCCCAAACA	CGCGAGCATC	TGCTTCTTGC	CAGACAAGTC	150
	GGTGTTCAGA	AAATCGTTGT	TTTCGTCAAC	AAGGTCGATG	CTGTAGAGGA	200
	TAAGGAGATG	TTGGAGCTTG	TGCAATTGGA	GATGAGAGAG	CTCTTGACCA	250
	CCTATGGGTT	CGAGGGTGAG	AAGACACCTA	TCATCTTTGG	TTCTGCGCTC	300
40	TGTGCTATGG	AGGGCCGTCA	GCCCGAGTTG	GGAGAGCAGA	AAATTGATGA	350
	ATTACTCGAG	GCTGTGGATA	CTTGGATCCC	TACGCCACAG	CGTGATACTG	400
	ACAAGCCCTT	CCTGATGTCC	ATTGAGGAGG	TGTTCTCTAT	CTCTGGACGA	450
	GGAACCGTTG	CCTCCGGCCG	CGTTGAGCGT	GGTATCCTCA	AGAAGGACTC	500
	CGAAGTTGAA	ATTATTGGCG	GCGGTGTTCC	CACAATCCTG	ACCAAGGTGA	550
45	CTGATATCGA	AACCTTCAAG	AAGTCTTGCG	ACGAGTCCAG	AGCCGGGGAC	600
	AACTCCGGCC	TCTTGTTGCG	CGGTGTCAAG	CGTGAGGATA	TCCGCCGTGG	650
	TATGGTCGTT	GCAGTTCCCG	GAAGCGTCAA	AGCACATGAC	AGATTCTTGG	700
	TGTGATGTA	CGTTCTGACC	GAGGCTGAGG	GTGGTCGCCG	CACTGGCTTC	750
	GGTCAGAACT	ATCGTCCTCA	AATGTTTCATC	CGCACAGCTG	GTACGTTTCA	800
50	TCTTTCACTA	TATTCCTATA	TGCATAGCCC	GATCCTCCCA	TTAACTAATT	850
	GACACAGACG	AGGCTGCTGA	ACTCAGCTGG	CCTGATGGAG	ACGACGAAGC	900
	CAAAATGGTC	ATGCCCGGTG	ACAATGTTGA	AATGGTCCTG	AAGTCACACC	950
	GCCCCGGGCC	GCTGAGGCTG	GACAGCGATT	CA		982

55

2) INFORMATION FOR SEQ ID NO: 505

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 931 bases

60

- (B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

5 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Penicillium marneffe*
(B) STRAIN: ATCC 58950

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 505

	CGCTGTTGTT	GTCGTCGCTG	CTTCTGATGG	TCAAATGTAA	CATATCCACG	50
	AGCTGCCAAT	TATGGACACT	GCTGATAAGA	ATAGGCCCCA	AACCCGTGAG	100
15	CACTTGCTCC	TCGCCCCGTC	GGTCGGTGTT	CAAAAGATCG	TCGTCTTCGT	150
	CAACAAGGTT	GATGCCGTCG	AGGACCCCGA	GATGTTGGAA	CTTGTCGAAT	200
	TGGAAATGCG	TGAACTCTTG	ACCACCTACG	GTTTCGAGGG	TGAAGAGACC	250
	CCTATCATTT	TCGGATCCGC	TCTTTGCGCC	TTGGAAGGCC	GCAAGCCCGA	300
	GATTGGCGAA	CAGAAGATTG	ACGAGCTCAT	GAACGCCGTT	GATACCTGGA	350
20	TCCCCACCCC	CCAGCGTGAC	CTTGACAAGC	CCTTCTTGAT	GTCCGTTGAG	400
	GAAGTTTCT	CCATCTCTGG	TCGTGGTACC	GTTGCATCTG	GTCGTGTTGA	450
	GCGTGGTATT	TTGCGCAAGG	ATTCTGAGGT	TGAGATTATC	GGATACCAGA	500
	AGAACCCTAT	CAAGACCAAG	GTTACCGACA	TTGAGACCTT	CAAGAAGTCT	550
	TGCGATGAAT	CTCGTGCTGG	TGACAACTCT	GGCTTGCTTC	TCCGTGGTAT	600
25	CAAGCGTGAG	GACATTCGTC	GTGGTATGGT	TATCGCTGCT	CCTGGAACCA	650
	CCAAGGCTCA	TGACAACTTC	TTGGTCTCCA	TGTATGTCTT	GA CTGAGGCT	700
	GAAGGTGGTC	GTCGTA CTGG	ATTCGGCGCC	AACTACCGTC	CTCAAGCTTT	750
	CATCCGTA CT	GCCGGTATGT	TCCCTTTCAA	AGTCAATTAA	TGAGCGATTT	800
	GCTAACGAGT	TATAGATGAG	GCTGCTACTC	TCAGCTTCCC	CGGTGACGAT	850
30	CAGTCCAAGC	AGGTCATGCC	CGGTGACAAC	GTTGAGATGA	TCTTGAAGAC	900
	ACACCGTCCC	GTTGCCGCCG	AAGCTGGTCA	G		931

35 2) INFORMATION FOR SEQ ID NO: 506

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 846 bases
(B) TYPE: Nucleic acid
40 (C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

45 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Pichia anomala*
(B) STRAIN: ATCC 18205

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 506

50

	TGGTGCTATT	ATTGTTGTTG	CTGCTTCTGA	TGGTCAAATG	CCTCAAACCA	50
	GAGAACATTT	RTTATTGGCT	AGACAAGTTG	GTGTTCAACA	CATTGTTGTC	100
	TTTGTTAACA	AAGTTGATAC	TATTGATGAC	CCAGAAATGT	TGGAATTAGT	150
	TGAAATGGAA	ATGAGAGAAT	TGTTAAGTAC	TTATGGTTTT	GATGGTGATA	200
55	ACGTCCCA GT	TGTTATGGGT	TCTGCTTTAT	GTGCCTTGGA	AGGTCGTGAA	250
	GAAGAAATTG	GTGTCAAAGC	TATTGATAAA	TTATTAGCTG	CTGTTGATGA	300
	ATATATCCCA	ACCCACAAA	GAGATTTAGA	AAAACCATTC	TTGATGGGTG	350
	TTGAAGATGT	CTTYTCAATC	TCAGGTAGAG	GTACCGTTGT	TACTGGTCGT	400
	GTTGAACGTG	GTAAC TTGAA	GAAAGGTGAT	GAAGTTGAAA	TTGTTGGTTT	450
60	AAACAAA ACT	CCATTGAAAA	CTACTGTYAC	NGGTATTGAA	ATGTTCAAAA	500

	AAGAATTGGA	CCAAGCTATG	GCTGGTGATA	ACTGTGGTAT	CTTATTACGT	550
	GGTATCAAAA	GAGATGACAT	YAAAAGAGGT	ATGGTTATTG	CTAAAACCGG	600
	TACCATCTCW	GCTCACACTA	AATTCTTAGC	CTCAATGTAT	ATTTTGACTA	650
	AAGAAGAAGG	TGGTCGTCAC	TCAGGTTTTG	GTGAACATTA	CAGACCTCAA	700
5	TTATTATCA	GAACCTGGTGA	TGTTACCGTT	GTTTTAACCT	TYCCAGAAGG	750
	TGGTGATTCA	TCTCAACAAA	TCTTACCAGG	TGACAATGTC	GAAATGGTTT	800
	GTGAATTGGT	TCACCCAAC	GCTTTAGAAG	CTGGTCAAAG	ATTCAA	846

10

2) INFORMATION FOR SEQ ID NO: 507

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 964 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Trichophyton mentagrophytes*
 (B) STRAIN: WSA-225

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 507

	GGAGCTGTTG	TCGTTGTCGC	AGCTTCTGAC	GGTCAAATGT	AATTGAATGC	50
	CCGCCCAGAC	GGATGAAAGG	ATTTGACGTT	TCTAACATCA	GTCTAGGCCT	100
	CAGACCAGAG	AACATTTGCT	CCTTGCCCCG	CAGGTCGGTG	TCCAGAAGCT	150
30	GGTCGTTTTT	GTTAACAAGG	TCGATGCCGT	TGAGGACCCA	GAGATGTTGG	200
	AGCTTGTCGA	ACTTGAAATG	CGTGAACCTC	TCAGCCACTA	CAGTTTTGAG	250
	GGTGAGGAGA	CCCCCATCAT	TTTTGGCTCT	GCTCTCTGTG	CCCTCGAGTC	300
	CCGTCGACCT	GAGCTTGGTG	TCGAGAAGAT	TGACGAGCTA	TTGAACGCCG	350
	TCGACACCTG	GATCCCCACC	CCCGAGCGCG	CCACTGATAA	GCCTTTCCTC	400
35	ATGTCCATTG	AGGAAGTGTT	CTCTATCTCT	GGTCGTGGTA	CCGTCGTCTC	450
	CGGTCGTGTT	GAGCGTGGTA	TCCTCAAGAA	GGATTCCGAC	GTCGAAATTG	500
	TTGGTGCGTC	TACCACCCCT	ATCAAGACCA	AGGTCACAGA	TATCGAAACC	550
	TTCAAGAAGT	CCTGCGATGA	ATCTCGAGCT	GGTGACAACT	CTGGTCTCCT	600
	TCTCCGAGGT	ATCAAGCGTG	AGGACTTGAA	GCGTGGAATG	GTTGTTGCTG	650
40	CCCCCGGATC	CACCAAGGCT	CACACCGACT	TCATGGTCTC	CCTCTACGTC	700
	CTGACTGAGG	CTGAGGGTGG	TCGTTCCAAC	GGCTTCACCC	ACAAGTACCG	750
	CCCTCAAATG	TTCATCCGTA	CTGCTGGTAT	GTAACCAAAG	TTTCCGCTAT	800
	TTACTAAGTA	GATCATTGCT	AACCTGTATT	CCCTTCCGTA	GACGAAGCCG	850
	CATCTTTCAG	CTGGCCTGGA	GAAGACCAAG	ACAAGAAGGC	TATGCCTGGT	900
45	GACAACGTCG	AGATGATTTG	CAAAACCCTC	CACCCCATTG	CTGCCGAGGC	950
	TGGCCAACGA	TTCA				964

50 2) INFORMATION FOR SEQ ID NO: 508

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 844 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Yarrowia lipolytica*
 (B) STRAIN: ATCC 38295

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 508

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5      GGTGCTATCA TTGTCGTTGC TGCTGGAGAC GGTTCCAAGC CCCAGACCCG      50
      AGAGCATCTG CTGCTTGCTC GACAGGTCGG TGTCCAGAAC CTGGTTGTGT      100
      TTGTTAACAA GGTTGATCAG ATTGATGATA AGGAGATTCT TGAGCTCGTT      150
      GACATGGAGA TGCAGATCT GCTGACCCAG TACGGTTTTG ATGGTGACAA      200
10     CACCCCCGTT GTCATGGGCT CTGCTCTGTG CGCTCTTGAG GGCAAGCAGA      250
      AGGATATTGG AGAGGACGCC ATCATGGCCC TTATGGATGC CGTTGATGAG      300
      CACATCCCTA CCCCTAACCG TGACCTTGAG AAGCCCTTCC TGATGCCCCG      350
      TGAGGACGTT TTCTCCATCT CTGGCCGAGG AACTGTTGTT ACTGGCCGAG      400
      TCGAGCGAGG AAACCTGAAG AAGGGTGAGG AAATCGAGAT TGTTGGCTAC      450
15     AACACAAGC CCATCAAGGC TGTGTGTTACC GGTATTGAGA TGTTCAAGAA      500
      GGAGCTCGAG TCCGCCATGG CCGGTGACAA CGCCGGTATC CTGCTCCGAG      550
      GTATCAAGCG AGACGAGATC AAGCGAGGTA TGGTCATGTG CAAGCCTGGC      600
      ACCGTCAACG CCCACACCAA GTTCCTTGCT TCTCTTTACA TCATCCCCAC      650
      CGAGGAGGGT GGTCAACCA GCTCTTTCGG CGCCAACTAC CGACCCGAGA      700
20     TGTTTCATCCG AACTTCTTCC GTCACCGCCA CTCTCACCTT CCCCAGAGGT      750
      ACCGACGAGT CCCAGACCGT CAACCCCGGT GACAACACTG AGATGGTTCT      800
      CGAGCTTGTT CACCCTACCG CCATTGAGGT CAACCAGCGA TTCA          844
  
```

25 2) INFORMATION FOR SEQ ID NO: 509

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1067 bases
 30 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Babesia bigemina*
 (B) STRAIN: Suarez-2

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 509

```

      CTTGGACAAG CTGAAGAGCG AGCGTGAGCG TGGTATCACC ATTGACATTA      50
      CCCTGTGGAA GTTCGAAACT GGCAAGTACT ACTACACCGT CATTGACGCC      100
      CCCGGTCACC GTGACTTCAT TAAGAACATG ATTACGGGTA CCTCCCAGGC      150
45     CGATGTTGCT ATGCTTGTCG TGCCCGCCGA GGCTGGTGGT TTCGAAGCTG      200
      CCTTCTCTAA GGAAGGTCAG ACCCGTGAGC ACGCTCTTTT GGCCTTCACC      250
      CTTGGTGTCA AGCAGATCAT TTGCGCCATC AACAAGATGG ACAAGTGC GA      300
      CTACAAGGAG GACCGTTACA GCGAAATCCA GAAGGAAGTT CAGGGTTACC      350
      TGAAGAAGGT CGGTTACAAC ATCGAGAAGG TGCCTTTCGT CGCCATCTCC      400
50     GGTTCATGCG GTGACAACAT GGTGTAGCGC TCCACCAACA TGCCGTGGTA      450
      CAAGGGCAAG ACCTTGGTCT AGGCCCTCGA CATGATGGAG CCCCCGAAGA      500
      GGCCCGTCGA CAAGCCCCTG CGTCTTCCCC TCCAGGGTGT GTACAAGATC      550
      GGTGGTATCG GTACCGTCCC TGTCGGTCTG GTGGAGACTG GTCAGCTCAA      600
      GGCCGGTATG GTCCTCACCT TCGCCCCCAA CCCGATCACT ACTGAGTGCA      650
55     AATCCGTCGA AATGCACCAC GAAGTTATCG ATGTTGCCAG CCCTGGTGAC      700
      AACGTTGGTT TCAACGTGAA GAACGTGTCC ACCTCTGACA TCCGCACTGG      750
      TCACGTCGCT TCTGACTCCA AGAACGACCC CGCCAAGGCC GCCGTGTCCT      800
      TCACCGCCCA GGTTCATCAT TTGAACCACC CTGGTACCAT CAAGGCCGGT      850
      TACTCCCCTG TGTTGACTG CCACACTGCC CACATCTCGT GCAAATTCGA      900
60     CGAGATCACC AGCCGTATGG ACAAGCGTAC CGGTAAGGCC CTTGAGGAGA      950
  
```

ACCCCAAGAC CATCAAGAAC GGCGACGCCG CTATGGTCGT CCTGAAGCCG 1000
 TGCAAGCCCA TGGTCGTCGA GGCCTTCACT GAATACGCTC CCCTTGGTGC 1050
 TTTCGCCGTG CGTGACG 1067

5

2) INFORMATION FOR SEQ ID NO: 510

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 1049 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

15 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Babesia bovis*
 (B) STRAIN: Suarez-3

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 510

GTGAACGTGA ACGTGGTATT ACTATTGATA TTACCTTATG GAAGTTCGAG 50
 ACCACCAAGT ACTACTACAC CGTCATTGAT GCCCCTGGTC ACCGTGACTT 100
 25 CATCAAGAAC ATGATTACGG GTACTTCTCA AGCCGATGTT GCTATGCTTG 150
 TTGTACCAGC TGAGGCTGGT GGTTTCGAGG CCGCTTTCTC CAAGGAAGGA 200
 CAGACCCGTG AGCACGCTCT TTTGGCTTTC ACCCTTGGTG TCAAACAGAT 250
 CATCTGTGCC ATTAACAAGA TGGACAAGTG CGACTACAAG GAGGACCGTT 300
 ACAGTGAAAT CCAGAAGGAA GTCCAGGGTT ACCTCAAGAA GGTCGGTTAC 350
 30 AATATTGAGA AGGTGCCCTT CGTTGCCATC TCCGGTTTCA TGGGAGACAA 400
 CATGGTTGAG CGTTCCACCA ACATGCCCTG GTATAAGGGA AAGACATTGG 450
 TCGAGGCCCT TGATCAGATG GAACCCCAA AGAGGCCCGT TGACAAGCCA 500
 CTTCGTCTTC CCCTCCAGGG TGTCTACAAG ATCGGTGGTA TCGGTACCGT 550
 CCCCCTCGGT CGTGTTGAAA CTGGTATGTT GAAGGCTGGT ATGATTCTAA 600
 35 CCTTTGCTCC TAACCCAATC ACCACTGAAT GCAAATCCGT TGAAATGCAC 650
 CACGAAACCG TTGAGGTGTC TTACCCCGGT GACAACGTCG GTTCAACGT 700
 AAAGAACGTT TCTACTTCTG ACATTCGCAG TGGTCACGTT GCCTCTGATT 750
 CTAAGAACGA CCCTGCCAAG GCTGCTGTTT CCTTCACTGC CCAGGTCATT 800
 GTGCTCAACC ACCCTGGTAC CATTAAGGCC GGTACTGCC CCGTCGTCGA 850
 40 TTGCCACACC GCTCACATTT CATGTAAATT CGAAGAGATC ACCAGCCGTA 900
 TGGACAAGCG TACCGGTAAA TCTCTTGAGG AAAACCCCAA GACCATCAAG 950
 AACGGTGACG CTGCCATGGT TGTGCTCAAG CCAATGAAGC CCATGGTTGT 1000
 CGAATCCTTC ACTGAGTATG CTCCTCTTGG TCGTTTCGCT GTTCGTGAC 1049

45

2) INFORMATION FOR SEQ ID NO: 511

(i) SEQUENCE CHARACTERISTICS:

- 50 (A) LENGTH: 1070 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

55 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Criethidia fasciculata*
 (B) STRAIN: ATCC 11745

60

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 511

	TGGACAAGCT	GAAGGCGGAG	CGCGAGCGCG	GTATCACGAT	CGATATTGCC	50
	CTGTGGAAGT	TCGAGTCGCC	CAAGTCCGTG	TTCACGATCA	TCGATGCCCC	100
5	CGGCCACCGC	GACTTCATCA	AGAACATGAT	CACCGGCACC	TCCAGGCCCG	150
	ATGCCGCCAT	TCTGATGATT	GACTCGACCC	AGGGTGGCTT	CGAGGCTGGC	200
	ATCTCCAAGG	ACGGCCAGAC	CCGCGAGCAC	GCCCTGCTTG	CCTTCACGCT	250
	GGGCGTGAAG	CAGATGGTTG	TGTGCTGCAA	CAAGATGGAC	GACAAGACGG	300
	TGCAGTACGC	CCAGGCCCGC	TACGAGGAGA	TCAGCAAGGA	GGTCGGCGCG	350
10	TACCTGAAGC	GCGTGGGCTA	CAACCCGGAG	AAGGTGCGCT	TCATCCCGAT	400
	CTCGGGCTGG	CAGGGCGACA	ACATGATCGA	GAAGTCCGAC	AACATGTCGT	450
	GGTACAAGGG	TCCCACGCTG	CTGGAGGCGC	TCGACCTGCT	GGAGGCCCCC	500
	GTGCGTCCGG	TGGACAAGCC	GCTGCGCCTG	CCCCTGCAGG	ACGTGTACAA	550
	GATCGGCGGT	ATCGGCACTG	TGCCCCGTGG	CCGTGTGGAG	ACCGGCGTGA	600
15	TGAAGCCGGG	CGACGTTGTG	GTGTTTCGCG	CTGCCAACGT	GACGACCGAG	650
	GTGAAGTCGA	TCGAGATGCA	CCACGAGCAG	CTGGCTGAGG	CCGTGCCCCG	700
	CGACAACGTG	GGCTTCAACG	TGAAGAACGT	GTCCGTGAAG	GATATCCGCC	750
	GTGGTAACGT	GTGCGGCAAC	ACGAAGAGCG	ACCCCCGAA	GGAGGCGGCC	800
	GACTTCACTG	CCCAGGTGAT	CGTGCTGAAC	CACCCCGGCC	AGATCAGCAA	850
20	CGGCTACGCG	CCGGTGCTGG	ACTGCCACAC	GAGCCACATC	GCGTGCAAGT	900
	TCGCGGACAT	CGAGTCCAAG	ATCGACCGCC	GCTCTGGCAA	GGAGCTGGAG	950
	AAGAGCCCGA	AGGCCATCAA	GTCCGGCGAT	GCGGCCATCG	TGAAGATGAT	1000
	CCCGCAGAAG	CCGATGTGCG	TGGAGGTGTT	CAACGACTAC	CCGCCGCTGG	1050
	GCCGCTTCGC	TGTCCGCGAT				1070
25						

2) INFORMATION FOR SEQ ID NO: 512

- 30 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1052 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Double
 - (D) TOPOLOGY: Linear
- 35 (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Entamoeba histolytica*
 - (B) STRAIN: HM1-IMMS
- 40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 512

	GCTGAAAGAG	AAAGAGGAAT	TACTATTGAT	ATTTTATTAT	GGAAATTCGA	50
45	AACATCTAAA	TACTACTTCA	CTATTATTGA	TGCCCCAGGT	CAYAGAGATT	100
	TCATTAAGAA	CATGATTACT	GGAACCTCAC	AAGCTGATGT	TGCCATCCTT	150
	ATTGTTGCTG	CTGGTACTGG	WGAATTTGAA	GCTGGTATTT	CAAAGAATGG	200
	ACAAACCAGA	GAACAYATTC	TTCTTTTATA	CACTCTTGGA	GTAAACAAA	250
	TGATTGTTGG	WGTTAACAAG	ATGGATGCTA	TTCAATATAA	ACAAGAAAGA	300
50	TATGAAGAAA	TTAAGAAAGA	AATTAGTGCA	TTCCTTAAGA	AGACWGGATA	350
	TAATCCAGAC	AAGATTCCAT	TTGTCCCAAT	TTCAGGATTC	CAAGGAGATA	400
	ATATGATTGA	ACCATCAACC	AACATGCCAT	GGTACAAAGG	ACCAACATTA	450
	ATTGGAGCAC	TTGATTCACT	CACACCACCA	GAAAGACCAG	TTGATAAACC	500
	ACTTAGACTT	CCACTTCAAG	ATGTTTAYAA	GATTTTCAGG	ATTGGAAGTG	550
55	TACCATGTGG	AAGAGTTGAA	ACTGGAGTTC	TTAGACCAGG	AACTATTGTT	600
	CAATTTGCAC	CATCAGGAGT	TTCATCTGAA	TGTAAATCAG	TTGAAATGCA	650
	TCACACAGCA	CTTGCTCAAG	CTATTCCAGG	TGATAATGTT	GGATTCAATG	700
	TTAGAAAYTT	AACAGTTAAA	GATATTAAGA	GAGGAAATGT	AGCATCAGAT	750
	GCTAAGAATC	AACCAGCTGT	TGGATGTGAA	GATTTCACTG	CTCAAGTCAT	800
60	TGTCATGAAC	CATCCAGGAC	AAATTAGAAA	GGGATATACA	CCAGTTCTTG	850

	ATTGCCATAC	ATCACACATT	GCATGTAAAT	TCGAAGAATT	ATTAAGCAAG	900
	ATTGATAGAA	GAACAGGTAA	ATCCATGGAA	GGAGGAGAAC	CAGAAATAT	950
	TAAGAATGGA	GATTCAGCAC	TTGTAAAGAT	TGTTCCAAC	AAACCACTTT	1000
	GTGTTGAAGA	ATTTGCTAAA	TTCCCACCAT	TGGGAAGATT	TGCTGTTAGA	1050
5	GA					1052

2) INFORMATION FOR SEQ ID NO: 513

10

(i) SEQUENCE CHARACTERISTICS:

	(A)	LENGTH: 1082 bases
	(B)	TYPE: Nucleic acid
	(C)	STRANDEDNESS: Double
15	(D)	TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

20	(A)	ORGANISM: <i>Giardia lamblia</i>
	(B)	STRAIN: Faubert-1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 513

25	GACGAGCGCG	AGCGCGGGAT	CACGATCAAC	ATCGCGCTCT	GGAAGTTCGA	50
	GACGAAGAAG	TACATCGTCA	CGATCATCGA	CGCCCCGGGC	CACCGCGACT	100
	TCATCAAGAA	CATGATCACG	GGGACGTCCC	AGGCCGACGT	CGCGATCCTC	150
	GTCGTCGCGG	CGGGCCAGGG	CGAGTTCGAG	GCCGGGATCT	CGAAGGACGG	200
	CCAGACGCGC	GAGCACGCGA	CCCTTGCGAA	CACGCTCGGG	ATCAAGACGA	250
30	TGATCATCTG	CGTCAACAAG	ATGGACGACG	GCCAGGTCAA	GTACTCGAAG	300
	GAGCGCTACG	ACGAGATCAA	GGGCGAGATG	ATGAAGCAGC	TCAAGAACAT	350
	CGGCTGGAAG	AAGGCCGAGG	AGTTCGACTA	CATCCCGACG	TCCGGCTGGA	400
	CCGGGGACAA	CATCATGGAG	AAGTCCGACA	AGATGCCCTG	GTACGAGGGC	450
	CCGTGCCTGA	TCGACGCGAT	CGACGGGCTC	AAGGCCCCGA	AGCGCCCGAC	500
35	CGACAAGCCC	CTCCGCCTCC	CGATCCAGGA	CGTCTACAAG	ATCTCGGGCG	550
	TCGGGACCGT	CCCCGCGGGC	CGCGTCGAGA	CGGGCGAGCT	CGCGCCCGGG	600
	ATGAAGGTCG	TCTTCGCCCC	GACGTCCCAG	GTCTCGGAGG	TCAAGTCCGT	650
	CGAGATGCAC	CACGAGGAGC	TCAAGAAGGC	CGGGCCCGGG	GACAACGTCG	700
	GCTTCAACGT	CCGCGGGCTC	GCCGTCAAGG	ACCTCAAGAA	GGGCTACGTC	750
40	GTCGGGGACG	TGACGAACGA	CCCGCCCGTC	GGCTGCAAGA	GCTTCACCGC	800
	CCAGGTCATC	GTCATGAACC	ACCCGAAGAA	GATCCAGCCC	GGCTACACGC	850
	CCGTCAATCGA	CTGCCACACC	GCGCACATCG	CGTGCCAGTT	CCAGCTCTTC	900
	CTCCAGAAGC	TCGACAAGCG	CACGCTCAAG	CCCGAGATGG	AGAACCCGCC	950
	CGACGCAGGC	CGCGGCGATT	GCATCATCGT	CAAGATGGTC	CCCCAGAAGC	1000
45	CCCTGTGCTG	CGAGACGTTT	AACGACTACG	CGCCCCCTCG	CCGCTTCGCC	1050
	GTCCGCGACA	TGCGCCAAAC	CGTTGCCGTC	GG		1082

50 2) INFORMATION FOR SEQ ID NO: 514

(i) SEQUENCE CHARACTERISTICS:

	(A)	LENGTH: 1098 bases
	(B)	TYPE: Nucleic acid
55	(C)	STRANDEDNESS: Double
	(D)	TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

60 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Leishmania tropica*
 (B) STRAIN: ATCC 30816

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 514

```

5  ACGCGTGGGT GCTCGACAAG CTGAAGGCGG AGCGCGAGCG CGGCATCACG      50
   ATCGACATTG CGCTGTGGAA GTTCGAGTCG CCCAAGTCCG TGTTCACGAT      100
   CATCGATGCG CCCGGCCACC GCGACTTCAT CAAGAACATG ATCACGGGCA      150
   CGTCGCAGGC GGACGCCGCC ATCCTGATGA TCGACTCGAC GCATGGTGGC      200
10  TTCGAGGCTG GCATCTCGAA GGACGGCCAG ACCCGCGAGC ACGCGCTGCT      250
   TGCCTTCACT CTTGGCGTGA AGCAGATGGT GGTGTGCTGC AACAAAGATGG      300
   ACGACAAGAC GGTGACGTAC GCGCAGTCGC GCTACGATGA GATCAGCAAG      350
   GAGGTGGGCG CGTACCTGAA GCGCGTGGGC TACAACCCGG AGAAGGTGCG      400
   CTTTCATCCCG ATCTCGGGCT GGCAGGGCGA CAACATGATC GAGAAGTCGG      450
15  ACAACATGCC GTGGTACAAG GGTCCCACGC TGCTGGACGC GCTCGACATG      500
   CTGGAGCCGC CGGTGCGCCC GGTGGACAAG CCGCTGCGCC TGCCCCTGCA      550
   GGACGTGTAC AAGATCGGCG GTATCGGGAC GGTGCCCCGTG GGGCGCGTGG      600
   AGACCGGCAT CATGAAGCCG GGCAGCTGGT TGACGTTCGC GCCCGCCAAC      650
   GTGACGACTG AGGTGAAGTC GATCGAGATG CACCACGAGC AGCTGGCGGA      700
20  GGCAGAGCCC GGCAGACAAC TCGGCTTCAA CGTGAAGAAC GTGTCGGTGA      750
   AGGACATCCG CCGTGGTAAC GTGTGCGGCA ACTCGAAGAA CGACCCGCCG      800
   AAGGAGGCGG CCGACTTCAC GGCAGAGGTG ATCGTGCTGA ACCACCCCGG      850
   CCAGATCAGC AACGGCTACG CGCCGGTGCT GGAATGCCAC ACGAGCCACA      900
   TTGCGTGCCG CTTTCGCGAA ATCGAGTCCA AGATCGACCG CCGCTCCGGC      950
25  AAGGAGCTGG AGAAGAACCC CAAGGCGATC AAGTCTGGCG ATGCCGCGAT     1000
   CGTGAAGATG GTGCCGAGA AGCCGATGTG CGTGAGAGTG TTCAACGACT     1050
   ACGCGCCGCT GGGCCGCTTT GCCGTGCGCG ACATGCGCCA AACCGTTG      1098
  
```

30

2) INFORMATION FOR SEQ ID NO: 515

(i) SEQUENCE CHARACTERISTICS:

```

35  (A) LENGTH: 1104 bases
   (B) TYPE: Nucleic acid
   (C) STRANDEDNESS: Double
   (D) TOPOLOGY: Linear
  
```

40 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Leishmania aethiopica*
 (B) STRAIN: ATCC 50119

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 515

```

   TACGCGTGGG TGCTCGACAA GCTGAAGGCG GAGCGCGAGC GCGGCATCAC      50
   GATCGACATT GCGCTGTGGA AGTTCGAGTC GCCCAAGTCC GTGTTACGGA      100
   TCATCGATGC GCCCGGCCAC CGCGACTTCA TCAAGAACAT GATCACGGGC      150
50  ACGTCGCAGG CGGACGCCGC CATCCTGATG ATCGACTCGA CGCATGGTGG      200
   CTTTCGAGGCT GGCATCTCGA AGGACGGCCA GACCCGCGAG CACGCGCTGC      250
   TTGCCTTAC TCTTGGCGTG AAGCAGATGG TGGTGTGCTG CAACAAGATG      300
   GACGACAAGA CGGTGACGTA CGCGCAGTCG CGCTACGAGG AGATCAGCAA      350
   GGAGGTGGGC GCGTACCTGA AGCGCGTGGG CTACAACCCG GAGAAGGTGC      400
55  GCTTCATCCC GATCTCGGGC TGGCAGGGCG ACAACATGAT CGAGAAGTCG      450
   GACAACATGC CGTGGTACAA GGGTCCCACG CTGCTGGACG CGCTCGACAT      500
   GCTGGAGCCG CCGGTGCGCC CGGTGGACAA GCCGCTGCGC CTGCCCCCTGC      550
   AGGACGTGTA CAAGATCGGC GGTATCGGGA CGGTGCCCCG GGGCCGCGTG      600
   GAGACCGGCA TCATGAAGCC GGGCGACGTG GTGACGTTG CGCCCGCCAA      650
60  CGTGACGACT GAGGTGAAGT CGATCGAGAT GCACCACGAG CAGCTGGCGG      700
  
```

	AGGCGCAGCC	CGGCGACAAC	GTCGGCTTCA	ACGTGAAGAA	CGTGTGGTG	-750
	AAGGACATCC	GCCGTGGCAA	CGTGTGCGGC	AACTCGAAGA	ACGACCCGCC	800
	GAAGGAGGCG	GCCGACTTCA	CGGCGCAGGT	GATCGTGCTG	AACCACCCCG	850
	GCCAGATCAG	CAACGGCTAC	GCGCCGGTGC	TGGACTGCCA	CACGAGCCAC	900
5	ATTGCGTGCC	GCTTCGCGGA	AATCGAGTCC	AAGATCGACC	GCCGCTCCGG	950
	CAAGGAGCTG	GAGAAGAACC	CCAAGGCGAT	CAAGTCTGGC	GATGCCGCGA	1000
	TCGTGAAGAT	GGTGCCGCAG	AAGCCGATGT	GCGTGGAGGT	GTTCAACGAC	1050
	TACGCGCCGC	TGGGCCGCTT	TGCCGTGCGC	GACATGCGCC	AAACCGTTGC	1100
10	CGTC					1104

2) INFORMATION FOR SEQ ID NO: 516

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1106 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Double
 - (D) TOPOLOGY: Linear

- (ii) MOLECULE TYPE: Genomic DNA

- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Leishmania tropica*
 - (B) STRAIN: ATCC 30815

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 516

	TACGCGTGGG	TGCTCGACAA	GCTGAAGGCG	GAGCGCGAGC	GCGGCATCAC	50
30	GATCGACATT	GCGCTGTGGA	AGTTCGAGTC	GCCCAAGTCC	GTGTTACGA	100
	TCATCGATGC	GCCCGGCCAC	CGCGACTTCA	TCAAGAACAT	GATCACGGGC	150
	ACGTCGCAGG	CGGACGCCGC	CATCCTGATG	ATCGACTCGA	CGCATGGTGG	200
	CTTCGAGGCT	GGCATCTCGA	AGGACGGCCA	GACCCGCGAG	CACGCGCTGC	250
	TTGCCTTAC	KCTTGGCGTG	AAGCAGATGG	TGGTGTGCTG	CAACAAGATG	300
35	GACGACAAGA	CGGTGACGTA	CGCGCAGTCG	CGCTACGATG	AGATCAGCAA	350
	GGAGGTGGGC	GCGTACCTGA	AGCGCGTGGG	CTACAACCCG	GAGAAGGTGC	400
	GCTTCATCCC	GATCTCGGGC	TGGCAGGGCG	ACAACATGAT	CGAGAAGTCG	450
	GACAAACATGC	CGTGGTACAA	GGGTCCACG	CTGCTGGACG	CGCTCGACAT	500
	GCTGGAGCCG	CCGGTGCGCC	CGGTGGACAA	GCCGCTGCGC	CTGCCCCCTGC	550
40	AGGACGTGTA	CAAGATCGGC	GGTATCGGGA	CGGTGCCCCGT	GGGGCGCGTG	600
	GAGACCGGCA	TCATGAAGCC	GGGCGACGTG	GTGACGTTTCG	CGCCCGCCAA	650
	CGTGACGACT	GAGGTGAAGT	CGATCGAGAT	GCACCACGAG	CAGCTGGCGG	700
	AGGCGCAGCC	CGGCGACAAC	GTCGGCTTCA	ACGTGAAGAA	CGTGTGCGTG	750
	AAGGACATCC	GCCGTGGTAA	CGTGTGCGGC	AACTCGAAGA	ACGACCCGCC	800
45	GAAGGAGGCG	GCCGACTTCA	CGGCGCAGGT	GATCGTGCTG	AACCACCCCG	850
	GCCAGATCAG	CAACGGCTAC	GCGCCGGTGC	TGGACTGCCA	CACGAGCCAC	900
	ATTGCGTGCC	GCTTCGCGGA	AATCGAGTCC	AAGATCGACC	GCCGCTCCGG	950
	CAAGGAGCTG	GAGAAGAACC	CCAAGGCGAT	CAAGTCTGGC	GATGCCGCGA	1000
	TCGTGAAGAT	GGTGCCGCAG	AAGCCGATGT	GCGTGGAGGT	GTTCAACGAC	1050
50	TACGCGCCGC	TGGGCCGCTT	TGCCGTGCGC	GACATGCGCC	AAACCGTTGC	1100
	CGTCGG					1106

2) INFORMATION FOR SEQ ID NO: 517

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1099 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

5 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Leishmania donovani*

(B) STRAIN: ATCC 50212

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 517

10

TACGCGTGGG	TGCTCGACAA	GCTGAAGGCG	GAGCGCGAGC	GCGGCATCAC	50
GATCGACATT	GCGCTGTGGA	AGTTCGAGTC	GCCCAAGTCC	GTGTTCACGA	100
TCATCGATGC	GCCCGGCCAC	CGCGACTTCA	TCAAGAACAT	GATCACGGGC	150
ACGTCGCAGG	CGGACGCCGC	CATCCTGATG	ATCGACTCGA	CGCATGGTGG	200
15 CTTTCGAGGCT	GGCATCTCGA	AGGACGGCCA	GACCCGCGAG	CACGCGCTGC	250
TTGCCTTCAC	GCTTGGCGTG	AAGCAGATGG	TGGTGTGCTG	CAACAAGATG	300
GACGACAAGA	CCGTGACGTA	CGCGCAGTCG	CGCTACGATG	AGATCAGCAA	350
GGAGGTGGGC	GCGTACCTGA	AGCGCGTGGG	CTACAACCCG	GAGAAGGTGC	400
GCTTCATCCC	GATCTCGGGC	TGGCAGGGCG	ACAACATGAT	CGAGAGGTTCG	450
20 GACAACATGC	CGTGGTACAA	GGGTCCACG	CTGCTGGACG	CGCTCGACAT	500
GCTGGAGCCG	CCGGTGCGCC	CGGTGGACAA	GCCGCTGCGC	CTGCCCCTGC	550
AGGACGTGTA	CAAGATCGGC	GGTATCGGGA	CTGTGCCCCGT	GGGCCGCGTG	600
GAGACCGGCA	TCATGAAGCC	GGGCGACGTG	GTGACGTTTCG	CGCCCGCCAA	650
CGTGACGACT	GAGGTGAACT	CGATCGAGAT	GCACCACGAG	CAGCTGGCGG	700
25 AGGCGCAGCC	CGGCGACAAC	GTCGGCTTCA	ACGTGAAGAA	CGTGTCGGTG	750
AAGGACATCC	GCCGTGGCAA	CGTGTGCGGC	AACTCGAAGA	ACGACCCGCC	800
GAAGGAGGCG	GCCGACTTCA	CGGCGCAGGT	GATCGTGTCTG	AACCACCCCG	850
GCCAGATCAG	CAACGGCTAC	GCGCCGGTGC	TGGACTGCCA	CACGAGCCAC	900
ATTGCGTGCC	GCTTCGCGGA	AATCGAGTCC	AAGATCGACC	GCCGCTCCGG	950
30 CAAGGAGCTG	GAGAAGAACC	CCAAGGCGAT	CAAGTCTGGC	GATGCCGCGA	1000
TCGTGAAGAT	GGTGCCGCAG	AAGCCGATGT	GCGTGGAGGT	GTTCAACGAC	1050
TACGCGCCGC	TGGGCCGCTT	TGCCGTGCGC	GACATGCGCC	AAACCGTTG	1099

35

2) INFORMATION FOR SEQ ID NO: 518

(i) SEQUENCE CHARACTERISTICS:

40 (A) LENGTH: 1098 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

45

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Leishmania infantum*

(B) STRAIN: MOU

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 518

TACGCGTGGG	TGCTCGACAA	GCTGAAGGCG	GAGCGCGAGC	GCGGCATCAC	50
GATCGACATT	GCGCTGTGGA	AGTTCGAGTC	GCCCAAGTCC	GTGTTCACGA	100
TCATCGATGC	GCCCGGCCAC	CGCGACTTCA	TCAAGAACAT	GATCACGGGC	150
55 ACGTCGCAGG	CGGACGCCGC	CATCCTGATG	ATCGACTCGA	CGCATGGTGG	200
CTTCGAGGCT	GGCATCTCGA	AGGACGGCCA	GACCCGCGAG	CACGCGCTGC	250
TTGCCTTCAC	GCTTGGCGTG	AAGCAGATGG	TGGTGTGCTG	CAACAAGATG	300
GACGACAAGA	CCGTGACGTA	CGCGCAGTCG	CGCTACGATG	AGATCAGCAA	350
GGAGGTGGGC	GCGTACCTGA	AGCGCGTGGG	CTACAACCCG	GAGAAGGTGC	400
60 GCTTCATCCC	GATCTCGGGC	TGGCAGGGCG	ACAACATGAT	CGAGAGGTTCG	450

	GACAACATGC	CGTGGTACAA	GGGTCCCACG	CTGCTGGACG	CGCTCGACAT	500
	GCTGGAGCCG	CCGGTGCGCC	CGGTGGACAA	GCCGCTGCGC	CTGCCCCTGC	550
	AGGACGTGTA	CAAGATCGGC	GGTATCGGGA	CTGTGCCCCG	GGGCCGCGTG	600
	GAGACCGGCA	TCATGAAGCC	GGGCGACGTG	GTGACGTTCG	CGCCCCGCAA	650
5	CGTGACGACT	GAGGTGAAGT	CGATCGAGAT	GCACCACGAG	CAGCTGGCGG	700
	AGGCGCAGCC	CGGCGACAAC	GTCGGCTTCA	ACGTGAAGAA	CGTGTCGGTG	750
	AAGGACATCC	GCCGTGGCAA	CGTGTGCGGC	AACTCGAAGA	ACGACCCGCC	800
	GAAGGAGGCG	GCCGACTTCA	CGGCGCAGGT	GATCGTGCTG	AACCACCCCG	850
	GCCAGATCAG	CAACGGCTAC	GCGCCGGTGC	TGGACTGCCA	CACGAGCCAC	900
10	ATTGCGTGCC	GCTTCGCGGA	AATCGAGTCC	AAGATCGACC	GCCGCTCCGG	950
	CAAGGAGCTG	GAGAAGAACC	CCAAGGCGAT	CAAGTCTGGC	GATGCCGCGA	1000
	TCGTGAAGAT	GGTGCCGCAG	AAGCCGATGT	GCGTGGAGGT	GTTCAAACGAC	1050
	TACGCGCCGC	TGGGCCGCTT	TGCCGTGCGC	GACATGCGCC	AAACCGTT	1098

15

2) INFORMATION FOR SEQ ID NO: 519

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 1071 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

25 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Leishmania enriettii*

(B) STRAIN: ATCC 50120

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 519

	CTCGACAAGC	TGAAGGCGGA	GCGCGAGCGC	GGCATCACGA	TCGACATTGC	50
	GCTGTGGAAG	TTCGAGTCGC	CCAAGTCTGT	GTTACGATC	ATCGATGCGC	100
35	CCGGCCACCG	CGACTTCATC	AAGAACATGA	TCACCGGCAC	GTCGCAGGCC	150
	GACGCCGCCA	TCCTGATGAT	CGACTCGACC	CAGGCGGGCT	TCGAGGTGG	200
	CATCTCGAAG	GACGGCCAGA	CCCGCGAGCA	CGCGCTGCTC	GCCTTCACGC	250
	TTGGTGTGAA	GCAGATGGTG	GTGTGCTGCA	ACAAGATGGA	CGACAAGACG	300
	GTGCAGTACT	CGCAGGCGCG	CTACGAGGAG	ATCAGCAAGG	AGGTGGGCGC	350
40	GTACCTGAAG	CGCGTCGGCT	ACAACCCGGA	GAAGGTGCGC	TTCATCCCGA	400
	TCTCGGGCTG	GCAGGGCGAC	AACATGATCG	ACAAGTCGGA	CAGCATGCCG	450
	TGGTACAAGG	GGCCACGCT	GCTGGACGCG	CTCGACATGC	TGGAGGCGCC	500
	GGTGCGCCCG	GTGGACAAGC	CGCTGCGCCT	GCCCCCTGCAG	GACGTGTACA	550
	AGATCGGCGG	TATCGGGACG	GTGCCCCGTGG	GCCGCGTGGA	GACCGGCATC	600
45	ATGAAGCCTG	GCGACGTGGT	GACGTTTGCG	CCCGCCAACG	TGACGACGGA	650
	GGTGAAGTCG	ATCGAGATGC	ACCACGAGCA	GCTGGCGGAG	GCGGTGCCCCG	700
	GCGACAACGT	CGGCTTCAAC	GTGAAGAACG	TGTCGGTGAA	GGACATCCGC	750
	CGTGGTAACG	TGTGCGGCAA	CTCGAAGAAC	GACCCGCCGA	AGGAGGCGGC	800
	CGACTTCACG	GCGCAGGTGA	TCGTGCTGAA	CCACCCTGGC	CAGATCAGCA	850
50	ACGGCTACGC	GCCGGTGCTG	GACTGCCACA	CGAGCCACAT	CGCGTGCCGC	900
	TTCGCGGATA	TCGAGTCCAA	GATCGACCGC	CGCTCTGGCA	AGGAGCTGGA	950
	GAAGAACCCC	AAGGCGATCA	AGTCCGGCGA	TGCGGCCATC	GTGAAGATGG	1000
	TGCCGCAGAA	GCCGATGTGC	GTGGAGGTGT	TCAACGACTA	CCCGCCGCTG	1050
	GGGCGCTTCG	CTGTGCGCGA	C			1071

55

2) INFORMATION FOR SEQ ID NO: 520

60 (i) SEQUENCE CHARACTERISTICS:

320

- (A) LENGTH: 1071 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

5

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Leishmania gerbilli*
 (B) STRAIN: ATCC 50121

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 520

	CTCGACAAGC	TGAAGGCGGA	GCGCGAGCGC	GGCATCACGA	TCGACATTGC	50
15	GCTGTGGAAG	TTCGAGTCGC	CCAAGTCCGT	GTTACAGATC	ATCGATGCGC	100
	CCGGCCACCG	CGACTTCATC	AAGAACATGA	TCACGGGCAC	GTCGCAGGCG	150
	GACGCCGCCA	TCCTGATGAT	CGACTCGACG	CATGGTGGCT	TCGAGGCTGG	200
	CATCTCGAAG	GACGGCCAGA	CCCGCGAGCA	CGCGCTGCTT	GCCTTCACTC	250
	TTGGCGTGAA	GCAGATGGTG	GTGTGCTGCA	ACAAGATGGA	CGACAAGACG	300
20	GTGACGTACG	CGCAGTCGCG	CTACGATGAG	ATCAGCAAGG	AGGTGGGCGC	350
	GTACCTGAAG	CGCGTGGGCT	ACAACCCGGA	GAAGGTGCGC	TTCATCCCGA	400
	TCTCGGGCTG	GCAGGGCGAC	AACATGATCG	AGAAGTCGGA	CAACATGCCG	450
	TGGTACAAGG	GTCCACGCT	GCTGGACGCG	CTCGACATGC	TGGAGCCGCC	500
	GGTGCGCCCG	GTGGACAAGC	CGCTGCGCCT	GCCCCCTGCAG	GACGTGTACA	550
25	AGATCGGCGG	TATCGGGACG	GTGCCCCTGG	GCCGCGTGGA	GACCGGCATC	600
	ATGAAGCCGG	GCGACGTGGT	GACGTTGCGG	CCCGCCAACG	TGACGACTGA	650
	GGTGAAGTCG	ATCGAGATGC	ACCACGAGCA	GCTGGCGGAG	GCGCAGCCCG	700
	GCGACAACGT	CGGCTTCAAC	GTGAAGAACG	TGTCGGTGAA	GGACATCCGC	750
	CGTGGTAAAC	TGTGCGGCAA	CTCGAAGAAC	GACCCGCCGA	AGGAGGCGGC	800
30	CGACTTCACG	GCGCAGGTGA	TCGTGCTGAA	CCACCCCGGC	CAGATCAGCA	850
	ACGGCTATGC	GCCGGTGCTG	GACTGCCACA	CGAGCCACAT	TGCGTGCCGC	900
	TTCGCGGAAA	TCGAGTCCAA	GATCGACCGC	CGCTCCGGCA	AGGAGCTGGA	950
	GAAGAACCCC	AAGGCGATCA	AGTCTGGCGA	TGCCGCGATC	GTGAAGATGG	1000
	TGCCGCAGAA	GCCGATGTGC	GTGGAGGTGT	TCAACGACTA	CGCGCCGCTG	1050
35	GGCCGCTTTG	CCGTGCGCGA	C			1071

2) INFORMATION FOR SEQ ID NO: 521

40

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1114 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

45

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Leishmania hertigi*
 (B) STRAIN: ATCC 50125

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 521

55	TCGTTCAAAGT	ACGCGTGGGT	GCTCGACAAG	CTGAAGGCGG	AGCGCGAGCG	50
	CGGTATCACG	ATCGACATTG	CGCTGTGGAA	GTTTCGAGTCG	CCCAAGTCGG	100
	TGTTACAGAT	CATCGATGCG	CCCGGCCACC	GCGACTTCAT	CAAGAACATG	150
	ATCACCGGCA	CGTCGCAGGC	GGATGCTGCC	ATTCTGATGA	TCGATTTCGAC	200
	GCAGGGTGGC	TTCGAGGCTG	GCATCTCGAA	GGACGGCCAG	ACGCGCGAGC	250
60	ACGCGCTGCT	GGCCTTCACG	CTGGGCGTGA	AGCAGATGGT	TGTGTGCTGC	300

	AACAAGATGG	ACGACAAGAC	GGTGCAGTAC	GCGCAGGCGC	GCTACGAGGA	350
	GATCAGCAAG	GAGGTGGGCG	CGTACCTGAA	GCGCGTGGGC	TACAACCCGG	400
	AGAAGGTGCG	CTTCATCCCG	ATCTCGGGCT	GGCAGGGCGA	CAACATGATC	450
	GAGAAGTCCG	ACAACATGTC	GTGGTACAAG	GGTCCCACGC	TGCTGGAGGC	500
5	GCTGGACATG	CTGGAGGCGC	CGGTGCGCCC	GGTGACAAG	CCGCTGCGCC	550
	TGCCCCGTGCA	GGACGTGTAC	AAGATCGGCG	GCATTGGCAC	GGTGCCGGTG	600
	GGCCGTGTGG	AGACCGGCAT	CATGAAGCCC	GGCGACGTGG	TGACGTTTCGC	650
	GCCCCCAAC	GTGACGACGG	AGGTGAAGTC	GATCGAGATG	CACCACGAGC	700
	AGCTGCAGGA	GGCTGTGCCC	GGCGACAACG	TGGGCTTCAA	CGTGAAGAAC	750
10	GTGTGCGGTGA	AGGACATCCG	CCGTGGTAAC	GTGTGTGGCA	ACTCGAAGAA	800
	CGACCCGCCG	AAGGAGGCGG	CTGACTTCAC	GGCGCAGGTG	ATCGTGCTGA	850
	ACCACCCCGG	CCAGATCAGC	AACGGCTACG	CGCCGGTGCT	GGACTGCCAC	900
	ACCAGCCACA	TCGCGTGCCG	CTTCGCGGAC	ATCGAGTCGA	AGATCGACCG	950
	CCGCTCCGGC	AAGGAGCTGG	AGAAGAACCC	CAAGTCCATC	AAGTCCGGCG	1000
15	ACGCCGCCAT	CGTGAAGATG	GTGCCGCAGA	AGCCGATGTG	CGTGGAGGTG	1050
	TTCAACGACT	ACCCGCCGCT	GGGCCGCTTT	GCGGTGCGCG	ACATGCGCCA	1100
	AACCGTTGCC	GTCG				1114

20

2) INFORMATION FOR SEQ ID NO: 522

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1106 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

30

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Leishmania major*
 (B) STRAIN: ATCC 50122

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 522

	TACGCGTGGG	TGCTCGACAA	GCTGAAGGCG	GAGCGCGAGC	GCGGCATCAC	50
	GATCGACATT	GCGCTGTGGA	AGTTCGAGTC	GCCCCAAGTCC	GTGTTTCACGA	100
	TCATCGATGC	GCCCCGCCAC	CGCGACTTCA	TCAAGAACAT	GATCACGGGC	150
40	ACGTGCGAGG	CGGACGCCGC	CATTCTGATG	ATCGACTCGA	CGCATGGCGG	200
	CTTCGAGGCT	GGCATCTCGA	AGGACGGCCA	GACCCGCGAG	CACGCGCTGC	250
	TTGCCTTAC	TCTTGCCGTG	AAGCAGATGG	TGGTGTGCTG	CAACAAGATG	300
	GACGACAAGA	CGGTGACGTA	CGCGCAGTCR	CGCTACGATG	AGATCAGCAA	350
	GGAGGTGGGC	GCGTACCTGA	AGCGCGTGGG	CTACAACCCG	GAGAAGGTGC	400
45	GCTTCATCCC	GATCTCGGGC	TGGCAGGGCG	ACAACATGAT	CGAGAAGTGC	450
	GACAACATGC	CGTGGTACAA	GGGTCCCACG	CTGCTGGACG	CGCTCGACAT	500
	GCTGGAGCCG	CCGGTGCGCC	CGGTGGACAA	GCCGCTGCGC	CTGCCCCCTGC	550
	AGGACGTGTA	CAAGATCGGC	GGTATCGGGA	CGGTGCCCCGT	GGGCCGCGTG	600
	GAGACCGGCA	TCATGAAGCC	GGGCGACGTG	GTGACGTTTCG	CGCCCGCCAA	650
50	CGTGACGACT	GAGGTGAAGT	CGATCGAGAT	GCACCACGAG	CAGCTGGCGG	700
	AGGCGCAGCC	CGGCGACAAC	GTCGGCTTCA	ACGTGAAGAA	CGTGTCGGTG	750
	AAGGACATCC	GCCGTGGTAA	CGTGTGCGGC	AACTCGAAGA	ACGACCCGCC	800
	GAAGGAGGCG	GCCGACTTCA	CGGCGCAGGT	GATCGTGCTG	AACCACCCCG	850
	GCCAGATCAG	CAACGGCTAT	GCGCCGGTGC	TGGACTGCCA	CACGAGCCAC	900
55	ATTGCGTGCC	GCTTCGCGGA	AATCGAGTCC	AAGATCGACC	GCCGCTCCGG	950
	CAAGGAGCTG	GAGAAGAACC	CCAAGGCGAT	CAAGTCTGGC	GATGCCGCGA	1000
	TCGTGAAGAT	GGTGCCGCAG	AAGCCGATGT	GCGTGGAGGT	GTTCAACGAC	1050
	TACGCGCCGC	TGGGCCGCTT	TGCCGTGCGC	GACATGCGCC	AAACCGTTGC	1100
	CGTCGG					1106

60

2) INFORMATION FOR SEQ ID NO: 523

- 5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1105 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

10

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 15 (A) ORGANISM: *Leishmania amazonensis*
 (B) STRAIN: ATCC 50131

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 523

20 TACGCGTGGG TGCTCGACAA GCTGAAGGCG GAGCGCGAGC GCGGCATCAC 50
 GATCGACATT GCGCTGTGGA AGTTCGAGTC GCCGAAGTCC GTGTTCACGA 100
 TCATCGATGC GCCCGGCCAC CGCGACTTCA TCAAGAACAT GATCACGGGC 150
 ACGTCGCAGG CGGACGCGGC CATCCTGATG ATCGACTCGA CGCATGGTGG 200
 CTTTCGAGGCT GGCATCTCGA AGGACGGCCA GACCCGCGAG CACGCGCTGC 250
 TTGCCTTCAC TCTTGCGCTG AAGCAGATGG TGGTGTGCTG CAACAAGATG 300
 25 GACGACAAGA CCGTGATGTA CGCGCAGTCG CGCTACGATG AGATCAGCAA 350
 GGAGGTGAGC GCGTACCTGA AGCGCGTGGG CTACAACCCG GAGAAGGTGC 400
 GCTTCATCCC GATCTCGGGG TGGCAGGGCG ACAACATGAT CGACAAGTCG 450
 GACAACATGC CGTGGTACAA GGGTCCCACG CTGCTGGACG CGCTCGACAT 500
 GCTGGAGCCG CCGGTGCGCC CGGTGGACAA GCCGCTGCGC CTGCCCCCTGC 550
 30 AGGACGTGTA CAAGATCGGC GGTATCGGGA CCGGTGCCCCGT GGGCCGCGTG 600
 GAGACCGGGA TCATGAAGCC GGGCGACGTG GTGACGTTTCG CGCCCGCCAA 650
 CGTGACGACT GAGGTGAAGT CGATCGAGAT GCACCACGAG CAGCTGGCGG 700
 AGGCGCAGCC CGGCGACAAC GTCGGCTTCA ACGTGAAGAA CGTGTCGGTG 750
 AAGGACATCC GCCGTGGTAA CGTGTGCGGC AACTCGAAGA ACGACCCGCC 800
 35 GAAGGAGGCG GCCGACTTCA CGGCGCAGGT GATCGTGCTG AACCACCCCG 850
 GCCAGATCAG CAACGGCTAC GCGCCGGTGC TGGACTGCCA CACGAGCCAC 900
 ATCGCGTGCC GCTTCGCGGA GATCGAGTCC AAGATCGACC GCCGCTCCGG 950
 CAAGGAGCTG GAGAAGAACC CCAAGGCGAT CAAGTCTGGC GACGCCGCGA 1000
 TCGTGAAGAT GGTGCCGCGA AAGCCGATGT CCGTGGAGGT GTTCAACGAC 1050
 40 TACGCGCCGC TGGGCCGCTT TGCCGTGCGC GACATGCGCC AAACCGTTGC 1100
 CGTCG 1105

45 2) INFORMATION FOR SEQ ID NO: 524

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1098 bases
 (B) TYPE: Nucleic acid
 50 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

55 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Leishmania mexicana*
 (B) STRAIN: ATCC 50156

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 524

60

	TACGCGTGGG	TGCTCGACAA	GCTGAAGGCG	GAGCGCGAGC	GCGGCATCAC	50
	GATCGACATT	GCGCTGTGGA	AGTTCGAGTC	GCCGAAGTCC	GTGTTACGA	100
	TCATCGATGC	GCCCCGCCAC	CGCGACTTCA	TCAAGAACAT	GATCACGGGC	150
	ACGTCGCAGG	CGGACGCGGC	CATCCTGATG	ATCGACTCGA	CGCATGGTGG	200
5	CTTCGAGGCT	GGCATCTCGA	AGGACGGCCA	GACCCGCGAG	CACGCGTGC	250
	TTGCCTTCAC	TCTTGGCGTG	AAGCAGATGG	TGGTGTGCTG	CAACAAGATG	300
	GACGACAAGA	CGGTGATGTA	CGCGCAGTCG	CGCTACGATG	AGATCAGCAA	350
	GGAGGTGAGC	GCGTACCTGA	AGCGCGTGGG	CTACAACCCG	GAGAAGGTGC	400
	GCTTCATCCC	GATCTCGGGG	TGGCAGGGCG	ACAACATGAT	CGACAAGTCG	450
10	GACAACATGC	CGTGGTACAA	GGGTCCCACG	CTGCTGGACG	CGCTCGACAT	500
	GCTGGAGCCG	CCGGTGCGCC	CGGTGGACAA	GCCGCTGCGC	CTGCCCCCTGC	550
	AGGACGTGTA	CAAGATCGGC	GGTATCGGGA	CGGTGCCCCGT	GGGCCGCGTG	600
	GAGACCGGGA	TCATGAAGCC	GGGCGACGTG	GTGACGTTTCG	CGCCCGCCAA	650
	CGTGACGACT	GAGGTGAAGT	CGATCGAGAT	GCACCACGAG	CAGCTGGCGG	700
15	AGGCGCAGCC	CGGCGACAAC	GTCGGCTTCA	ACGTGAAGAA	CGTGTCGGTG	750
	AAGGACATCC	GCCGTGGTAA	CGTGTGCGGC	AACTCGAAGA	ACGACCCGCC	800
	GAAGGAGGCG	GCCGACTTCA	CGGCGCAGGT	GATCGTGCTG	AACCACCCCG	850
	GCCAGATCAG	CAACGGCTAC	GCGCCGGTGC	TGGACTGCCA	CACGAGCCAC	900
	ATCGCGTGCC	GCTTCGCGGA	GATCGAGTCC	AAGATCGACC	GCCGCTCCGG	950
20	CAAGGAGCTG	GAGAAGAACC	CCAAGGCGAT	CAAGTCTGGC	GACGCCGCGA	1000
	TCGTGAAGAT	GGTGCCGCAG	AAGCCGATGT	GCGTGGAGGT	GTTCAACGAC	1050
	TACGCGCCGC	TGGGCCGCTT	TGCCGTGCGC	GACATGCGCC	AAACCGTT	1098

25

2) INFORMATION FOR SEQ ID NO: 525

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1081 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

35

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Leishmania tarentolae*
 (B) STRAIN: II WT

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 525

	GCTGAAGGCG	GAGCGCGAGC	GCGGCATCAC	GATCGACATT	GCGCTGTGGA	50
	AGTTCGAGTC	GCCCAAGTCG	GTGTTACGA	TCATCGATGC	GCCCCGCCAC	100
	CGCGACTTCA	TCAAGAACAT	GATCACGGGC	ACGTCGCAGG	CGGACGCGGC	150
45	CATCCTGATG	ATCGACTCGA	CGCACGGTGG	GTTCGAGGCT	GGCATCTCGA	200
	AGGACGGGCA	GACGCGCGAG	CACGCGCTGC	TTGCCTTCAC	TCTTGGCGTG	250
	AAGCAGATGG	TTGTGTGCTG	CAACAAGATG	GACGACAAGA	CGGTGATGTA	300
	CGCGCAGTCG	CGCTACGATG	AGATCAGCAA	GGAGGTGGGC	GCGTACCTGA	350
	AGCGCGTGGG	CTACAACCCG	GAGAAGGTGC	GCTTCATCCC	GATCTCGGGC	400
50	TGGCAGGGCG	ACAACATGAT	CGAGAAGTCG	GACAACATGC	CGTGGTACAA	450
	GGGTCCCACG	CTGCTGGACG	CGCTCGACAT	GCTGGAGGCG	CCGGTGCGCC	500
	CGGTGGACAA	GCCGCTGCGC	CTGCCCCCTGC	AGGACGTGTA	CAAGATCGGC	550
	GGCATCGGCA	CGGTGCCCCGT	GGGCCGCGTG	GAGACCGGCA	TCATGAAGCC	600
	GGGCGACGTG	GTGACGTTTCG	CGCCCGCGAA	CGTGACGACG	GAGGTGAAGT	650
55	CGATCGAGAT	GCACCACGAG	CAGCTGGCGG	AGGCGCAGCC	CGGCGACAAC	700
	GTCGGCTTCA	ACGTGAAGAA	CGTGTGCGTG	AAGGACATCC	GCCGTGGGAA	750
	CGTGTGCGGT	AACTCGAAGA	ACGACCCGCC	GAAGGAGGCC	GCCGACTTCA	800
	CGGCGCAGGT	GATCGTGCTG	AACCACCCCG	GCCAGATCAG	CAACGGCTAC	850
	GCGCCGGTGC	TGGACTGCCA	CACGAGCCAC	ATCGCGTGCC	GGTTCGCGGA	900
60	CATCGAGTCC	AAGATTGACC	GCCGCTCCCG	CAAGGAGCTG	GAGAAGAACC	950

CCAAGGCGAT	CAAGTCCGGC	GATGCCGCGA	TCGTGAAGAT	GGTGCCGCGAG	1000
AAGCCGATGT	GCGTGGAGAT	GTTCAACGAC	TACGCGCCGC	TTGGCCGCTT	1050
TGCTGTGCGC	GACATGCGCC	AAACCGTTGC	C		1081

5

2) INFORMATION FOR SEQ ID NO: 526

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 1102 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

15 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Leishmania tropica*
 (B) STRAIN: ATCC 50129

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 526

AAATACGCGT	GGGTGCTCGA	CAAGCTGAAG	GCGGAGCGCG	AGCGCGGCAT	50
CACGATCGAC	ATTGCGCTGT	GGAAGTTCGA	GTCGCCCAAG	TCCGTGTTCA	100
25 CGATCATCGA	TGCGCCCGGC	CACCGCGACT	TCATCAAGAA	CATGATCACG	150
GGCACGTGCG	AGGCGGACGC	CGCCATCCTG	ATGATCGACT	CGACGCATGG	200
TGGCTTCGAG	GCTGGCATCT	CGAAGGACGG	CCAGACCCGC	GAGCACGCGC	250
TGCTTGCTT	CACKCTTGGC	GTGAAGCAGA	TGGTGGTGTG	CTGCAACAAG	300
ATGGACGACA	AGACGGTGAC	GTACGCGCAG	TCGCGCTACG	ATGAGATCAG	350
30 CAAGGAGGTG	GGCGCGTACC	TGAAGCGCGT	GGGCTACAAC	CCGGAGAAGG	400
TGCGCTTCAT	CCCGATCTCG	GGCTGGCAGG	GCGACAACAT	GATCGAGAAG	450
TCGGACAACA	TGCCGTGGTA	CAAGGGTCCC	ACGCTGCTGG	ACGCGCTCGA	500
CATGCTGGAG	CCGCCGGTGC	GCCCCGTGGA	CAAGCCGCTG	CGCCTGCCCC	550
TGCAGGACGT	GTACAAGATC	GGCGGTATCG	GGACGGTGCC	CGTGGGGCGC	600
35 GTGGAGACCG	GCATCATGAA	GCCGGGCGAC	GTGGTGACGT	TCGCGCCCGC	650
CAAGTGACG	ACTGAGGTGA	AGTCGATCGA	GATGCACCAC	GAGCAGCTGG	700
CGGAGGCGCA	GCCCCGGCGA	AACGTCGGCT	TCAACGTGAA	GAACGTGTCTG	750
GTGAAGGACA	TCCGCCGTGG	TAACGTGTGC	GGCAACTCGA	AGAACGACCC	800
GCCGAAGGAG	GCGGCCGACT	TCACGGCGCA	GGTGATCGTG	CTGAACCACC	850
40 CCGGCCAGAT	CAGCAACGGC	TACGCGCCGG	TGCTGGACTG	CCACACGAGC	900
CACATTGCGT	GCCGCTTCGC	GGAAATCGAG	TCCAAGATCG	ACCGCCGCTC	950
CGGCAAGGAG	CTGGAGAAGA	ACCCCAAGGC	GATCAAGTCT	GGCGATGCCG	1000
CGATCGTGAA	GATGGTGCCG	CAGAAGCCGA	TGTGCGTGGA	GGTGTTCAAC	1050
GACTACGCGC	CGCTGGGCCG	CTTTGCCGTG	CGCGACATGC	GCCAAACCGT	1100
45 TG					1102

2) INFORMATION FOR SEQ ID NO: 527

50

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1105 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 55 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 60 (A) ORGANISM: *Neospora caninum*
 325

(B) STRAIN: Suarez-4

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 527

5	GGACRAACTT	AAAGCTGAAC	GTGAGCGTGG	TATCACCATT	GATATCTCCC	50
	TGTGGAAATT	TGAGACCAGC	AAGTACTATG	TTACCATCAT	TGATGCCCCA	100
	GGACACAGAG	ACTTCATCAA	AAACATGATT	ACAGGCACAT	CCCAGGCTGA	150
	CTGTGCTGTC	CTGATTGTTG	CTGCTGGTGT	TGGTGAATTT	GAAGCCGGTA	200
	TCTCCAAGAA	CGGGCAGACC	CGTGAGCATG	CCCTTNTGGC	TTACACCCTG	250
10	GGTGTGAAAC	AACTAATTGT	TGGCGTTAAC	AAAAKGGATT	CCACTGAGCC	300
	ACCCTATAGC	CARAAGAGAT	ACGARGAAAT	TGTTAAGGAA	GTCAGCMCCT	350
	AYNTTAAAAA	AATTGGYTAC	AACCCCGACA	CAGTANCATT	TGKGCCAATT	400
	TNTGGCTGGA	ATGGTGACAA	CATGCTGGAN	CCAAGTGCTA	ATATGCCATG	450
	GTTCAAGGGA	TGGAAAGTCM	CCCGTAAGGA	CGGCAATGCC	AGKGGAAACM	500
15	CCCTGCTTGA	AGCTYTGGAT	TGCATTYTGC	CACCAAYTTG	CCCAACTGAC	550
	AAACCCCTGC	GTTTGCCTYT	CCAGGATGTC	TATAAAATTG	GKGGTATTGG	600
	TACTGTCCCT	GTGGGTCGTG	TGGAGACTGG	TGTTCTCAA	CCTGGCATGG	650
	TGGTCACCTT	TGCTCCAGTC	AATGTAACAA	CTGAAGTGAA	GTCTGTAGAA	700
	ATGCACCATG	AAGCATTGAG	TGAAGCCCTT	CCTGGGGACA	ATGTGGGCTT	750
20	CAATGTCAAG	AACGTGTCTG	TCAAAGATGT	CCGTCGTGGC	AATGTGGCTG	800
	GTGACAGCAA	AAATGATCCA	CCCATGGAAG	CTGCTGGCTT	CACAGCTCAG	850
	GTGATTATTT	TGAACCATCC	AGGCCAAATC	AGTGCTGGAT	ATGCACCTGT	900
	GCTGGATTGT	CACACAGCTC	ACATTGCTTG	CAAGTTTGCT	GAGCTGAAGG	950
	AGAAGATTGA	TCGTCGTTCT	GGGAAAAAGC	TGGAAGATGG	CCCTAAATTC	1000
25	TTGAAATCTG	GTGACGCTGC	CATCGTTGAT	ATGGTTCCTG	GCAAGCCCAT	1050
	GTGTGTCGAG	AGCTTCTCTG	ATTATCCTCC	CCTGGGCCGT	TTTGCTGTGC	1100
	GTGAC					1105

30

2) INFORMATION FOR SEQ ID NO: 528

(i) SEQUENCE CHARACTERISTICS:

- | | | |
|----|-----|----------------------|
| 35 | (A) | LENGTH: 935 bases |
| | (B) | TYPE: Nucleic acid |
| | (C) | STRANDEDNESS: Double |
| | (D) | TOPOLOGY: Linear |

(ii) MOLECULE TYPE: Genomic DNA

40

(vi) ORIGINAL SOURCE:

- | | | |
|--|-----|--|
| | (A) | ORGANISM: <i>Trichomonas vaginalis</i> |
| | (B) | STRAIN: ATCC 30001 |

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 528

	GCACATCCCA	GGCTGATGCT	GCTATCCTTG	TCATCGACTC	CACACTCGGT	50
	GGYTTGGAAG	CCGGTATCGC	TGAACAAGGC	CAGACACGTG	AACACGCTCT	100
	TCTTGCCTTC	AACTTCGGCA	TCAAGCAGGT	CATTGTCGCC	GTCAACAAGA	150
50	TGGATGACAA	GACAGTCAAC	TACAACAAGG	CYCGTTTCGA	CGAAATCACA	200
	GCCGAAATGA	CACGCATCCT	TACAGGCATC	GGCTACAAGC	CAGAAATGTT	250
	CCGCTTCGTC	CCAATCTCCG	GCTGGGCTGG	CGACAACATG	ACAGAGAAGT	300
	CTCCAAACAT	GCCATGGTAC	AATGGCCCAT	ACCTTCTTGA	AGCCCTCGAT	350
	TCCCTTCAGC	CACCAAAGCG	CCCATTGAC	AAGCCACTCC	GTCTTCCACT	400
55	CCAGGATGTC	TACAAGATCA	ACGGTATCGG	TACAGTTCCA	GTCGGCCGTG	450
	TCGAATCCGG	CACAATGAAG	CCAGGCATGA	TCGTTAACTT	CGCCCCATCC	500
	ACAGTTACAG	CTGAAGTTAA	GTCCATCGAA	ATGCACCACG	AATCCCTTCC	550
	AGAGGCTCTT	CCAGGTGACA	ACATCGGCTT	CAACGTCAAG	AACGTTTCCA	600
	CAGCTGATGT	CAAGCGTGGC	TACGTCGTTG	GTGATACAAA	GCGTGACCCA	650
60	CCAGTCGAAT	GCGCTTCCTT	CACAGCTCAR	ATGATCATCT	CCAACCACCC	700

	AGGCAAGATC	CACGCCGGCT	ACCAGCCAGT	TTTCGACTGC	CACACAGCTC	750
	ACATCGCCTG	CAAGTTCGAC	AAGCTCATCC	AGCGTATCGA	TCGTGCGCAC	800
	GGCAAGAAGG	CTACAGAGAA	CCCAGAATAC	ATTCAGAAGG	ATGATGCCGC	850
	TATCGTCGAG	GTTGTCCCAT	CCAAGCCACT	CGTCGTGAG	TCCTTCCAGG	900
5	AGTACCCACC	ACTCGGCCGT	TTCGCCATCC	GTGAT		935

2) INFORMATION FOR SEQ ID NO: 529

10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1065 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 15 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 20 (A) ORGANISM: *Trypanosoma brucei* subsp. *brucei*
 (B) STRAIN: EATRO795

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 529

25	AAGCTGAAGG	CTGAGCGCGA	ACGTGGTATC	ACGATCGACA	TTGCACTGTG	50
	GAAATTCGAG	TCACCCAAGT	CTGTCTTCAC	TATTATTGAT	GCTCCTGGGC	100
	ACCGTGACTT	CATCAAGAAC	ATGATCACCG	GCACATCGCA	AGCCGACGCA	150
	GCCATCCTCA	TCATTGCCTC	TGCGCAGGGT	GAGTTCGAGG	CTGGTATCTC	200
	CAAGGATGGA	CAGACCCGCG	AGCACGCGTT	GCTGGCCTTC	ACTTTGGGTG	250
30	TGAAGCAGAT	GGTTGTGTGC	TGCAACAAGA	TGGACGACAA	GACTGTGAAC	300
	TACGGACAGG	AGCGGTATGA	CGAGATTGTG	AAGGAGGTGT	CTGCTTACAT	350
	CAAGAAGGTT	GGGTACAACG	TGGAGAAGGT	GCGCTTCGTC	CCCATCTCCG	400
	GATGGCAGGG	CGACAACATG	ATTGAGAAAT	CCGAGAAGAT	GCCATGGTAC	450
	AAGGGTCCAA	CGCTCCTGGA	GGCACTAGAC	ATGCTGGAGC	CACCAAGTGC	500
35	TCCGAGCGAC	AAGCCCCTGC	GTCTGCCACT	GCAGGACGTG	TACAAGATCG	550
	GTGGTATTGG	CACCGTGCCC	GTTGGTCGTG	TGGAGACCGG	CGTGATGAAG	600
	CCTGGTGATG	TGGTGACGTT	TGCCCCCGCC	AACGTGACGA	CCGAGGTGAA	650
	ATCGATCGAG	ATGCACCACG	AGCAGTCTCG	TGAGGCGACC	CCCGGTGACA	700
	ACGTCGGCTT	TAACGTGAAG	AACGTTTCTG	TAAAGGACAT	CCGCCGTGGC	750
40	AACGTCTGCG	GTAACACCAA	GAACGACCCC	CCAAAGGAGG	CCGCCGACTT	800
	CACGGCACAG	GTGATCATCC	TGAACCACCC	CGGACAGATT	GGAAACGGTT	850
	ATGCGCCCCG	GCTGGACTGC	CACACATCGC	ACATTGCCTG	CAAGTTCGCG	900
	GAGATCGAGT	CGAAGATCGA	CCGTCGCTCT	GGCAAGGAGC	TGGAGAAGGC	950
	TCCCAAGTCG	ATCAAGTCTG	GCGACGCCGC	GATCGTGCGC	ATGGTGCCGC	1000
45	AGAAGCCTAT	GTGCGTGGAG	GTCTTCAACG	ACTACGCGCC	ACTCGGCCGC	1050
	TTTGCCGTGC	GTGAC				1065

50 2) INFORMATION FOR SEQ ID NO: 530

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1297 bases
 (B) TYPE: Nucleic acid
 55 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

60 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Crithidia rasciculata*

(B) STRAIN: ATCC 11745

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 530

5
TTCGCGGAGG GCGTGCCGCC GGTGCTGACG GCGCTGGACG TGACGGAGGA 50
CCTCGGCCGC GACGAGCCGC TGACGCTGGA GATTGTGCAG CACTTGGACG 100
CGAACACCGG CCGCTGCATT GCCATGCAGA CGACGGATCT GCTGAAGCTG 150
AAGTCGAAGG TTGTGTCGAC GGGCGGCAAC ATCTCCGTGC CGGTTGGCCG 200
10 CGAGACGCTG GGCCGCATCT TCAACGTGCT CGGCGACGCG ATCGACCAGC 250
GCGGTGTGGT GGGCGAGAAG ATGCGCATGC CGATCCACGC CGAGGCGCCG 300

AAGCTGGCGG ACCAGGCCGC GGAGGACGCG ATTCTGACGA CCGGCATCAA 350
GGTGATCGAC CTGATTCTGC CGTACTGCAA GGGTGGCAAG ATCGGGCTGT 400
TCGGCGGTGC TGGTGTGGGC AAGACTGTGA TCATCATGGA GCTGATCAAC 450
15 AACGTGGCCA AGGGCCACGG TGGTTTCTCC GTGTTCGCCG GCGTTGGCGA 500
GCGCACCCGC GAGGGCACGG ATCTGTACCT GGAGATGATG CAGTCGAAGG 550
TCATTGACCT GAAGGGCGAG TCGAAGTGCG TGCTGGTGTA CGGCCAGATG 600
AACGAGCCCC CGGGTGCGCG TCGCGTGTG GCGCAGTCTG CGCTGACGAT 650
GGCGGAGTAC TTCCGTGACG TGGAGGGCCA GAACGTGCTG CTGTTCATCG 700
20 ACAACATCTT CCGCTTCACC CAGGCCAACT CCGAGGTGTC CGCCCTGCTG 750
GGCCGCATTC CCGCCGCCGT GGGCTACCAG CCGACGCTTG CCGAGGATCT 800
TGGTATGCTG CAGGAGCGCA TTACGTCGAC GACGAAGGGC TCGATTACGT 850
CTGTGCAGGC CGTGTACGTG CCGGCCGATG ATATCACGGA TCCGGCGCCG 900
GCGACGACCT TCTCGCACCT GGATGCGACG ACGGTGCTGG ACCGCGCGGT 950
25 TGCCGAGTCT GGCATCTACC CCGCCGTGAA CCCGCTGGAG TGCGCGTCCG 1000
GTATCATGGA CCCCAGATGT ATCGACGTGG ACCACTACAA CGTTGCGCAG 1050
GATATCGTGC AGATGCTGAC CAAGTACAAG GAGCTGCAGG ATATCATTGC 1100
CGTGCTGGGT ATCGACGAGC TGAGCGAGGA GGACAAGCTT GTGGTGGACC 1150
GCGCTCGCAA GGTGACGCGC TTCCTGTGCG AGCCGTTCCA GGTGGCCGAG 1200
30 GTGTTACCGG GCATGACGGG CCACTACGTG CAGCTGGAGG ACACAGTGGA 1250
GTCGTTCTCT GGCCTGCTGA TGGGCTCGTA CGACCAGATC CCGGAGA 1297

35 2) INFORMATION FOR SEQ ID NO: 531

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1298 bases
(B) TYPE: Nucleic acid
40 (C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

45 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Leishmania tropica*

(B) STRAIN: ATCC 30816

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 531

50
CTTCTCGGAG GGCGTGCCGC CCGTGCTGAC GGCGCTGGAT GTGACGGAGG 50
ACCTTGGCCG CGATGAGCCG CTGACGCTGG AGATCGTGCA GCACTTGGAC 100
GCGAACACGG GCCGCTGCAT TGCGATGCAG ACGACGGACC TGCTGAAGCT 150
GAAGTCGAAG GTCGTGTCGA CCGGCGGCAA CATCTCTGTG CCGGTGGGCC 200
55 GTGAGACGCT GGGCCGCATC TTCAAYGTTT TGGGCGACGC GATCGACCAG 250
CGCGGCCCCG TGGGCGAGAA GATGCGCATG GCGATCCACG CCGAGGCCCC 300
GAAGCTGGCG GATCAGGCCG CGGAGGACAC GATCCTGACG ACCGGCATCA 350
AGGTGATCGA CCTGATTCTG CCCTACTGCA AGGGTGGCAA GATCGGCCTG 400
TTCGGCGGTG CCGGTGTGGG CAAGACTGTG ATCATCATGG AGCTGATCAA 450
60 CAACGTCGCG AAGGGCCACG GCGGTTTCTC CGTGTTTGCC GCGTTGGCG 500

	AGCGCACGCG	CGAGGGCAGC	GACCTGTACC	TGGAGATGAT	GCAGTGAAG	550
	GTGATTGACC	TGAAGGGCGA	GTCGAAGTGY	GTGCTTGTGT	ATGGGCAGAT	600
	GAACGAGCCC	CCGGGTGCGC	GCGCGCGCGT	TGCGCAGTCT	GCGCTGACGA	650
	TGGCGGAGTA	CTTCCGCGAC	GTGGAGGGCC	AGAACGTGCT	GCTGTTTCATC	700
5	GACAACATCT	TCCGCTTCAC	GCAGGCGAAC	TCCGAGGTGT	CTGCGCTGCT	750
	GGGCCGCATT	CCGGCCGCCG	TGGGCTACCA	GCCGACGCTT	GCGGAGGATC	800
	TTGGTATGCT	GCAGGAGCGC	ATCACGTCGA	CAACGAAGGG	GTCGATCACG	850
	TCCGTGCAGG	CCGTGTACGT	GCCAGCGGAT	GATATCACGG	ATCCCGCGCC	900
	CGCGAGCAGC	TTCTCGCACC	TGGACGCGAC	GACTGTGCTG	GACCGCGCGG	950
10	TGGCGGAGTG	GGGCATCTAC	CCTGCCGTGA	ACCCGCTGGA	GTGCGCGTGC	1000
	CGTATCATGG	ACCCTGATGT	GATCGATGTG	GACCACTACA	ACGTTGCGCA	1050
	GGATATCGTG	CAGATGCTGA	CCAAGTACAA	GGAGCTGCAG	GATATCATTG	1100
	CGGTGCTTGG	CATCGACGAG	CTGAGCGAGG	AAGACAAGGT	TGTTGTGGAC	1150
	CGCGCGCGCA	AGGTGACCCG	GTTCTGTGTC	CAGCCGTTCC	AGGTTGCGGA	1200
15	GGTGTTCACG	GGCATGACGG	GCCACTACGT	GCAGCTGGTC	GACACGGTGG	1250
	AGTCGTTCTC	TGGCCTGCTG	ATGGGGTCGT	ACGACCAGAT	CCCGGAGA	1298

20 2) INFORMATION FOR SEQ ID NO: 532

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1297 bases
 (B) TYPE: Nucleic acid
 25 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

30 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Leishmania aethiopica*
 (B) STRAIN: ATCC 50119

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 532

35	TTCTCGGAGG	GCGTGCCGCC	CGTGCTGACG	GCGCTGGATG	TGACGGAGGA	50
	CCTTGGCCGC	GATGAGCCGC	TGACGCTGGA	GATCGTGCAG	CACTTGGACG	100
	CGAACACCGG	CCGCTGCATT	GCGATGCAGA	CGACGGACCT	GCTGAAGCTG	150
	AAGTCGAAGG	TTGTGTGCGC	CGGCGGCAAC	ATCTCTGTGC	CGGTGGGCCG	200
40	TGAGACGCTG	GGCCGCATCT	TCAACGTTCT	GGCGACGCG	ATCGACGACG	250
	GCGGCCCCGT	GGCGGAGAAG	ATGCGCATGG	GATCCACGC	CGAGGCCCCA	300
	AAGCTGGCGG	ATCAGGCCGC	GGAGGACACG	ATCCTGACGA	CCGGCATCAA	350
	GGTGATCGAC	CTGATTCTGC	CCTACTGCAA	GGGTGGCAAG	ATCGGCCTGT	400
	TCGGCGGTGC	CGGTGTGGGC	AAGACTGTGA	TCATCATGGA	GCTGATCAAC	450
45	AACGTCGCGA	AGGGCCACGG	TGGTTTCTCC	GTGTTTGCCG	GCGTTGGCGA	500
	GCGCACGCGC	GAGGGCACGG	ACCTGTACCT	GGAGATGATG	CAGTCGAAGG	550
	TGATTGACCT	GAAGGGCGAG	TCGAAGTGCG	TGCTTGTGTA	CGGGCAGATG	600
	AACGAGCCCC	CGGGTGCGCG	GCGCGCGGTT	GCGCAGTCTG	CGCTGACGAT	650
	GGCGGAGTAC	TTCCGCGACG	TGGAGGGCCA	GAACGTGCTG	CTGTTTCATCG	700
50	ACAACATCTT	CCGCTTCACG	CAGGCGAACT	CCGAGGTGTC	TGCGCTGCTG	750
	GGCCGCATTC	CAGCCGCCGT	GGGCTACCAG	CCGACGCTTG	CGGAGGATCT	800
	TGGTATGCTG	CAGGAGCGCA	TCACGTCGAC	AACGAAGGGG	TCGATCACGT	850
	CCGTGCAGGC	CGTGTACGTG	CCAGCGGATG	ATATCACGGA	TCCCGCGCCC	900
	GCGACGACGT	TCTCGCACCT	GGACGCGACG	ACTGTGCTGG	ACCGCGCGGT	950
55	GGCGGAGTCG	GGCATCTACC	CTGCCGTGAA	CCCGCTGGAG	TGCGCGTCGC	1000
	GTATCATGGA	CCCCGACGTG	ATCGATGTGG	ACCACTACAA	CGTTGCGCAG	1050
	GATATCGTGC	AGATGCTGAC	CAAGTACAAG	GAGCTGCAGG	ATATCATTGC	1100
	GGTGCTTGGC	ATCGACGAGC	TGAGCGAGGA	AGACAAGGTT	GTTGTGGACC	1150
	GCGCGCGCAA	GGTGACCCCG	TTCCTGTGCG	AGCCGTTCCA	GGTTGCGGAG	1200
60	GTGTTACGCG	GCATGACGGG	CCACTACGTG	CAGCTGGTCG	ACACGGTGGG	1250

5 2) INFORMATION FOR SEQ ID NO: 533

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1298 bases
 (B) TYPE: Nucleic acid
 10 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

15 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Leishmania donovani*
 (B) STRAIN: ATCC 50212

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 533

20 CTTCTCGGAG GCGGTGCCGC CCGTACTGAC GCGCTGGAT GTGACGGAGG 50
 ACCTTGGCCG CGATGAGCCG CTGACGCTGG AGATCGTGCA GCACTTGGAT 100
 GCGAACACCG GCCGCTGCAT TGCGATGCAG ACGACGGACC TGCTGAAGCT 150
 GAAGTCGAAG GTTGTGTCGA CCGGCGGCAA CATCTCTGTG CCGGTGGGCC 200
 25 GTGAGACGCT GGGCCGCATC TTCAACGTTT TGGGCGACGC GATCGACCAG 250
 CGCGGCCCCG TGGGCGAGAA GATGCGCATG GCGATCCACG CCGAGGCCCC 300
 GAAGCTGGCG GACCAGGCCG CGGAGGACAC GATCCTGACG ACCGGCATCA 350
 AGGTGATCGA CCTCATTTCT CCCTACTGCA AGGGCGGCAA GATCGGCCTG 400
 TTCGGCGGTG CCGGTGTGGG CAAGACTGTG ATCATCATGG AGCTGATCAA 450
 30 CAACGTCGCG AAGGGCCACG GTGGCTTCTC CGTGTTTGCC GCGGTTGGCG 500
 AGCGCACGCG CGAGGGCACG GACCTATAAC TGGAGATGAT GCAGTCGAAG 550
 GTGATTGACC TGAAGGGCGA GTCGAAGTGC GTGCTTGTGT ACGGGCAGAT 600
 GAACGAGCCC CCGGGTGCGC GCGCGCGCGT TCGCAGTCT GCGCTGACGA 650
 TGGCGGAGTA CTTCCGCGAC GTGGAGGGCC AGAACGTGCT GCTGTTTCATC 700
 35 GACAACATCT TCCGCTTCAC GCAGGCGAAC TCCGAGGTGT CTGCGCTGCT 750
 TGGCCGCATT CCGGCCGCCG TGGGCTACCA CCGACGCTT GCCGAGGATC 800
 TTGGTATGCT GCAGGAGCGC ATCACATCGA CGACGAAGGG GTCGATCACG 850
 TCCGTGCAGG CCGTGTACGT GCCGGCGGAT GATATCACGG ATCCCGCGCC 900
 CGCGACGACG TTCTCGCACC TGGACGCGAC GACTGTGCTG GACCGCGCGG 950
 40 TGGCGGAGTC GGGCATCTAC CCTGCCGTGA ACCCGCTGGA GTGCGCGTCG 1000
 CGTATCATGG ACCCCGATGT GATCGATGTG GACCACTACA ACGTTGCGCA 1050
 GGATATCGTG CAGATGCTGA CCAAGTACAA GGAGCTGCAG GATATCATTG 1100
 CCGTGCTTGG CATCGACGAG CTGAGCGAGG AGGACAAGGT TGTGGTGGAC 1150
 CGCGCGCGCA AGGTGACCCG GTTCCTGTG CAGCCGTTCC AGGTTGCGGA 1200
 45 GGTGTTACG GGCATGACGG GCCACTACGT GCAGCTGGCC GACACGGTGG 1250
 AGTCGTTCTC TGGCCTGCTG ATGGGGTCGT ACGACCAGAT CCCGGAGA 1298

50 2) INFORMATION FOR SEQ ID NO: 534

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1298 bases
 (B) TYPE: Nucleic acid
 55 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

60 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Leishmania infantum*
 (B) STRAIN: MOU

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 534

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5      CTTCTCGGAG GGCCTGCCGC CCGTACTGAC GGCGCTGGAT GTGACGGAGG      50
      ACCTTGGCCG CGATGAGCCG CTGACGCTGG AGATCGTGCA GCACTTGGAT      100
      GCCAACACCG GCCGCTGCAT TGCATGTCAG ACGACGGACC TGCTGAAGCT      150
      GAAGTCGAAG GTTGTGTCGA CCGGCGGCAA CATCTCTGTG CCGGTGGGCC      200
10     GTGAGACGCT GGGCCGCATC TTCAACGTTT TGGGCGACGC GATCGACCAG      250
      CGCGGCCCCG TGGGCGAGAA GATGCGCATG GCGATCCACG CCGAGGCCCC      300
      AAAGCTGGCG GACCAGGCCG CGGAGGACAC GATCCTGAAG ACCGGCATCA      350
      AGGTGATCGA CCTCATTTCT CCCTACTGCA AGGGCGGCAA GATCGGCCTG      400
      TTCGGCGGTG CCGGTGTGGG CAAGACTGTG ATCATCATGG AGCTGATCAA      450
15     CAACGTCGCG AAGGGCCACG GTGGCTTCTC CGTGTGTTGCC GCGTTGGCG      500
      AGCGCACGCG CGAGGGCACG GACCTATACC TGGAGATGAT GCAGTCGAAG      550
      GTGATTGACC TGAAGGGCGA GTCGAAGTGC GTGCTTGTGT ACGGGCAGAT      600
      GAACGAGCCC CCGGTGCGC GCGCGCGCGT TGCAGTCT GCGCTGACGA      650
      TGGCGGAGTA CTTCCGCGAC GTGGAGGGCC AGAACGTGCT GCTGTTTCATC      700
20     GACAACATCT TCCGCTTCAC GCAGGCGAAC TCCGAGGTGT CTGCGCTGCT      750
      GGGCCGCATT CCGGCCGCCG TGGGCTACCA GCCGACGCTT GCCGAGGATC      800
      TTGGTATGCT GCAGGAGCGC ATCACATCGA CGACGAAGGG GTCGATCACG      850
      TCCGTGCAGG CCGTGTACGT GCCGGCGGAT GATATCACTG ATCCCGCGCC      900
      CGCGACGACG TTCTCGCACC TGGACGCGAC GACTGTGCTG GACCGCGCGG      950
25     TGGCGGAGTC GGGCATCTAC CCTGCCGTGA ACCCGCTGGA GTGCGCGTCG      1000
      CGTATCATGG ACCCCGATGT GATCGATGTG GACCACTACA ACGTTGCGCA      1050
      GGATATCGTG CAGATGCTGA CCAAGTACAA GGAGCTGCAG GATATCATTG      1100
      CCGTGCTTGG CATCGACGAG CTGAGCGAGG AGGACAAGGT TGTGGTGGAC      1150
      CGCGCGCGCA AGGTGACCCG GTTCCTGTCT CAGCCGTTCC AGGTTGCGGA      1200
30     GGTGTTACG GGCATGACGG GCCACTACGT GCAGCTGGCC GACACGGTGG      1250
      AGTCGTCTC TGGCCTGCTG ATGGGGTCTG ACGACCAGAT CCCGGAGA      1298
  
```

35 2) INFORMATION FOR SEQ ID NO: 535

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1301 bases
 (B) TYPE: Nucleic acid
 40 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

45 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Leishmania gerbilli*
 (B) STRAIN: ATCC 50121

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 535

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50     GCACTTCTCG GAGGGCGTGC CGCCCGTGCT GACGGCGCTG GATGTGACGG      50
      AGGACCTTGG CCGCGATGAG CCGCTGACGC TGGAGATCGT GCAGCACTTG      100
      GACGCGAACA CCGGCCGCTG CATTGCGATG CAGACGACGG ACCTGCTGAA      150
      GCTGAAGTCG AAGGTTGTGT CGACCGGTGG CAACATCTCT GTGCCGGTGG      200
55     GCCGTGAGAC GCTGGGCCGC ATCTTCAACG TTCTGGGCGA TGCGATCGAC      250
      CAGCGCGGCC CCGTGGGCGA GAAGATGCGC ATGGCGATCC ACGCCGAGGC      300
      CCCGAAGCTG GCGGATCAGG CCGCGGAGGA CACGATCCTG ACGACCGGCA      350
      TCAAGGTGAT CGACCTGATT CTGCCCTACT GCAAGGGTGG CAAGATCGGY      400
      CTGTTCCGGC GTGCCGGTGT GGGCAAGACT GTGATCATCA TGGAGCTGAT      450
60     CAACAACGTC GCGAAGGGCC ACGGTGGTTT CTCCGTGTTT GCCGGCGTTG      500
  
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	GCGAGCGCAC	GCGCGAGGGC	ACGGACCTGT	ACCTGGAGAT	GATGCAATCG	550
	AAGGTGATTG	ACCTGAAGGG	CGAGTCGAAG	TGCGTGCTTG	TGTACGGGCA	600
	GATGAACGAG	CCCCCGGGTG	CGCGCGCGCG	CGTTGCGCAG	TCTGCGCTGA	650
	CGATGGCGGA	GTACTTCCGC	GACGTGGAGG	GCCAGAACGT	GCTGCTGTTC	700
5	ATCGACAACA	TCTTCCGCTT	CACGCAGGCG	AACTCCGAGG	TGTCCGCGCT	750
	GCTGGGCGCG	ATTCCGGCCG	CCGTGGGCTA	CCAGCCGACG	CTTGCGGAGG	800
	ATCTTGGTAT	GCTGCAGGAG	CGCATCACGT	CGACAACGAA	GGGGTCGATC	850
	ACGTCCGTGC	AGGCCGTGTA	CGTGCCAGCG	GATGATATCA	CGGATCCCGC	900
	GCCCCGCGACG	ACGTTCTCGC	ACCTTGACGC	GACGACTGTG	CTGGACCGCG	950
10	CGGTGGCGGA	GTCGGGCATC	TACCCTGCCG	TGAACCCGCT	GGAGTGCGCG	1000
	TCGCGTATCA	TGGACCCCGA	TGTGATCGAT	GTGGACCACT	ACAACGTTGC	1050
	GCAGGATATC	GTGCAGATGC	TGACCAAGTA	CAAGGAGCTG	CAGGACATCA	1100
	TTGCGGTGCT	TGGCATCGAC	GAGCTGAGCG	AGGAAGACAA	GGTTGTGGTG	1150
	GACCGCGCGC	GCAAGGTGAC	CCGGTTCCTG	TCGCAGCCGT	TCCAGGTTGC	1200
15	GGAGGTGTTC	ACGGGCATGA	CGGGCCACTA	CGTGCAGCTG	GTCGACACGG	1250
	TGGAGTCGTT	CTCTGGCTTG	CTGATGGGGT	CGTACGACCA	GATCCCGGAG	1300
	A					1301

20

2) INFORMATION FOR SEQ ID NO: 536

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1298 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

30

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Leishmania hertigi*
 (B) STRAIN: ATCC 50125

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 536

	CTTCGCGGAG	GGCGTGCCGC	CGGTGCTGAC	GTCGCTGGAT	GTGACGGAGA	50
	ACCTCGGCCG	CGATGAGCCG	CTGACGCTGG	AGATTGTGCA	GCACTTGAC	100
	GCGAACACCG	GTCGCTGCAT	TGCGATGCAG	ACGACGGACC	TGCTGAAGCT	150
40	GAAGTCGAAG	GTCGTGTCGA	CCGGTGGCAA	CATCTCTGTG	CCTGTTGGCC	200
	GCGAGACGCT	GGGTGCGATC	TTCAACGTGC	TTGGCGATGC	GATTGACCAG	250
	CGCGGCCCTG	TGGGTGAGAA	GATGCGCATG	GCGATCCACG	CCGAGGCGCC	300
	GAAGCTGGCG	GATCAGGCGG	CAGAGGACAC	GATCCTGACG	ACCGGCATCA	350
	AGGTGATCGA	TCTTATTCTG	CCGTACTGCA	AGGGTGGTAA	GATCGGTCTG	400
45	TTCGGTGGTG	CCGGTGTAGG	CAAGACTGTG	ATTATTATGG	AGCTGATCAA	450
	TAACGTGGCG	AAGGGCCACG	GTGGGTTTTT	CGTGTTTGCT	GGCGTGGGCG	500
	AGCGCACGCG	CGAGGGCACT	GACCTGTACC	TGGAGATGAT	GCAGTCGAAG	550
	GTGATTGACC	TGAAGGGCGA	ATCAAAGTGC	GTGCTTGTGT	ACGGACAGAT	600
	GAACGAGCCC	CCGGGTGCGC	GTGCGCGCGT	TGCGCAGTCT	GCGCTGACGA	650
50	TGGCCGAGTA	CTTCCGCGAT	GTGGAGGGCC	AGAACGTGCT	GCTGTTTATT	700
	GACAACATCT	TCCGCTTCAC	GCAGGCCAAC	TCCGAGGTGT	CTGCGCTGCT	750
	GGGTGCGATT	CCTGCCGCCG	TGGGCTACCA	GCCGACGCTT	GCGGAGGATC	800
	TGGGCATGCT	GCAGGAGCGC	ATTACGTCGA	CGACGAAGGG	CTCGATTACG	850
	TCTGTGCAGG	CCGTGTACGT	GCCTGCGGAT	GATATCACGG	ACCCGGCGCC	900
55	CGCGACGACG	TTCTCGCACC	TGGACGCGAC	GACTGTGCTG	GACCGTGCGG	950
	TGGCAGAGTC	GGGCATTTAC	CCTGCGGTGA	ACCCGCTGGA	GTGCGCGTGC	1000
	CGTATCATGG	ACCCCGATGT	GATCGATGTG	GACCACTACA	ACGTTGCGCA	1050
	GGATATCGTG	CAGATGCTGA	CCAAGTACAA	GGAGCTGCAG	GATATCATTT	1100
	CCGTGCTTGG	TATCGACGAG	CTGAGCGAGG	AGGACAAGGT	TGTGGTGGAC	1150
60	CGCGCGCGCA	AGGTGACCCG	GTTCTGTGTC	CAGCCGTTCC	AGGTTGCGGA	1200

GGTGTTCAC T GGCATGACGG GTCAC TACGT TCAGCTGGAG GACACGGTGG 1250
 AGTCGTTCTC TGGCCTACTG ATGGGGTCAT ACGACCAGAT CCCGGAGA 1298

5

2) INFORMATION FOR SEQ ID NO: 537

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1297 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

15

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Leishmania major*
 (B) STRAIN: ATCC 50122

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 537

CTTCTCGGAG GCGGTGCCGC CCGTGCTGAC GCGCTGGAT GTGACGGAGG 50
 ACCTTGGCCG TGATGAGCCG CTGACGCTGG AGATCGTGCA GCACTTGGAC 100
 GCCAACACCG GCCGCTGCAT TGCATGACAG ACGACGGACC TGCTGAAGCT 150
 25 GAAGTCGAAG GTTGTGTCGA CCGGCGGCAA CATCTCTGTG CCGGTGGGCC 200
 GTGAGACGCT GGGCCGCATC TTCAACGTTT TGGGCGATGC GATCGACCAG 250
 CGCGGCCCCG TGGGCGAGAA GATGCGCATG GCGATCCACG CCGAGGCCCC 300
 GAAGCTGGCG GATCAGGCCG CAGAGGACAC GATCCTGACG ACCGGCATCA 350
 AGGTGATCGA CTTGATCCTG CCCTACTGCA AGGGTGGCAA GATCGGCCTG 400
 30 TTCGGCGGTG CCGGTGTGGG CAAGACTGTG ATCATCATGG AGCTGATCAA 450
 CAATGTCGCG AAGGGCCACG GTGGTTTCTC CGTGTGTTGCC GCGGTGGCG 500
 AGCGCACGCG CGAGGGCACG GACCTGTACC TGGAGATGAT GCAGTCGAAG 550
 GTGATTGACC TGAAGGGCGA GTCGAAGTGC GTGCTTGTGT ACGGGCAGAT 600
 GAACGAGCCC CCGGGTGCGC GCGCGCGCGT TGCAGTCT GCGCTGACGA 650
 35 TGGCGGAGTA CTTCCGCGAC GTGGAGGGCC AGAACGTGCT GCTGTTCATC 700
 GACAACATCT TCCGCTTAC GCAGGCGAAC TCCGAGGTGT CCGCGCTGCT 750
 GGGCCGCATT CCGGCCGCCG TGGGCTACCA GCCGACGCTT GCGGAGGATC 800
 TTGGTATGCT GCAGGACGCG ATCAGCTCGA CAACGAAGGG GTCGATCACG 850
 TCCGTGCAGG CCGTGTACGT GCCAGCGGAT GATATCACGG ATCCCGCGCC 900
 40 CGCGACGACG TTCTCGCACC TGGATGCGAC GACTGTGCTG GACCGCGCGG 950
 TGGCGGAGTC GGGCATCTAC CCTGCCGTGA ACCCGCTGGA GTGCGCGTCG 1000
 CGTATCATGG ACCCCGATGT GATCGATGTG GACCACTACA ACGTTGCGCA 1050
 GGATATCGTG CAGATGCTGA CCAAGTACAA GGAGCTGCAG GACATCATTG 1100
 CCGTGCTTGG CATCGACGAG CTGAGCGAGG AAGACAAGGT TGTGGTGGAC 1150
 45 CGCGCGCGCA AGGTGACCCG GTTCCTGTG CAGCCGTTCC AGGTTGCGGA 1200
 GGTGTTCACG GGCATGACGG GCCACTACGT GCAGCTGGTC GACACGGTGG 1250
 AGTCGTTCTC TGGCCTGCTG ATGGGGTCGT ACGACCAGAT CCCGGAG 1297

50

2) INFORMATION FOR SEQ ID NO: 538

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1297 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

60

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Leishmania amazonensis*

(B) STRAIN: ATCC 50131

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 538

```

TTCTCGGAGG GCGTGCCGCC CGTGCTGACG GCGCTGGATG TGACGGAGGA      50
CCTTGGCCGC GATGAGCCGC TGACGCTGGA GATCGTGCAG CACCTGGACG      100
CGAACACCGG CCGCTGCATT GCGATGCAGA CGACGGACCT GTTGAAGCTG      150
10 AAGTCGAAGG TTGTGTCGAC CGGCGCAAC ATCTCTGTGC CGGTGGGCCG      200
TGAGACGCTG GGCCGCATCT TCAACGTGCT GGGCGACGCG ATCGACCAGC      250
-----
GCGGCCCGT GGGTGAGAAG ATGCGCATGG CGATCCACGC CGAGGCCCGG      300
AAGCTGGCGG ATCAGGCCGC GGAGGACACG ATCCTGACGA CCGGCATCAA      350
GGTGATCGAC CTGATTCTGC CCTACTGCAA GGGTGGCAAG ATCGGCCTGT      400
15 TTGGTGGCGC CCGTGTGGGC AAGACCGTGA TCATCATGGA GTTGATTAAC      450
AACGTCGCGA AGGGCCACGG TGGTTTCTCG GTGTTTGCCG GCGTTGGCGA      500
GCGCACGCGC GAGGGCACGG ACCTGTACCT GGAGATGATG CAGTCGAAGG      550
TGATTGACCT GAAGGGCGAG TCGAAGTGCG TGCTTGTTGTA CGGGCAGATG      600
AACGAGCCCC CGGGTGCGCG CGCGCGCGTT GCGCAGTCTG CGCTGACGAT      650
20 GCGGAGTAC TTCCGAGACG TGGAGGGCCA GAATGTGCTG CTGTTTCATCG      700
ACAACATCTT CCGCTTCACG CAGGCGAACT CCGAGGTGTC TCGCGTGCTG      750
GGCCGCATTC CGGCCGCCGT GGGCTACCAG CCGACGCTTG CGGAGGATCT      800
TGGTATGCTG CAGGAGCGCA TCACGTCGAC GACGAAGGGG TCGATCACGT      850
CCGTGCAGGC CGTGACGTG CCTGCGGATG ATATCACGGA TCCGGCGCCC      900
25 GCGACGACGT TCTCGCACCT GGACGCGACG ACTGTGCTGG ACCGCGCGGT      950
GGCGGAGTCG GGGATCTACC CTGCCGTGAA CCCGCTGGAG TCGCGGTCGC     1000
GTATCATGGA CCCCATGTG ATCGACGTGG ACCACTACAA CGTTGCGCAG     1050
GATATCGTGC AGATGCTGAC CAAGTACAAG GAGCTGCAGG ATATCATTGC     1100
GGTGCTTGGT ATCGACGAGC TGAGCGAGGA GGACAAGGTC GTGGTGGACC     1150
30 GCGCGCGCAA GGTGACCCGG TTCCTGTCGC AGCCGTTCCA GGTGCGGAG     1200
GTGTTACCGG GCATGACGGG CCACTACGTG CAGCTGGCCG ACACGGTGGA     1250
GTCGTTCTCT GGGCTGCTGA TGGGGTCGTA CGACCAGATC CCGGAGA       1297

```

35

2) INFORMATION FOR SEQ ID NO: 539

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 27 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

45 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 539

CCITACATCC TBGTYGCICT IAACAAG

27

50

2) INFORMATION FOR SEQ ID NO: 540

(i) SEQUENCE CHARACTERISTICS:

- 55 (A) LENGTH: 23 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

60 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 540

GGDGCITCYT CRTCGWAITC CTG

23

5

2) INFORMATION FOR SEQ ID NO: 541

10 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

15

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 541

20 GTKGAAATGT TCCGCAAGCT GCT

23

2) INFORMATION FOR SEQ ID NO: 542

25

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

30

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 542

35

CGGAARTAGA ACTGSGGACG GTAG

24

40 2) INFORMATION FOR SEQ ID NO: 543

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

45

(ii) MOLECULE TYPE: DNA

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 543

ATCTTAGTAG TTTCTGCTGC TGA

23

55

2) INFORMATION FOR SEQ ID NO: 544

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 bases

(B) TYPE: Nucleic acid

60

335

(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 544

AYGTTGTCGC CMGGCATTMC CAT

23

10

2) INFORMATION FOR SEQ ID NO: 545

(i) SEQUENCE CHARACTERISTICS:

15

(A) LENGTH: 26 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 545

TACATCCTBG TYGCICTIAA CAAGTG

26

25

2) INFORMATION FOR SEQ ID NO: 546

(i) SEQUENCE CHARACTERISTICS:

30

(A) LENGTH: 23 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 546

CCRCGICCGG TRATGGTGAA GAT

23

2) INFORMATION FOR SEQ ID NO: 547

45

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 547

55

GTACAGTTGC TTCAGGACGT ATC

23

60 2) INFORMATION FOR SEQ ID NO: 548

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 bases
(B) TYPE: Nucleic acid
5 (C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

- 10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 548

ACGTTTCGATT TCATCACGTT G

21

15

2) INFORMATION FOR SEQ ID NO: 549

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 bases
20 (B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

25

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 549

GAACGTGATA CTGACAAACC TTTA

24

30

2) INFORMATION FOR SEQ ID NO: 550

- (i) SEQUENCE CHARACTERISTICS:
35 (A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

40 (ii) MOLECULE TYPE: DNA

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 550

GAAGAAGAAC ACCAACGTTG

20

45

2) INFORMATION FOR SEQ ID NO: 551

- 50 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
55 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 551

60 GAAGAAAAA TCTTCGAACT GGCTA

25

2) INFORMATION FOR SEQ ID NO: 552

5

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

10

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 552

15

TACACGGCCG GTGACTACG

19

20 2) INFORMATION FOR SEQ ID NO: 553

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

25

(ii) MOLECULE TYPE: DNA

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 553

GGCCGTGTTG AACGTGGTCA AATCA

25

35

2) INFORMATION FOR SEQ ID NO: 554

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

40

(ii) MOLECULE TYPE: DNA

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 554

GTTCCCTTACA TCGTTGTTTT TCTC

24

50

2) INFORMATION FOR SEQ ID NO: 555

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

55

60

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 555

5 TCTCGAACTT TCTCTATGTA TGCA

24

2) INFORMATION FOR SEQ ID NO: 556

10

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

15 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 556

20

CGGCGCNATC YTS GTTGTTG C

21

25 2) INFORMATION FOR SEQ ID NO: 557

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 bases

(B) TYPE: Nucleic acid

30 (C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 557

CCMAGGCATR ACCATCTCGG TG

22

40

2) INFORMATION FOR SEQ ID NO: 558

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 bases

45 (B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 558

TCITTYAART AYG CITGGGT

20

55

2) INFORMATION FOR SEQ ID NO: 559

(i) SEQUENCE CHARACTERISTICS:

60 (A) LENGTH: 23 bases

339

- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

5 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 559

10 CCGACRGCRA YIGTYTGICK CAT 23

2) INFORMATION FOR SEQ ID NO: 560

- 15 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 23 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

20 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 560

25 GAYTTCATYA ARAAYATGAT YAC 23

2) INFORMATION FOR SEQ ID NO: 561

- 30 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 23 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear
- 35

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 561

40 ACIGTICGGC CRCCCTCACG GAT 23

45 2) INFORMATION FOR SEQ ID NO: 562

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 30 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear
- 50

(ii) MOLECULE TYPE: DNA

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 562

CARATGRAYG ARCCICCI GG IGYIMGIATG 30

60

2) INFORMATION FOR SEQ ID NO: 563

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 563

GGYTGRTAIC CIACIGCIGA IGGCAT 26

15

2) INFORMATION FOR SEQ ID NO: 564

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 29 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 564

TAYGGICARA TGAAYGARCC ICCIGGIAA 29

30

2) INFORMATION FOR SEQ ID NO: 565

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 565

GGYTGRTAIC CIACIGCIGA IGGDAT 26

45

2) INFORMATION FOR SEQ ID NO: 566

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 566

60

5 2) INFORMATION FOR SEQ ID NO: 567

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 bases
(B) TYPE: Nucleic acid
10 (C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear
-

(ii) MOLECULE TYPE: DNA

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 567

TCRTCIGCIG GIACRTAIAY IGCYTG

26

20 2) INFORMATION FOR SEQ ID NO: 568

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 bases
25 (B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 568

RTIATIGGIG CIGTIRTIGA YGT

23

35 2) INFORMATION FOR SEQ ID NO: 569

- (i) SEQUENCE CHARACTERISTICS:
40 (A) LENGTH: 23 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

45 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 569

RTIRTIGGIS CIGTIRTIGA TAT

23

50

2) INFORMATION FOR SEQ ID NO: 570

- 55 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
60 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 570

5 RTIRYIGGIC CIGTIRTIGA YGT

23

2) INFORMATION FOR SEQ ID NO: 571

10

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

15 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 571

20

RTIRTIGGIC CIGTIRTIGA TGT

23

25 2) INFORMATION FOR SEQ ID NO: 572

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 bases

(B) TYPE: Nucleic acid

30 (C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 572

RTIRTIGGIS CIGTIRTIGA

20

40

2) INFORMATION FOR SEQ ID NO: 573

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 bases

45 (B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 573

CCICCIACCA TRTARAAIGC

20

55

2) INFORMATION FOR SEQ ID NO: 574

(i) SEQUENCE CHARACTERISTICS:

60 (A) LENGTH: 23 bases

343

- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

5 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 574

10 ATIGCIATGG AYGGIACIGA RGG 23

2) INFORMATION FOR SEQ ID NO: 575

- 15 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 25 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

20 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 575

25 TIACCATTTC AGTACCTTCT GGTA 25

2) INFORMATION FOR SEQ ID NO: 576

- 30 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 26 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

35 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 576

40 AACTTCRTCA AGAAGGTYGG TTACAA 26

45 2) INFORMATION FOR SEQ ID NO: 577

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 20 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

50 (ii) MOLECULE TYPE: DNA

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 577

CATGATTGAA CCATCCACCA 20

60

2) INFORMATION FOR SEQ ID NO: 578

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 578

CATGATTGAA GCTTCCACCA

20

15

2) INFORMATION FOR SEQ ID NO: 579

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 579

GAAGGCCGTG CTGGTGAGAA

20

30

2) INFORMATION FOR SEQ ID NO: 580

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 580

GCTAAACCAG CTACAATCAC TCCAC

25

45

2) INFORMATION FOR SEQ ID NO: 581

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 581

60

5 2) INFORMATION FOR SEQ ID NO: 582

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 28 bases
 (B) TYPE: Nucleic acid
10 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 582

TTTCAACTTC GTCGTTGACA CGAACAGT

28

20

2) INFORMATION FOR SEQ ID NO: 583

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 35 bases
25 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 583

CAACTGCTTT TTGGATATCT TCTTTAATAC CAACG

35

35

2) INFORMATION FOR SEQ ID NO: 584

- (i) SEQUENCE CHARACTERISTICS:
40 (A) LENGTH: 20 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

45 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 584

ACATGACACA TCTAAAACAA

20

50

2) INFORMATION FOR SEQ ID NO: 585

- 55 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
60 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 585

5 ACCACATACT GAATTCAAAG 20

2) INFORMATION FOR SEQ ID NO: 586

10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

15

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 586

20

CAGAAGTATA CGTATTATCA 20

2) INFORMATION FOR SEQ ID NO: 587

25

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

30

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 587

35

CGTATTATCA AAAGACGAAG 20

2) INFORMATION FOR SEQ ID NO: 588

40

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

45

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 588

50

TCTTCTCAAA CTATCGTCCA 20

2) INFORMATION FOR SEQ ID NO: 589

55

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases

60

- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

5 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 589

GCACGAAACT TCTAAAACAA

20

10

2) INFORMATION FOR SEQ ID NO: 590

15 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 590

25 TATACGTATT ATCTAAAGAT

20

2) INFORMATION FOR SEQ ID NO: 591

30

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 591

40

TCCTGGTTCT ATTACACCAC

20

2) INFORMATION FOR SEQ ID NO: 592

45

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 592

55

CAAAGCTGAA GTATACGTAT

20

60

2) INFORMATION FOR SEQ ID NO: 593

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 593

TTCACCTAACT ATCGCCCACA

20

15

2) INFORMATION FOR SEQ ID NO: 594

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

25 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 594

ATTGGTATCC ATGACACTTC

20

30

2) INFORMATION FOR SEQ ID NO: 595

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

40

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 595

45 TTAAAGCAGA CGTATACGTT

20

50

2) INFORMATION FOR SEQ ID NO: 596

(i) SEQUENCE CHARACTERISTICS:

- 55 (A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 596

60

5 2) INFORMATION FOR SEQ ID NO: 597

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 bases
 (B) TYPE: Nucleic acid
10 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 597

ATTGGTATCA AAGAACTTC

20

20

2) INFORMATION FOR SEQ ID NO: 598

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 bases
25 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 598

AATTACACCT CACACAAAAT

20

35

2) INFORMATION FOR SEQ ID NO: 599

- (i) SEQUENCE CHARACTERISTICS:
40 (A) LENGTH: 20 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

45 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 599

CGGTGAAGAA ATCGAAATCA

20

50

2) INFORMATION FOR SEQ ID NO: 600

- 55 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
60 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 600

5 ATGCAAGAAG AATCAAGCAA 20

2) INFORMATION FOR SEQ ID NO: 601

10

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

15 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 601

20

GTTTCACGTG ATGATGTACA 20

25 2) INFORMATION FOR SEQ ID NO: 602

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 bases

(B) TYPE: Nucleic acid

30 (C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 602

AAGTTGAAGT TGTGGTATT 20

40

2) INFORMATION FOR SEQ ID NO: 603

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 bases

45 (B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 603

GGTATTAAAG ACGAAACATC 20

55

2) INFORMATION FOR SEQ ID NO: 604

(i) SEQUENCE CHARACTERISTICS:

60 (A) LENGTH: 20 bases

351

- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

5 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 604

GGTGATGAAG TAGAAATCGT

20

10

2) INFORMATION FOR SEQ ID NO:605

15 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 605

25 GAAATGTTCC GTAAATTATT

20

2) INFORMATION FOR SEQ ID NO:606

30

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 606

40

ATTAGACTAC GCTGAAGCTG

20

2) INFORMATION FOR SEQ ID NO: 607

45

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 821 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: Genomic DNA

55 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus faecalis*
- (B) STRAIN: ATCC 29212

60

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 607

	CGGAGCTATC	TTAGTAGTTT	CTGCTGCTGA	TGGTCCTATG	CCTCAAAACAC	50
	GTGAACATAT	CTTATTATCA	CGTAACGTTG	GTGTACCATA	CATCGTTGTA	100
	TTCTTAAACA	AAATGGATAT	GGTTGATGAC	GAAGAATTAT	TAGAATTAGT	150
	AGAAATGGAA	GTTTCGTGACT	TATTATCAGA	ATACGATTTT	CCAGGCGATG	200
5	ATGTTCCAGT	TATCGCAGGT	TCTGCTTTGA	AAGCTTTAGA	AGGCGACGAG	250
	TCTTATGAAG	AAAAAATCTT	AGAATTAATG	GCTGCAGTTG	ACGAATATAT	300
	CCCAACTCCA	GAACGTGATA	CTGACAAACC	ATTCATGATG	CCAGTCGAAG	350
	ACGTATTCTC	AATCACTGGA	CGTGGTACTG	TTGCTACAGG	ACGTGTTGAA	400
	CGTGGTGAAG	TTCGCGTTGG	TGACGAAGTT	GAAATCGTTG	GTATTAAAGA	450
10	CGAAACTACT	AAAACAACCTG	TTACAGGTGT	TGAAATGTTT	CGTAAATTAT	500
	TAGACTACGC	TGAAGCAGGC	GACAACTTCG	GTGCTTTATT	ACGTGGTGTA	550
	GCACGTGAAG	ATATCGAACG	TGGACAAGTA	TTAGCTAAAC	CAGCTACAAT	600
	CACTCCACAC	ACAAAATTCA	AAGCTGAAGT	ATACGTATTA	TCAAAAGAAG	650
	AAGGCGGACG	TCACACTCCA	TTCTTCACTA	ACTACCGTCC	TCAATTCTAC	700
15	TTCCGTACAA	CAGACGTTAC	TGGTGTGTA	GAATTGCCAG	AAGGTACTGA	750
	AATGGTAATG	CCTGGTGATA	ACGTTGCTAT	GGACGTTGAA	TTAATTACAC	800
	CAATCGCTAT	CGAAGACGGA	A			821

20

2) INFORMATION FOR SEQ ID NO: 608

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 751 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

30

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus faecium*
 (B) STRAIN: ATCC 19434

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 608

	CGGAGCTATC	TTGGTAGTTT	CTGCTGCTGA	CGGCCCAATG	CCTCAAACCTC	50
	GTGAACACAT	CCTATTGTCT	CGTCAAGTTG	GTGTTCCCTA	CATCGTTGTA	100
	TTCTTGAACA	AAGTAGACAT	GGTTGATGAC	GAAGAATTAC	TAGAATTAGT	150
40	TGAAATGGAA	GTTTCGTGACC	TATTAACAGA	ATACRAATTC	CCTGGTGRCG	200
	ATGTTCCCTGT	AGTTGCTGGA	TCAGCTTTGA	AAGCTCTAGA	AGGCGACGCT	250
	TCATACGAAG	AAAAAATTCT	TGAATTAATG	GCTGCAGTTG	ACGAATACAT	300
	CCCAACTCCA	GAACGTGACA	ACGACAAACC	ATTCATGATG	CCAGTTGAAG	350
	ACGTGTTCTC	AATTACTGGA	CGTGGTACTG	TTGCTACAGG	TCGTGTTGAA	400
45	CGTGGACAAG	TTCGCGTTGG	TGACGAAGTT	GAAGTTGTTG	GTATTGCTGA	450
	AGAAACTTCA	AAAACAACAG	TTACTGGTGT	TGAAATGTTT	CGTAAATTGT	500
	TAGACYACGC	TGAAGCTGGA	GACRACATTG	GTGCTTTACT	ACGTGGTGTT	550
	GCACGTGAAG	ACATCCAACG	TGGACAAGTT	TTAGCTAAAC	CAGGTACAAT	600
	CACACCTCRT	ACAAAATTCT	CTGCAGAAGT	ATACGTGTTG	ACAAAAGAAG	650
50	AAGGTGGACG	TCATACTCCA	TTCTTCACTA	ACTACCGTCC	ACAATTCTAC	700
	TTCCGTACAA	CTGACGTAAC	AGGTGTTGTT	GAATTACCAG	AAGGAACTGA	750
	A					751

55

2) INFORMATION FOR SEQ ID NO: 609

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 751 bases
 (B) TYPE: Nucleic acid

60

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

5

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Enterococcus gallinarum*

(B) STRAIN: ATCC 49573

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 609

	CGGTGCGATC	TTAGTAGTAT	CTGCTGCTGA	CGGTCCTATG	CCTCAAACCTC	50
	GTGAACACAT	CTTGTTATCA	CGTAACGTTG	GCGWACCATA	CATCGTTGTT	100
	TTCTTGAACA	AAATGGATAT	GGTTGAYGAC	GAAGAATTGC	TAGAATTAGT	150
15	TGAAATGGAA	GTTTCGTGACC	TATTGTCTGA	ATATGACTTC	CCAGGCGACG	200
	ATGTTCTGT	AATCGCCGGT	TCTGCTTTGA	AAGCTCTTGA	AGGAGATCCT	250
	TCATACGAAG	AAAAAATCAT	GGAATTGATG	GCTGCAGTTG	ACGAATACGT	300
	TCCAACCTCA	GAACGTGATA	CTGACAAACC	ATTCATGATG	CCAGTCGAAG	350
	ACGTATTCTC	AATCACTGGA	CGTGGTACTG	TTGCTACAGG	CCGTGTTGAA	400
20	CGTGGACAAG	TTCGCGTTGG	TGATGAAGTA	GAAATCGTTG	GTATTGCTGA	450
	CGAAACTGCT	AAAACAACCTG	TAACAGGTGT	TGAAATGTTT	CGTAAATTGT	500
	TAGACTATGC	TGAAGCAGGG	GATAACATTG	GTGCATTGCT	ACGTGGGGTT	550
	GCTCGTGAAG	ACATCCAACG	TGGACAAGTA	TTGGCTAAAG	CTGGTACRAT	600
	CACACCTCAT	ACAAAATTCA	AAGCTGAAGT	TTATGTTTTG	ACAAAAGAAG	650
25	AAGGTGGRCG	TCACACTCCA	TTCTTCACTA	ACTACCGTCC	TCAGTTCTAC	700
	TTCCGTACAA	CTGACGTAAC	TGGTGTGTTT	GAATTACCAG	AAGGAACTGA	750
	A					751

30

2) INFORMATION FOR SEQ ID NO: 610

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 891 bases

35

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

40

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Haemophilus influenzae* Rd

(B) STRAIN: KW20

(C) ACCESSION NUMBER: extracted from U32739

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 610

	AATATGATTA	CTGGTGCGGC	ACAAATGGAT	GGTGCTATTT	TAGTAGTAGC	50
	AGCAACAGAT	GGTCCTATGC	CACAAACTCG	TGAACACATC	TTATTAGGTC	100
50	GCCAAGTAGG	TGTTCCATAC	ATCATCGTAT	TCTTAAACAA	ATGCGACATG	150
	GTAGATGACG	AAGAGTTATT	AGAATTAGTC	GAAATGGAAG	TTCGTGAACT	200
	TCTATCTCAA	TATGACTTCC	CAGGTGACGA	TACACCAATC	GTACGTGGTT	250
	CAGCATTACA	AGCGTTAAAC	GGCGTAGCAG	AATGGGAAGA	AAAAATCCTT	300
	GAGTTAGCAA	ACCACTTAGA	TACTTACATC	CCAGAACCAG	AACGTGCGAT	350
55	TGACCAACCG	TTCCTTCTTC	CAATCGAAGA	TGTGTTCTCA	ATCTCAGGTC	400
	GTGGTACTGT	AGTAACAGGT	CGTGTAAGAC	GAGGTATTAT	CCGTACAGGT	450
	GATGAAGTAG	AAATCGTCGG	TATCAAAGAT	ACAGCGAAAA	CTACTGTAAC	500
	GGGTGTTGAA	ATGTTCCGTA	AATTACTTGA	CGAAGGTCGT	GCAGGTGAAA	550
	ACATCGGTGC	ATTATTACGT	GGTACCAAAC	GTGAAGAAAT	CGAACGTGGT	600
60	CAAGTATTAG	CGAAACCAGG	TTCAATCACA	CCACACACTG	ACTTCGAATC	650

	AGAAGTGTAC	GTATTATCAA	AAGATGAAGG	TGGTCGTCAT	ACTCCATCTCT	700
	TCAAAGGTTA	CCGTCCACAA	TTCTATTTCC	GTACAACAGA	CGTGACTION	750
	ACAATCGAAT	TACCAGAAGG	CGTGGAATG	GTAATGCCAG	GCGATAACAT	800
	CAAGATGACA	GTAAGCTTAA	TCCACCCAAT	TGCGATGGAT	CAAGGTTTAC	850
5	GTTTCGCAAT	CCGTGAAGGT	GGCCGTACAG	TAGGTGCAGG	C	891

2) INFORMATION FOR SEQ ID NO: 611

10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 818 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 15 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 20 (A) ORGANISM: *Staphylococcus epidermidis*
 (B) STRAIN: ATCC 14990

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 611

25	CGGCGGTATC	TTAGTTGTAT	CTGCTGCTGA	CGGTCCAATG	CCACAAACTC	50
	GTGAACACAT	CTTATTATCA	CGTAACGTTG	GTGTACCAGC	ATTAGTTGTA	100
	TTCTTAAACA	AAGTTGACAT	GGTAGACGAC	GAAGAATTAT	TAGAATTAGT	150
	TGAAATGGAA	GTTTCGTGACT	TATTAAGCGA	ATATGACTTC	CCAGGTGACG	200
	ATGTACCTGT	AATCGCTGGT	TCTGCATTAA	AAGCATTAGA	AGGCGATGCT	250
30	GAATACGAAC	AAAAAATCTT	AGACTTAATG	CAAGCAGTTG	ATGATTACAT	300
	TCCAACCTCA	GAACGTGATT	CTGACAAACC	ATTCATGATG	CCAGTTGAGG	350
	ACGTATTCTC	AATCACTGGT	CGTGGTACTG	TTGCTACAGG	CCGTGTTGAA	400
	CGTGGTCAAA	TCAAAGTTGG	TGAAGAAGTT	GAAATCATCG	GTATGCACGA	450
	AACTTCTAAA	ACAACTGTTA	CTGGTGTAGA	AATGTTCCGT	AAATTATTAG	500
35	ACTACGCTGA	AGCTGGTGAC	AACATCGGTG	CTTTATTACG	TGGTGTGCA	550
	CGTGAAGACG	TACAACGTGG	TCAAGTATTA	GCTGCTCCTG	GTTCTATTAC	600
	ACCACACACA	AAATTCAAAG	CTGAAGTATA	CGTATTATCT	AAAGATGAAG	650
	GTGGACGTCA	CACTCCATTC	TTCACCTAAT	ATCGCCCA	ATTCTATTTT	700
	CGTACTACTG	ACGTAACCTG	TGTTGTAAAC	TTACCAGAAG	GTACAGAAAT	750
40	GGTTATGCCT	GGCGACAACG	TTGAAATGAC	AGTTGAATTA	ATCGCTCCAA	800
	TCGCTATCGA	AGACGGAA				818

45 2) INFORMATION FOR SEQ ID NO: 612

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 825 bases
 (B) TYPE: Nucleic acid
 50 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 55 (A) ORGANISM: *Salmonella choleraesuis* subsp. *choleraesuis*
 serotype Paratyphi A
 (B) STRAIN: ATCC 9150

60 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 612

355

	GGCGCGATCC	TGGTTGTTGC	TGCGACTGAC	GGCCCGATGC	CGCAGACCCG	50
	TGAGCACATC	CTGCTGGGTC	GTCAGGTAGG	CGTTCCGTAC	ATCATCGTGT	100
	TCCTGAACAA	ATGCGACATG	GTTGATGACG	AAGAGCTGCT	GGAAGTGGTT	150
5	GAAATGGAAG	TTCGTGAACT	TCTGTCTCAG	TACGACTTCC	CGGGCGACGA	200
	CACGCCGATC	GTTCTGTTT	CTGCTCTGAA	AGCGCTGGAA	GGCGACGCAG	250
	AGTGGGAAGC	GAAAATCATC	GAAGTGGCTG	GCTTCCTGGA	TTCTTACATC	300
	CCGGAACCAG	AGCGTGCGAT	TGACAAGCCG	TTCCTGCTGC	CGATCGAAGA	350
	CGTATTCTCC	ATCTCCGGTC	GTGGTACCGT	TGTTACCGGT	CGTGTAGAAC	400
10	GCGGTATCAT	CAAAGTGGGC	GAAGAAGTTG	AAATCGTTGG	TATCAAAGAG	450
	ACTCAGAAGT	CTACCTGTAC	TGGCGTTGAA	ATGTTCCGCA	AACTGCTGGA	500
	CGAAGGCCGT	GCCGGTGAGA	ACGTAGGTGT	TCTGCTGCGT	GGTATCAAAC	550
	GTGAAGAAAT	CGAACGTGGT	CAGGTACTGG	CTAAGCCGGG	CACCATCAAG	600
	CCGCACACCA	AGTTCGAATC	TGAAGTGTAC	ATTCTGTCCA	AAGATGAAGG	650
15	CGGCCGTCAT	ACTCCGTTCT	TCAAAGGCTA	CCGTCCGCAG	TTCTACTTCC	700
	GTACTACTGA	CGTGACTGGC	ACCATCGAAC	TGCCGGAAGG	CGTAGAGATG	750
	GTAATGCCGG	GCGACAACAT	CAAAATGGTT	GTTACCCTGA	TCCACCCGAT	800
	CGCAATGGAC	GACGGTCTGC	GTTTC			825

20

2) INFORMATION FOR SEQ ID NO: 613

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 778 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

30 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Serratia ficaria*
 (B) STRAIN: ATCC 33105

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 613

	GGCGCTATCC	TGGTTGTTGC	TGCGACTGAC	GGCCCAATGC	CTCAGACCCG	50
	TGAGCACATC	CTGCTGGGTC	GYCAGGTTGG	CGTTCCTTTC	ATCATCGTRT	100
40	TCATGAACAA	ATGCGACATG	GTTGATGATG	AAGAGCTGCT	GGAAGTGGTA	150
	GAAATGGAAG	TTCGCGAACT	GCTGTCCGCT	TACGACTTCC	CTGGCGATGA	200
	CCTGCCGGTG	ATTGCGGTT	CCGCGCTGAA	AGCGCTGGAA	GGCGAAGCCG	250
	AGTGGGAAGC	TAAAATCATC	GAGCTGGCTG	AMCMSCTGGA	TACTTACATC	300
	CCAGAACCAG	AGCGCGCTAT	CGACAAGCCG	TTCCTGCTGC	CAATCGAAGA	350
45	CGTATTCTCC	ATCTCCGGTC	GTGGTACCGT	GGTTACCGGT	CGTGTGAGC	400
	GCGGTATCAT	CAAAGTTGGC	GAAGAAGTTG	AAATCGTTGG	TATCAAAGAC	450
	ACCGTCAAGT	CTACCTGTAC	CGGCGTTGAA	ATGTTCCGCA	AACTGCTGGA	500
	CGAAGGCCGT	GCCGGTGAGA	ACGTAGGTGT	TCTGCTGCGT	GGTATCAAGC	550
	GTGAAGACAT	CGAACGTGGT	CAGGTTCTGG	CTAAACCAGG	TTCCATCAAG	600
50	CCGCACACCC	AGTTCGATTC	AGAAGTGTAC	ATCCTGAGCA	AAGAAGAAGG	650
	TGGTCGTCAC	ACKCCATTCT	TCAAAGGCTA	CCGTCCACAG	TTCTACTTCC	700
	GTACTACTGA	CGTGACCGGT	ACCATCGAAC	TGCCAGAAGG	CGTTGAGATG	750
	GTAATGCCTG	GCGACAACGT	GAACATGA			778

55

2) INFORMATION FOR SEQ ID NO: 614

(i) SEQUENCE CHARACTERISTICS:

- 60 (A) LENGTH: 653 bases

356

- (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

5 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus malodoratus*
 (B) STRAIN: ATCC 43197

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 614

	GTGCGATCTT	AGTAGTATCA	GCTACTGATG	GTCCAATGCC	TCAAACCTCGT	50
	GAACACATTT	TGTTATCACG	TCAAGTTGGT	GTTAAGCACT	TGATCGTTTTT	100
15	CTTGAACAAA	GTAGATTTAG	TTGATGACGA	AGAATTGATC	GACTTAGTTG	150
	AAATGGAAGT	ACGTGAATTA	CTTTCTGAAT	ATGGTTTCCC	AGGTGATGAT	200
	ATTCCAGTGC	TTAAAGGTTC	TGCTTTGAAA	GCATTAGAAG	GCGATCCAGA	250
	ACAAGAACAA	GTTATTCTTG	ATTTGATGGA	TACCGTTGAT	GAATATATCC	300
	CAACACCTGA	ACGTGACAAT	GACAAACCGT	TCTTGTTACC	AGTTGAGGAT	350
20	GTTTTCTCGA	TCACAGGACG	TGGTACTGTA	GCTTCTGGTC	GTATCGACCG	400
	TGGCGAAGTT	AAAGTCGGCG	ATGAAATTGA	AATCATCGGG	ATCAAACCTG	450
	AAGTTCAAAA	AGCAATCGTT	ACTGGACTTG	AAATGTTCCG	TAAAACATTG	500
	GATTATGGTG	AAGCTGGCGA	TAACGTTGGG	GTTCTATTAC	GTGGGATTAC	550
	ACGTGATGAA	ATCGAACGTG	GCCAAGTATT	AGCTAAACCA	GGTTCAATCA	600
25	CACCACATAC	TAAGTTCAAA	GCCGAAGTAT	ATGTGTTGAC	GAAAGAAGAA	650
	GGT					653

30 2) INFORMATION FOR SEQ ID NO: 615

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 829 bases
 (B) TYPE: Nucleic acid
 35 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

40 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus durans*
 (B) STRAIN: ATCC 19432

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 615

45	CCATTCTAGT	TGTATCTGCA	ACAGATGGAC	CAATGCCACA	AACACGTGAA	50
	CATATTTTAT	TGTCACGTCA	AGTAGGTGTT	AAATATTGGA	TCGTCTTCTT	100
	GAACAAAATC	GACTTAGTAG	ATGATGAAGA	ATTGATTGAT	CTTGTCGAAA	150
	TGGAAGTTTC	TGAATTATTA	AGCGAATATG	GTTTCCCAGG	TGACGATACA	200
50	CCAGTCATCA	AAGGTTTCAGC	ATTAAAAGCT	TTACAAGGAG	ATCCTGATGC	250
	AGAAGCAGCT	ATCATGGAAT	TGATGGATAC	TGTTGATGAA	TATATCCCAA	300
	CACCAGAACG	TGATACAGAC	AAACCATTAT	TGTTACCAGT	GGAAGATGTC	350
	TTCTCAATCA	CAGGTCGTGG	GACTGTTGCT	TCAGGTCGTA	TCGATCGTGG	400
	TGCAGTTCGT	GTAGGTGATG	AAATCGAAAT	CGTCGGTATC	AAACCTGAAA	450
55	CACAAAAGC	TGTTGTAAC	GGGGTCGAAA	TGTTCCGCAA	GACATTAGAC	500
	TATGGTGAAG	CAGGAGATAA	CGTTGGGGTA	TTGTTACGTG	GTATCCAACG	550
	TGAAGATATC	GAACGTGGAC	AAGTAATCGC	AAAACCAGGT	TCAATCACAC	600
	CACATACAAA	ATTCAAAGCA	GAAGTGACG	TATTGACAAA	AGAAGAAGGT	650
	GGACGTCATA	CACCATTCTT	CAATAACTAT	CGTCCACAAT	TCTACTTCCG	700
60	TACAACTGAC	GTAACCTGAA	CAATCGTTTT	ACCTGGAGGC	ACTGAAATGG	750

TTATGCCTGG AGATAACGTA ACGATCGACG TTGAATTGAT CCATCAGTT 890
GCCATCGAAA ACGGAACAAC TTTCTCTAT 829

5

2) INFORMATION FOR SEQ ID NO: 616

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 669 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus pseudoavium*
(B) STRAIN: ATCC 49372

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 616

GGTGCAATTT TAGTAGTATC TGCTACTGAT GGCCCAATGC CACAAACACG 50
TGAACATATC TTGTTATCAC GTCAAGTAGG GGTAAACAC TTAATCGTCT 100
TCTTGAACAA AGTTGATTGA GTTGATGATG AAGAATTGAT CGATTTAGTT 150
25 GAAATGGAAG TTCGGAATT GCTTTCTGAA TATGGTTTCC CAGGCGATGA 200
TATTCCAGTA CTTAAAGGTT CTGCTTTGAA AGCTTTAGAA GGCGATCCTG 250
AACAAGAACA AGTAATCCTT GACTTGATGG ATACGGTTGA TGAATACATC 300
CCAACGCCTG AACGTGATAC TGACAAACCA TTCTTGTTAC CAGTCGAAGA 350
TGTCTTCTCA ATCACAGGAC GTGGTACGGT TGCATCTGGT CGTATCGATC 400
30 GTGGGGAAGT TAAAGTCGGT GATGAAGTTG AAATCATCGG GATCAAACCT 450
GAAGTGCAA AAGCTGTCGT AACTGGACTA GAAATGTTCC GTAAGACATT 500
GGATTACGGT GAAGCTGGCG ATAACGTTGG GGTTCTATTA CGTGGGATTA 550
CTCGTGATGA AATCGAACGT GGACAAGTAT TAGCTAAACC AGGTTCAATC 600
ACTCCACATA CGAAATTCAG TGCAGAAAGT TATGTATTGA CGAAAGAAGA 650
35 AGGTGGCCGT CATACGCCA 669

40

2) INFORMATION FOR SEQ ID NO: 617

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 835 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus dispar*
(B) STRAIN: ATCC 51266

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 617

CGGGGCAATT TTAGTTGTAT CTGCAACTGA TGGCCCAATG CCACAAACAC 50
GTGAACACAT TTTGTTAGCT CGTCAAGTAG GGGTTAAATA TTTAATCGTC 100
TTCTTGAACA AAACAGATTT AGTTGATGAT GAAGAATTAT TGGAACAGT 150
TGAAATGGAA GTTCGTGAAT TATTAAATGA ATACAATTTC CCTGGCGATG 200
ATATTCCTGT TATTCGCGGA TCTGCTTTAA AAGCATTAGA AGGCGATCCA 250
60 GAACAAGAAG AAGTAATTAT GAACTTGATG GATACTGTGG ATGAATATAT 300

	CCCAACTCCA	GAACGTGACA	ATGATAAACC	ATTCTTGTTA	CCAGTGAAG	350
	ATGTCTTCAC	AATTACTGGT	CGTGGTACTG	TTGCTTCAGG	TCGTATCGAC	400
	CGTGGTAAAG	TCAACGTTGG	TGATGAAATT	GAAATTATCG	GAATTAAACC	450
	AGAAACACAA	AAAGCTGTTG	TAACCGGTTT	GGAAATGTTC	CGTAAACTT	500
5	TGGATTATGG	TGAAGCTGGT	GATAACGTTG	GGGTCTTATT	ACGTGGGATT	550
	ACTCGTGATG	AAGTAGAACG	TGGTCAAGTA	TTAGCAAAAC	CAGGTTCCAT	600
	TACACCGCAT	ACCAAATTTA	AAGGTGAACT	TTATATCTTA	ACAAAAGAAG	650
	AAGGTGGACG	TCATACTCCT	TTCTTTAATA	ACTATCGTCC	TCAATTTTAT	700
	TTCCGTACAA	CTGATGTGAC	TGGTAACATC	GCATTACCTG	AAGGAACTGA	750
10	AATGGTAATG	CCTGGTGATA	ATGTAACAAT	TGAAGTTGAA	TTGATTCATC	800
	CAATCGCCGT	TGAAAAGGG	ACTACTTTCT	CAATT		835

15 2) INFORMATION FOR SEQ ID NO: 618.

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 673 bases
 (B) TYPE: Nucleic acid
 20 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

25 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus avium*
 (B) STRAIN: ATCC 14025

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 618

30	GGTGCAATCC	TAGTAGTATC	AGCTACTGAT	GGTCCAATGC	CGCAAACACG	50
	TGAACATATT	TTGCTATCAC	GGCAAGTGGG	TGTTAAACAC	TTAATCGTAT	100
	TTTTAAACAA	AGTTGATTTA	GTCGATGATG	AAGAATTGAT	CGATCTAGTT	150
	GAAATGGAAG	TCCGTGAATT	ACTTTCTGAA	TATGGTTTCC	CAGGTGACGA	200
35	TATTCAGTT	CTCAAAGGTT	CAGCTTTGAA	AGCATTAGAA	GGCGATCCTG	250
	AACAAGAACA	AGTAATCCTT	GATTTAATGG	ATACAGTTGA	CGAATATATC	300
	CCAATCCAG	AACGTGACAC	TGACAAGCCA	TTCTTGTTAC	CAGTCGAAGA	350
	TGTATTTTCT	ATCACTGGTC	GTGGGACTGT	AGCGTCTGGA	CGGATTGATC	400
	GTGGTGAAGT	TAAAGTCGGC	GATGAAGTTG	AAATCATCGG	GATCAAACCT	450
40	GAAATTCAAA	AAGCAGTCGT	AACTGGACTT	GAAATGTTCC	GTAAAACTTT	500
	AGATTATGGT	GAAGCTGGCG	ATAACGTTGG	GGTTCTATTA	CGTGGGATTA	550
	CACGTGATGA	AATCGAACGT	GGTCAAGTCT	TAGCTAAACC	AGGTTCAATC	600
	ACACCACATA	CAAAATTCAG	TGCAGAAGTT	TACGTATTGA	CGAAAGAAGA	650
45	AGGTGGACGT	CATACACCAT	CTT			673

2) INFORMATION FOR SEQ ID NO: 619

50 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1713 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 55 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Saccharomyces cerevisiae*
 60 (C) ACCESSION NUMBER: K00428

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 619

	TTTCATATTT	TTAAGGATTT	TGTTTTAGCA	CCCATCCGAC	CTCAGTCAAT	50
5	ATATCCTTTC	GCGACCAGGC	TTTCCTCCCT	TTTGCTGCTA	ACTGGTTACA	100
	GATTTTCTTA	TTTTTGGTCA	TTTTTATCTT	TGAAACTGAT	TAAGCTGAAA	150
	AAATTTGAGC	TTCTTTGTTG	TAAACTATTT	TGTGCTTTCA	GTTTTATTCT	200
	AGCTCGACAA	AGGTAACAGA	CAAAAATGTC	AGCTTTATTA	CCAAGATTAC	250
	TCACAAGAAC	AGCTTTTAAA	GCTTCTGGGA	AACTTCTGAG	GCTCTCTTCA	300
10	GTAATTTCTA	GGACCTTTTC	TCAAACACT	ACTTCCTATG	CAGCTGCTTT	350
	TGATCGTTCC	AAACCGCATG	TAAATATAGG	TACGATCGGC	CATGTTGATC	400
	ATGGGAAGAC	AACTTTAACC	GCAGCCATTA	CGAAAACGTT	AGCCGCAAAA	450
	GGTGGTGCCA	ACTTCTTGGA	CTATGCTGCC	ATCGATAAGG	CTCCGGAAGA	500
	AAGAGCTCGT	GGTATTACAA	TTTCTACTGC	ACACGTGGAA	TACGAAACGG	550
15	CCAAGAGACA	TTATTCTCAC	GTCGACTGTC	CAGGCCACGC	TGATTACATC	600
	AAGAATATGA	TTACCGGTGC	TGCTCAAATG	GATGGTGCTA	TCATTGTTGT	650
	AGCTGCTACC	GATGGACAAA	TGCCCCAAAC	TAGAGAACAT	TTACTTTTGG	700
	CCAGACAAGT	TGGTGTCCAA	CATATTGTCG	TTTTTGTAA	CAAGGTTGAT	750
	ACCATTGATG	ATCCAGAAAT	GTTAGAGTTA	GTCGAAATGG	AAATGAGAGA	800
20	ACTTTTAAAC	GAATATGGGT	TTGACGGTGA	TAATGCTCCA	ATTATCATGG	850
	GTTCTGCCCT	TTGCGCTTTG	GAAGGTCGCC	AACCTGAAAT	TGGGGAGCAG	900
	GCCATCATGA	AACTTTGGGA	TGCAGTGGAT	GAGTATATTC	CTACACCTGA	950
	AAGAGATTTG	AACAAGCCTT	TCTTGATGCC	CGTTGAAGAT	ATCTTCTCTA	1000
	TCTCCGGTAG	AGGTACTGTG	GTCAGTGGTC	GTGTGGAAAG	GGGTAATTTA	1050
25	AAGAAAGGTG	AGGAATTGGA	AATTGTTGGT	CACAACTCCA	CCCCATTGAA	1100
	AACAACAGTT	ACTGGTATTG	AAATGTTTAG	AAAGGAATTG	GACTCTGCTA	1150
	TGGCAGGTGA	CAATGCCGGT	GTTTTACTTA	GAGGTATCAG	GAGAGATCAA	1200
	TTGAAGAGAG	GTATGGTCTT	AGCTAAGCCA	GGTACCGTTA	AAGCCCATAC	1250
	AAAGATTCTA	GCCTCTTTGT	ACATTTTATC	CAAAGAGGAA	GGTGGTAGAC	1300
30	ATTCTGGGTT	TGGTGAAAAC	TACAGACCAC	AAATGTTTAT	AAGAACAGCT	1350
	GATGTTACAG	TTGTGATGAG	ATTTCTTAAG	GAGGTGAAG	ATCATTCTAT	1400
	GCAAGTTATG	CCAGGTGACA	ATGTTGAAAT	GGAATGTGAT	TTGATCCATC	1450
	CTACCCCAT	AGAAGTTGGT	CAACGTTTCA	ATATCAGAGA	GGGTGGAAGA	1500
	ACTGTTGGTA	CCGGTCTAAT	CACACGTATT	ATTGAATAGA	CTTATTGATG	1550
35	CAACTGGAGT	ATATTTCTAT	ATATTCTGTT	CATTTCCCCT	CTCATAATAT	1600
	ATACTTGTTT	CGTTAAAATT	TTATACGTGT	AAATAAAGTG	CCATAAATTT	1650
	TTCAGCTTTA	CTTTTGGTAG	AGTCCTGCTA	GCACTAGATT	TTACAATTTT	1700
	ATGTGCACAC	ACC				1713

40

2) INFORMATION FOR SEQ ID NO: 620

(i) SEQUENCE CHARACTERISTICS:

45	(A)	LENGTH: 18 bases
	(B)	TYPE: Nucleic acid
	(C)	STRANDEDNESS: Single
	(D)	TOPOLOGY: Linear

50 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 620

55 ATTGGTGCAT TGCTACGT

18

2) INFORMATION FOR SEQ ID NO: 621

60 (i) SEQUENCE CHARACTERISTICS:

360

- (A) LENGTH: 751 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

5

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus faecium*
 (B) STRAIN: ATCC 19434

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 621

	TGGTGCAATC	TTAGTTGTTT	CTGCAACTGA	CGGTCCGATG	CCTCAAACAC	50
15	GTGAACACAT	TTTATTGTCA	CGCCAAGTTG	GTGTAAAATA	CCTGATTGTT	100
	TTCTTGAACA	AAGTTGATTT	AGTCGATGAT	GAAGAATTGA	TCGATTGTTG	150
	AGAAATGGAA	GTTTCGCGAGT	TATTGAGCGA	ATATGGTTTC	CCAGGCGATG	200
	ACACTCCTGT	GATCAAAGGT	TCCGCATTAA	AAGCATTGCA	AGGCGATCCA	250
	GATGCTGAAG	CTGCTATTAT	GGAATTGATG	GATACAGTAG	ATGAATATAT	300
20	CCCAACACCA	GAACGTGATA	CAGATAAACC	ATTACTATTG	CCAGTGGAAG	350
	ACGTCTTCTC	AATTACAGGT	CGAGGAACTG	TTGCCTCAGG	TCGTATTGAT	400
	CGTGGTGCTG	TTCGTGTCCG	TGATGAGGTA	GAGATCGTAG	GGATCAAACC	450
	TGAAACACAA	AAAGCAGTTG	TAACAGGTGT	AGAAATGTTC	CGTAAAACGT	500
	TAGATTACGG	GGAAGCTGGG	GATAACGTAG	GCGTGTTGTT	ACGGGGGATC	550
25	CAACGTGACG	ATATCGAACG	TGGACAAGTA	CTTGCTAAAC	CAGGTTCCAT	600
	TACTCCACAT	ACAAAATTCA	AAGCAGAAGT	GTACGTGTTG	ACAAAAGAAG	650
	AAGGTGGACG	TCATACTCCA	TTCTTCAACA	ACTATCGTCC	ACAGTTCTAC	700
	TTCCGCACAA	CTGATGTTAC	AGGAACAATC	ACATTGCCAG	AAGATACAGA	750
	A					751

30

2) INFORMATION FOR SEQ ID NO: 622

35 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 750 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

40

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Saccharomyces cerevisiae*
 (B) STRAIN: ATCC 13264

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 622

	GTCAAATGGG	ACGAATCCAG	ATTCCAAGAA	ATTGTCAAGG	AAACCTCCAA	50
50	CTTTATCAAG	AAGGTTGGTT	ACAACCCAAA	GACTGTTCCA	TTCGTCCCAA	100
	TCTCTGGTTG	GAACGGTGAC	AACATGATTG	AAGCTACCAC	CAACGCTCCA	150
	TGGTACAAGG	GTTGGGAAAA	GGAAACCAAG	GCCGGTGTCTG	TCAAGGGTAA	200
	GACTTTGTTG	GAAGCCATTG	ACGCCATTGA	ACAACCATCT	AGACCAACTG	250
	ACAAGCCATT	GAGATTGCCA	TTGCAAGATG	TTTACAAGAT	TGGTGGTATT	300
55	GGTACTGTGC	CAGTCGGTAG	AGTTGAAACC	GGTGTCATCA	AGCCAGGTAT	350
	GGTTGTTACT	TTCGCCCCAG	CTGGTGTTAC	CACTGAAGTC	AAGTCCGTTG	400
	AAATGCATCA	CGAACAATTG	GAACAAGGTG	TTCCAGGTGA	CAACGTTGGT	450
	TTCAACGTCA	AGAACGTTTC	CGTTAAGGAA	ATCAGAAGAG	GTAACGTCTG	500
	TGGTGACGCT	AAGAACGATC	CACCAAAGGG	TTGCGCTTCT	TTCAACGCTA	550
60	CCGTCATTGT	TTTGAACCAT	CCAGGTCAAA	TCTCTGCTGG	TTACTCTCCA	600

GTTTTGGATT	GTCACACTGC	TCACATTGCT	TGTAGATTCTG	ACGAATTGTT	650
GGAAAAGAAC	GACAGAAGAT	CTGGTAAGAA	GTTGGAAGAC	CATCCAAAGT	700
TCTTGAAGTC	CGGTGACGCT	GCTTTGGTCA	AGTTCGTTCC	ATCTAAGCCA	750

5

2) INFORMATION FOR SEQ ID NO:623

- (i) SEQUENCE CHARACTERISTICS:
- 10 (A) LENGTH: 1269 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear
- 15 (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Cryptococcus neoformans*
- (B) STRAIN: ATCC 44104
- 20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 623

TCTTGAAAGC	TTAAGGCCGA	GCGAGAGCGA	GGTATCACCA	TCGACATTGC	50
TCTTTGGAAG	TTCGAGACCC	CCAGGTACCA	GGTCACCGTC	ATTGACGCCC	100
25 CCGGTCACCG	AGACTTCATC	AAGAACATGA	TCACCGGTAC	CTCCCAGGCT	150
GACTGTGCCA	TCCTCATCAT	TGCCACCGGT	ATCGGTGAGT	TCGAGGCCGG	200
TATCTCCAAG	GACGGTCAGA	CCCGAGAGCA	CGCCCTCCTC	GCCTTCACCC	250
TCGGTGTGAG	GCAGCTCATT	GTTGCTTGCA	ACAAGATGGA	CACCTGCAAG	300
TGGTCCGAGG	ACCGATTCAA	CGAAATCGTC	AAGGAGACCA	ACGGTTTCAT	350
30 CAAGAAGGTT	GGTTACAACC	CCAAGGCTGT	CCCCCTCGTC	CCCATCTCTG	400
GTTGGCACGG	TGACAACATG	TTGGAGGAGA	CCACCAAGTC	AGTGAATCCG	450
CTTCTACGTG	ATGAGATGTT	TTTCTGACTT	TCCGTGCAGC	ATGCCCTGGT	500
ACAAGGGATG	GACCAAGGAG	ACCAAGTCTG	GTGTTTCCAA	GGGTAAGACC	550
CTCCTCGAGG	CCATCGACGC	CATCGAGCCC	CCTACCCGAC	CCACCGACAA	600
35 GCCCCTCCGT	CTCCCTCTCC	AGGACGTCTA	CAAGATCGGT	GGTATCGGCA	650
CAGTCCCTGT	CGGCCGAGTC	GAGACCGGTG	TCATCAAGGC	CGGTATGTTG	700
TCTCATCTCT	CTTGTCTCGT	AACATGCGTC	TCGTAACATG	CGCTTACTTC	750
ATTTTCAGGT	ATGGTCGTCA	AGTTCGCCCC	CACCAACGTC	ACCACTGAAG	800
TCAAGTCCGT	TGAGATGCAC	CACGAGCAGA	TCCCCGAGGG	TCTTCCCGGA	850
40 GACAACGTTG	GTTTCAACGT	CAAGAACGTT	TCCATCAAGG	ACATCCGACG	900
AGGTAACGTC	TGTGGTGACT	CCAAGAACGA	CCCCCCTATG	GAGGCTGCTT	950
CTTTCAACGC	CCAGGTTATC	GTCCTTAACC	ACCCTGGTCA	GATCGGTGCC	1000
GGTTACACCC	CCGTTCTCGA	CTGTCACACT	GCCCCGTAAGC	CTGACCCCAAT	1050
ACCTCCAACA	TACCTTTGAA	GCTGACCCTT	TCTAGACATT	GCCTGCAAGT	1100
45 TTGCTGAGTT	GATCGAGAAG	ATTGACCGAC	GAACCGGTAA	GGTCATGGAG	1150
GCCGCCCCCA	AGTTCGTCAA	GTCTGGTGAC	GCCGCCATTG	TCAAGCTTGT	1200
TGCCCAGAAG	CCCCTCTGTG	TTGAGACCTA	CGCCGACTAC	CCCCCTCTTG	1250
GTCGATTTCG	CGTCCGAGA				1269

50

2) INFORMATION FOR SEQ ID NO: 624

- (i) SEQUENCE CHARACTERISTICS:
- 55 (A) LENGTH: 753
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

- 60 (ii) MOLECULE TYPE: Genomic DNA

362

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Candida albicans*

(B) STRAIN: ATCC 36801

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 624

	TCTGTCAAAT	GGGACAAAAA	CAGATTTGAA	GAAATCATCA	AGGAAACCTC	50
	CAACTTCGTC	AAGAAGGTTG	GTTACAACCC	AAAGACTGTT	CCATTCGTTC	100
10	CAATCTCTGG	TTGGAATGGT	GACAACATGA	TTGAACCATC	CACCAACTGT	150
	CCATGGTACA	AGGGTTGGGA	AAAGGAAACC	AAATCCGGTA	AAGTTACTGG	200
	TAAGACCTTG	TTAGAAGCTA	TTGACGCTAT	TGAACCACCA	ACCAGACCAA	250
	CCGACAAACC	ATTGAGATTG	CCATTGCAAG	ATGTTTACAA	GATCGGTGGT	300
	ATTGGTACTG	TGCCAGTCGG	TAGAGTTGAA	ACTGGTATCA	TCAAAGCCGG	350
15	TATGGTTGTT	ACTTTCGCCC	CAGCTGGTGT	TACCACTGAA	GTCAAATCCG	400
	TTGAAATGCA	TCACGAACAA	TTGGCTGAAG	GTGTTCCAGG	TGACAATGTT	450
	GGTTTCAACG	TTAAGAACGT	TTCCGTAA	GAAATTAGAA	GAGGTAACGT	500
	TTGTGGTGAC	TCCAAGAACG	ATCCACCAA	GGGTTGTGAC	TCTTCAATG	550
	CCCAAGTCAT	TGTTTTGAAC	CATCCAGGTC	AAATCTCTGC	TGGTTACTCT	600
20	CCAGTCTTGG	ATTGTCACCC	TGCCCACATT	GCTTGTAAT	TCGACACTTT	650
	GGTTGAAAAG	ATTGACAGAA	GAAGTGGTAA	GAAATTGGAA	GAAAATCCAA	700
	AATTCGTCAA	ATCCGGTGAT	GCTGCTATCG	TCAAGATGGT	CCCAACCAA	750
	CCA					753

25

2) INFORMATION FOR SEQ ID NO: 625

(i) SEQUENCE CHARACTERISTICS:

30

(A) LENGTH: 26 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 625

	CGTTGAAGAC	ACGACCCAAA	GTATCC	26
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40

2) INFORMATION FOR SEQ ID NO: 626

(i) SEQUENCE CHARACTERISTICS:

45

(A) LENGTH: 26 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 626

55	TACCACCTTT	TAAGTAAGGT	GCTAAT	26
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2) INFORMATION FOR SEQ ID NO: 627

60

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
5 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 627

10

ATTGTCTATA AAAATGGCGA TAAGTC

26

15 2) INFORMATION FOR SEQ ID NO: 628

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 bases
(B) TYPE: Nucleic acid
20 (C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 628

AAAATGGCGA TAAGTCACAA AAAGTA

26

30

2) INFORMATION FOR SEQ ID NO: 629

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 bases
(B) TYPE: Nucleic acid
35 (C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 629

AAGTTCCATC TCAACAAGGT CAATA

25

45

2) INFORMATION FOR SEQ ID NO: 630

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 bases
(B) TYPE: Nucleic acid
50 (C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

55 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 630

CGGAGCTATC CTAGTCGTTT CA

22

60

cont AM

2) INFORMATION FOR SEQ ID NO: 631

- 5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

10

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 631

15 CAGACCAACY GAIAARCCAT TRAGAT

26

2) INFORMATION FOR SEQ ID NO: 632

20

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

25

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 632

30

CCCTTTGGTG GRTCSTKCTT GGA

23

35 2) INFORMATION FOR SEQ ID NO: 633

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

40

(ii) MOLECULE TYPE: DNA

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 633

CAGACCAACY GAIAARCCIT TRAGAT

26

50

2) INFORMATION FOR SEQ ID NO: 634

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

55

(ii) MOLECULE TYPE: DNA

60

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 634

AACACYGTCA GRCIATTGC YATGGA

26

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2) INFORMATION FOR SEQ ID NO: 635

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 26 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

15 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 635

AAACCRGTIA RRGCRACCTT IGCTCT

26

20

2) INFORMATION FOR SEQ ID NO: 636

25 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

30

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 636

35 ACTGGYGTTG AIATGTTCCG YAA

23

2) INFORMATION FOR SEQ ID NO: 637

40 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

45

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 637

50

ACGTCAGTIG TACGGAARTA GAA

23

2) INFORMATION FOR SEQ ID NO: 638

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single

60

366

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 638

CCAATGCCAC AAACICGTGA RCACAT

26

10

2) INFORMATION FOR SEQ ID NO: 639

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 28 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 639

TTTACGGAAC ATTCWACAC CWGTIACA

28

25

2) INFORMATION FOR SEQ ID NO: 640

(i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 23 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

35 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 640

TCCATGGTIT WYGGICARAT GAA

23

40

2) INFORMATION FOR SEQ ID NO: 641

(i) SEQUENCE CHARACTERISTICS:

45 (A) LENGTH: 26 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 641

55 TGATAACCWA CIGCIGAIGG CATACG

26

60

2) INFORMATION FOR SEQ ID NO: 642

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 23 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 642

GGCGTIGGIG ARCGIACICG TGA

15 2) INFORMATION FOR SEQ ID NO: 643

20 (1) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 643

ACTGGIGTIG ARATGTTCCG YAA

30 2) INFORMATION FOR SEQ ID NO: 644

35 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 644

ACGTCIGTIG TICKGAARTA GAA

45

2) INFORMATION FOR SEQ ID NO: 645

50 (1) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

55 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 645

ACGTCIGTIG TICKGAARTA RAA

2) INFORMATION FOR SEQ ID NO: 646

- 5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
10 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 646

15 ATCGACAAGC CITTCTIAT GSC 23

2) INFORMATION FOR SEQ ID NO: 647

- 20 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
25 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 647

30 ACGTCCGTSG TRCGGAAGTA GAACTG 26

35 2) INFORMATION FOR SEQ ID NO: 648

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 bases
(B) TYPE: Nucleic acid
40 (C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 648

ACGTCSGTSG TRCGGAAGTA GAACTG 26

50 2) INFORMATION FOR SEQ ID NO: 649

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 bases
55 (B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

60

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 649

GTCCTATGCC TCARACWCGI GAGCAC

26

5

2) INFORMATION FOR SEQ ID NO: 650

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 23 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

15 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 650

TTACGGAACA TYTCAACACC IGT

23

20

2) INFORMATION FOR SEQ ID NO: 651

25 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

30

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 651

35 TGACGACCAC CITCYTCYTT YTTCA

25

2) INFORMATION FOR SEQ ID NO: 652

40 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

45

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 652

50

CCWAYAGTIY KICCICCYTC YCTIATA

27

2) INFORMATION FOR SEQ ID NO: 653

55 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single

60

370

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 653

GAYTTCATIA ARAAYATGAT

20

10

2) INFORMATION FOR SEQ ID NO: 654

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 654

TACAARATYK GIGGTATYGG

20

25

2) INFORMATION FOR SEQ ID NO: 655

(i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

35 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 655

CCRATACCIC MRATYTTGTA

20

40

2) INFORMATION FOR SEQ ID NO: 656

(i) SEQUENCE CHARACTERISTICS:

45 (A) LENGTH: 22 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 656

55 AATTAATGGC TGCAGTTGAY GA

22

60

2) INFORMATION FOR SEQ ID NO: 657

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 657

TTGTCCACGT TCGATRTCTT CA 22

2) INFORMATION FOR SEQ ID NO: 658

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 658

GATYTAGTCG ATGATGAAGA ATT 23

2) INFORMATION FOR SEQ ID NO: 659

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 659

GCTTTTTTGIG TTTCWGGTTT RAT 23

2) INFORMATION FOR SEQ ID NO: 660

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 660

GTAGAATTGA GGACGGTAGT TAG 23

2) INFORMATION FOR SEQ ID NO: 661

- 5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 23 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

10

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 661

15 GTAGAAATGT GGWCGATART TRT

23

2) INFORMATION FOR SEQ ID NO: 662

20

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 832 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

25

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

30

- (A) ORGANISM: *Corynebacterium diphtheriae*
 (B) STRAIN: ATCC 27010

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 662

35	CGGCGCAATC CTCGTTGTTG CTGCCACCGA CGGCCCAATG CCTCAGACCC	50
	GTGAGCACGT TCTGCTCGCT CGCCAGGTCG GCGTTCCTTA CATCCTCGTT	100
	GCTCTGAACA AGTGCGACAT GGTTGATGAT GAGGAAATCA TCGAGCTCGT	150
	CGAGATGGAG ATCCRTGAGT TGCTCGCTGA GCAGGATTAC GACGAAGAGG	200
	CTCCAATCAT CCACATCTCC GCCTGAAGG CTCTTGAGGG CGACGAGAAG	250
40	TGGACCCAGT CCATCATCGA CCTCATGCAG GCTTGCKATG ATTCCATCCC	300
	AGACCCAGAG CGTGAGACCG ACAAGCCATT CCTCATGCCT ATCGAGGACA	350
	TCTTCAACCAT CACCGGCCGC GGTACCGTTG TTACCGGCCG TGTGAGCGT	400
	GGCTCCCTGA AGGTCAACGA GGACGTCGAG ATCATCGGTA TCCGCGAGAA	450
	KGCTACCACC ACCACCGTTA CCGGTATCGA GATGTTCCGT AAGCTTCTCG	500
45	ACTACACCGA GGCTGGCGAC AACTGTGGTC TGCTTCTCCG TGGCGTTAAG	550
	CGCGAAGACG TTGAGCGTGG CCAGGTTGTT GTTAAGCCAG GCGCTTACAC	600
	CCCTCACACC GAGTTCGAGG GCTCTGTCTA CGTTCTGTCC AAGGACGAGG	650
	GTGGCCGCCA CACCCCATTC TTCGACAACCT ACCGCCACA GTTCTACTTC	700
	CGCACCACCG ACGTTACCGG TGTTGTGAAG CTTCTGAGG GCACCGAGAT	750
50	GGTCATGCCT GGCGACAACG TCGACATGTC CGTCACCCTG ATCCAGCCTG	800
	TCGCTATGGA TGAGGGCCTG CGCTTCGCTA TC	832

55 2) INFORMATION FOR SEQ ID NO: 663

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1192 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single

60

373

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

5 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Candida catenulata*

(B) STRAIN: ATCC 10565

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 663

```

10 AACGGCGAGC AAGACTTGGT GTTGGAGGTT TCTCAGCACT TGGGTGAGAA      50
   CACCGTGCGT ACCATTGCCA TGGACGGTAC CGAGGGTTTG GTGAGAGGTA      100
   CCGCTGTCAC TGACACCGGT GCTCCCATCT CGGTCCCCGT TGGTCAGGGT      150
   ACCTTGGGCC GGATCATCAA CGTTGTCGGT GAGCCCATCG ACGAGCGTGG      200
15 TCCCATCCAG TGCAAGCAGA GAAACCCCAT TCACGCCGAG CCCCCGTCTT      250
   TCCACGAGCA GTCCGTCGAG GCTGAGGTGT TGGAGACCGG TATCAAGGTT      300
   GTCGACTTGT TGGCTCCCTA CGCCCGTGGT GGTAAGATTG GTCTTTTCGG      350
   TGGTGCCGGT GTCGGTAAGA CCGTGTTTAT CCAGGAGTTG ATTAACAACA      400
   TTGCCAAGGC CCACGGTGGT TTCTCCGTGT TCACTGGTGT CCGTGAGCGT      450
20 ACTCGTGAGG GTAACGACTT GTACCGTGAA ATGAAGGAGA CCGGTGTCAT      500
   CAACTTGAGG GGCGACTCCA AGGTGGCCTT GGTGTTTCGGT CAGATGAACG      550
   AGCCCCCGGG GGCTCGTGCC CGTGTCGCCT TGACCGGTTT GACCATTGCC      600
   GAGTACTTCC GTGACGAGGA AGGCCAGGAC GTGTTGTTGT TCGTTGACAA      650
   CATTTTCAGA TTCACCCAGG CCGGTTCCGA GGTGTCGGCG TTGTTGGGTC      700
25 GTATCCCCTC CGCCGTCGGT TACCAGCCCA CTTTGGCCAC CGACATGGGT      750
   TTGTTGCAGG AGAGAATTAC CACCACCAAG AAGGGTTCCG TCACCTCTGT      800
   GCAGGCCGTG TACGTCCCTG CCGATGACTT GACTGACCCT GCCCCCGCCA      850
   CCACTTTCGC TCACTTGGAC GCCACCACCG TGTTGTCGCG TGGTATCTCC      900
   GAGTTGGGTA TCTACCCCGC CGTCGACCCC TTGGACTCCA AGTCGAGATT      950
30 GTTGGACGTC GAGGTTGTTG GCCAGGAGCA CTACGACGTC GCCACCGGTG      1000
   TCCAGGAGTG CTTGCAGGCC TACAAGTCGT TGCAGGACAT CATTGCCATT      1050
   TTGGGTATGG ACGAGTTGTC CGAGCAGGAC AAGTTGACCG TCGAGAGAGC      1100
   CCGTAAGATC CAGCGTTTCT TGTCGCAGCC CTTGCTGTGC GCCGAGGTTT      1150
   TCACTGGTAT CCCCGGTAGA TTGGTGAGAT TGCAGGACAC CG              1192
35

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2) INFORMATION FOR SEQ ID NO: 664

40 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 29 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

45

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 664

50 AAYATGATIA CIGGIGCIGC ICARATGGA

29

2) INFORMATION FOR SEQ ID NO: 665

55

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1377 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

60

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 5 (A) ORGANISM: *Saccharomyces cerevisiae*
(C) ACCESSION NUMBER: extracted from X00779

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 665

```

10 ATGGGTAAAG AGAAGTCTCA CATTACGTT GTCGTTATCG GTCATGTCTGA 50
   TTCTGGTAAG TCTACCACTA CCGGTCATTT GATTTACAAG TGTGGTGGTA 100
   TTGACAAGAG AACCATCGAA AAGTTCGAAA AGGAAGCCGC TGAATTAGGT 150
   AAGGGTTCTT TCAAGTACGC TTGGGTTTTG GACAAGTTAA AGGCTGAAAG 200
   AGAAAGAGGT ATCACTATCG ATATTGCTTT GTGGAAGTTC GAAACTCCAA 250
15 AGTACCAAGT TACCGTTATT GATGCTCCAG GTCACAGAGA TTTCATCAAG 300
   AACATGATTA CTGGTACTTC TCAAGCTGAC TGTGCTATCT TGATTATTGC 350
   TGGTGGTGTC GGTGAATTTC AAGCCGGTAT CTCTAAGGAT GGTCAAACCA 400
   GAGAACACGC TTTGTTGGCT TTCACCTTGG GTGTTAGACA ATTGATTGTT 450
   GCTGTCAACA AGATGGACTC CGTCAAATGG GACGAATCCA GATTCCAAGA 500
20 AATTGTCAAG GAAACCTCCA ACTTTATCAA GAAGGTTGGT TACAACCCAA 550
   AGACTGTTCC ATTCGTCCCA ATCTCTGGTT GGAACGGTGA CAACATGATT 600
   GAAGCTACCA CCAACGCTCC ATGGTACAAG GGTGCGGAAA AGGAAACCAA 650
   GGCCGGTGTC GTCAAGGGTA AGACTTTGTT GGAAGCCATT GACGCCATTG 700
   AACAACCATC TAGACCAACT GACAAGCCAT TGAGATTGCC ATTGCAAGAT 750
25 GTTTACAAGA TTGGTGGTAT TGGTACTGTG CCAGTCGGTA GAGTTGAAAC 800
   CCGGTGTCATC AAGCCAGGTA TGGTTGTTAC TTTTGCCCCA GCTGGTGTTA 850
   CCACTGAAGT CAAGTCCGTT GAAATGCATC ACGAACAATT GGAACAAGGT 900
   GTTCCAGGTG ACAACGTTGG TTTCAACGTC AAGAACGTTT CCGTTAAGGA 950
   AATCAGAAGA GGTAACGTCT GTGGTGACGC TAAGAACGAT CCACCAAAGG 1000
30 GTTGCGCTTC TTTCAACGCT ACCGTCATTG TTTTGAACCA TCCAGGTCAA 1050
   ATCTCTGCTG GTTACTCTCC AGTTTTGGAT TGTCACACTG CTCACATTGC 1100
   TTGTAGATTG GACGAATTGT TGGAAAAGAA CGACAGAAGA TCTGGTAAGA 1150
   AGTTGGAAGA CCATCCAAAG TTCTTGAAGT CCGGTGACGC TGCTTTGGTC 1200
   AAGTTCGTTT CATCTAAGCC AATGTGTGTT GAAGCTTTCA GTGAATACCC 1250
35 ACCATTAGGT AGATTGCTG TCAGAGACAT GAGACAAACT GTCGCTGTCTG 1300
   GTGTTATCAA GTCTGTTGAC AAGACTGAAA AGGCCGCTAA GGTTACCAAG 1350
   GCTGCTCAAA AGGCTGCTAA GAAATAA 1377

```

40

2) INFORMATION FOR SEQ ID NO: 666

(i) SEQUENCE CHARACTERISTICS:

- 45 (A) LENGTH: 1536 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

50

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Saccharomyces cerevisiae*
(C) ACCESSION NUMBER: extracted from M12082

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 666

```

   ATGGTTTTGC CAAGACTATA TACTGCTACA TCCCGTGCTG CTTTTAAAGC 50
   AGCCAAACAA TCCGCTCCGC TTCTATCCAC TTCGTGGAAA AGATGTATGG 100
   CCTCAGCTGC TCAATCTACT CCAATCACCG GTAAAGTTAC CGCTGTCATT 150
60 GGTGCCATTG TTGACGTTCA TTTTGAACAA TCAGAGTTGC CCGCTATTTT 200

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	GAACGCTTTA	GAAATTAAAA	CACCTCAAGG	TAAGTTGGTT	TTGGAAGTTG	250
	CTCAACATTT	GGGTGAAAAC	ACTGTCAGAA	CCATTGCTAT	GGATGGTACC	300
	GAAGGTTTGG	TCCGTGGTGA	AAAGGTTCTT	GACACTGGTG	GCCCTATCTC	350
	CGTCCCAGTT	GGGAGAGAAA	CTTTAGGGAG	AATCATCAAC	GTTATCGGTG	400
5	AACCTATTGA	TGAAAGAGGT	CCAATTAAGT	CCAAACTAAG	AAAGCCAATT	450
	CACGCAGACC	CTCCTAGTTT	TGCAGAACAA	TCTACTTCGG	CTGAAATTTT	500
	GGAAACAGGT	ATCAAAGTCG	TCGATCTATT	AGCTCCTTAT	GCCAGAGGTG	550
	GTAAGATTGG	TCTTTTTCGGT	GGTGCAGGTG	TCGGTAAGAC	TGTGTTTCATT	600
	CAAGAATTGA	TTAACAATAT	CGCCAAGGCC	CATGGTGGTT	TTTCCGTTTT	650
10	CGCCGGTGTT	GGTGAAAGGA	CCAGAGAGGG	TAATGACTTG	TACCGTGAAA	700
	TGAAGGAAAC	TGGAGTCATT	AACCTGGAAG	GTGAATCCAA	GGTCGCCTTA	750
	GTTTTTCGGTC	AAATGAACGA	ACCTCCAGGA	GCCAGAGCCA	GAGTEGCTTT	800
	AACTGGTTTG	ACGATCGCTG	AATATTTTCAG	AGATGAAGAA	GGTCAAGACG	850
	TCTTGTTGTT	TATCGACAAT	ATCTTTAGAT	TTACTCAAGC	TGGTTCAGAA	900
15	GTCTCTGCCC	TTTTGGGTCG	TATTCCATCT	GCCGTCGGTT	ATCAACCAAC	950
	TTTGGCCACT	GATATGGGTC	TCTTACAAGA	AAGAATTACC	ACCACAAAGA	1000
	AGGGTTCTGT	CACCTTCTGTG	CAAGCCGTTT	ATGTTCCAGC	CGATGATTTA	1050
	ACAGATCCGT	CTCCGTCCAC	ATCTTTTGCC	CATTTGGACG	CATCATCCGT	1100
	CTTGTCAGA	GGTATTTTCAG	AATTAGGTAT	TTACCCTGCA	GTGGATCCAT	1150
20	TGGATTCTAA	ATCAAGGTTA	TTGGATGCCG	CCGTTGTCGG	TCAAGAACAT	1200
	TATGACGTCG	CCTCCAAGGT	TCAAGAAACT	TTACAGACCT	ATAAATCTTT	1250
	ACAAGATATC	ATTGCTATTT	TGGGTATGGA	TGAATTGTCC	GAACAAGATA	1300
	AACTAACTGT	CGAAAGGGCA	AGAAAGATTC	AAAGATTCTT	ATCTCAACCA	1350
	TTTGCTGTCTG	CCGAAGTCTT	TACTGGTATC	CCAGGTAAAT	TAGTGAGATT	1400
25	AAAGGACACC	GTTGCCTCGT	TCAAAGCCGT	TTTGGAAGGT	AAATACGATA	1450
	ATATACCAGA	ACATGCTTTC	TATATGTTTG	GTGGTATTGA	AGATGTTGTT	1500
	CGTAAAGCTG	AAAAGTTAGC	CCGTGAAGCC	AACTAG		1536

30

2) INFORMATION FOR SEQ ID NO: 667

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 1293 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

40 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Trypanosoma cruzi*
(B) STRAIN: Y

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 667

	CGGAAGGCGT	GCCGCCGGTG	TTAACTGCTT	TGGATGTGGT	GGAAAACTT	50
	GGCCGTGACG	AGCCCTTGAC	ACTTGAAATT	GTACAGCACT	TGGACGCCCA	100
	CACCGGCCGT	TGCATTGCGA	TGCAGACGAC	AGATCTGCTT	AAGCTGAAAT	150
50	CGAAGGTAGT	CTCGAGTGGC	GGGAACATTT	CTGTGCCTGT	GGGTCGGGAG	200
	ACACTTGGCA	GAATCTTCAA	TGTGCTGGGC	GATGCCATTG	ACCAGCGCGG	250
	CCATGTTGGA	GAGAAGCAAC	GCATGCCTAT	TCACGCTGTG	GCACCAAAGT	300
	TGGCGGATCA	GGCGGCAGAG	GACACCATTC	TCACAACGGG	TATCAAGGTG	350
	ATTGATCTGA	TTTTGCCCTA	CTGCAAGGGT	GGGAAGATTG	GTCTTTTTTG	400
55	TGGTGCTGGC	GTGGGCAAGA	CGGTTATTAT	CATGGAACCT	ATTAACAACG	450
	TTGCCAAGGG	CCATGGTGGG	TTCTCCGTCT	TTGCGGGTGT	TGGTGAACGC	500
	ACGCGTGAGG	GGACGGATCT	TTACCTGGAG	ATGATGCAAT	CCAAAGTTAT	550
	TGACCTGAAG	GGTGAATCGA	AGTGTGTGTT	GGTGTATGGT	CAGATGAACG	600
	AGCCTCCGGG	TGCCCCGTGCT	CGTGTGGCGC	AGTCTGCCTT	GACAATGGCC	650
60	GAGTACTTCC	GTGATGTGGA	AGGGCAAGAC	GTGTTGCTTT	TTATCGACAA	700

	CATTTTCCGC	TTTACGCAGG	CAAACCTCTGA	GGTGTCTAGCG	CTGTTGGGTC	750
	GTATTCCCGC	TGCCGTCGGC	TACCAGCCTA	CCCTTGCTGA	GGATCTTGGG	800
	CAGTTGCAGG	AGCGCATTAC	GTCCACGACA	AAAGGTTCCA	TTACCTCTGT	850
	GCAGGCTGTG	TACGTGCCAG	CCGATGATAT	TACCGACCCT	GCGCCAGCAA	900
5	CGACCTTTTC	CCACCTCGAT	GCCACGACGG	TGCTGGACCG	TGCCGTTGCC	950
	GAATCCGGCA	TTTACCCCGC	TGTCAACCCA	CTGGAGTGTG	CCTCGCGTAT	1000
	CATGGACCCG	GATGTAATCA	GCGTTGACCA	CTACAACGTG	GCGCAGGATG	1050
	TGGTGCAGAT	GCTTACCAAG	TACAAGGAGC	TGCAGGATAT	CATTGCGGTG	1100
	CTTGGCATTG	ATGAGCTCAG	TGAGGAGGAT	AAACTTATCG	TGGACCGTGC	1150
10	GCGTAAGGTG	ACAAAGTTTC	TCTCCCAGCC	TTTCCAGGTG	GCGGAGGTGT	1200
	TTACTGGCAT	GACAGGCCAC	TACGTGCAGC	TGGAGGAGAC	CATTGAGTCT	1250
	TTTTCGGGCC	TGTTGATGGG	CACATATGAT	CAGGTGCCCG	AGA	1293

15

2) INFORMATION FOR SEQ ID NO: 668

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1191 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

- (ii) MOLECULE TYPE: Genomic DNA

25

- (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Corynebacterium glutamicum*
- (C) ACCESSION NUMBER: X77034

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 668

	GTGGCAAAGG	CGAAGTTCGA	GCGTACCAAG	CCCCACGTAA	ACATCGGCAC	50
	CATCGGTAC	GTTGACCACG	GTAAGACCAC	CACCACCGCG	GCTATCACCA	100
	AGGTTCTGGC	TGACACTTAC	CCTGAGCTCA	ACGAGGCTTT	CGCCTTCGAC	150
35	TCCATCGATA	AGGCTCCTGA	GGAGAAGGAG	CGTGGCATCA	CGATCAACAT	200
	CTCCCACGTT	GAGTACCAGA	CTGAAAAGCG	CCACTACGCA	CACGTTGACG	250
	CTCCAGGCCA	CGCCGACTAC	ATCAAGAACA	TGATTACCGG	CGCTGCTCAG	300
	ATGGACGGCG	CAATCCTCGT	TGTTGCTGCT	ACCGACGGCC	CAATGCCTCA	350
	GACCCGTGAG	CACGTTCTTC	TTGCTCGCCA	GGTTGGCGTT	CCTTACATCC	400
40	TCGTTGCTCT	TAACAAGTGC	GACATGGTTG	AGGATGAGGA	AATCATCGAG	450
	CTCGTCGAGA	TGGAAGTTTC	TGAACCTCTT	GCTGAGCAGG	ACTACGACGA	500
	AGAGGCTCCA	ATTGTTTACA	TCTCCGCTCT	GAAGGCTCTT	GAGGGCGACG	550
	AGAAGTGGGG	CAAGCAGATC	CTTGAGCTCA	TGCAGGCTTG	CGATGACAAC	600
	ATCCCTGACC	CAGTTCGTGA	GACCGACAAG	CCATTCTCTA	TGCCTATCGA	650
45	GGACATCTTC	ACCATCACCG	GTCGTGGCAC	CGTTGTTACC	GGTCGTGTTG	700
	AGCGCGGTAC	CCTGAACGTG	AACGATGATG	TTGACATCAT	CGGCATCAAG	750
	GAGAAGTCCA	CCTCCACCAC	CGTTACCGGT	ATCGAGATGT	TCCGTAAGCT	800
	TCTTGACTCC	GCTGAGGCTG	GCGACAACCT	TGGTCTGCTT	CTCCGTGGTA	850
	TCAAGCGCGA	AGATGTTGAG	CGTGGCCAGG	TTATCGTTAA	GCCAGGCGCT	900
50	TACACCCCTC	ACACCGAGTT	CGAGGGCTCT	GTCTACGTTT	TGTCCAAGGA	950
	TGAAGGTGGC	CGCCACACCC	CATTCTTCGA	CAACTACCGT	CCTCAGTTCT	1000
	ACTTCCGCAC	CACCGACGTT	ACCGGTGTTG	TGAAGCTTCC	AGAGGGCACC	1050
	GAGATGGTCA	TGCCTGGCGA	CAACGTCGAC	ATGTCCGTCA	CCCTGATCCA	1100
	GCCTGTCGCT	ATGGACGAGG	GCCTGCGTTT	CGCTATCCGC	GAAGGCTCCC	1150
55	GCACCGTTGG	CGCTGGTCTG	GTCACCAAGA	TCATCAAGTA	A	1191

60

2) INFORMATION FOR SEQ ID NO: 669

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1383 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
(A) ORGANISM: *Escherichia coli*
(C) ACCESSION NUMBER: extracted from V00267

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 669

15	ATGGCTACTG	GAAAGATTGT	CCAGGTAATC	GGCGCCGTAG	TTGACGTCTGA	50
	ATTCCCTCAG	GATGCCGTAC	CGCGCGTGTA	CGATGCTCTT	GAGGTGCAAA	100
	ATGGTAATGA	GCGTCTGGTG	CTGGAAGTTC	AGCAGCAGCT	CGGCGGCGGT	150
	ATCGTACGTA	CCATCGCAAT	GGGTTCCTCC	GACGGTCTGC	GTCGCGGTCT	200
	GGATGTAAAA	GACCTCGAAC	ACCCGATTGA	AGTCCCGGTA	GGTAAAGCGA	250
20	CTCTGGGCCG	TATCATGAAC	GTACTGGGTG	AACCGGTCGA	CATGAAAGGC	300
	GAGATCGGTG	AAGAAGAGCG	TTGGGCGATT	CACCGCGCAG	CACCTTCCTA	350
	CGAAGAGCTG	TCAAACCTCTC	AGGAACCTGCT	GGAAACCGGT	ATCAAAGTTA	400
	TCGACCTGAT	GTGTCCGTTC	GCTAAGGGCG	GTAAAGTTGG	TCTGTTCCGT	450
	GGTGCGGGTG	TAGGTAAAAC	CGTAAACATG	ATGGAGCTCA	TTCGTAACAT	500
25	CGCGATCGAG	CACTCCGGTT	ACTCTGTGTT	TGCGGGCGTA	GGTGAACGTA	550
	CTCGTGAGGG	TAACGACTTC	TACCACGAAA	TGACCGACTC	CAACGTTATC	600
	GACAAAGTAT	CCCTGGTGTA	TGGCCAGATG	AACGAGCCGC	CGGGAAACCG	650
	TCTGCGCGTT	GCTCTGACCG	GTCTGACCAT	GGCTGAGAAA	TTCCGTGACG	700
	AAGGTCGTGA	CGTTCTGCTG	TTCGTTGACA	ACATCTATCG	TTACACCCTG	750
30	GCCGGTACGG	AAGTATCCGC	ACTGCTGGGC	CGTATGCCTT	CAGCGGTAGG	800
	TTATCAGCCG	ACCCTGGCGG	AAGAGATGGG	CGTTCTGCAG	GAACGTATCA	850
	CCTCCACCAA	AACTGGTTCT	ATCACCTCCG	TACAGGCAGT	ATACGTACCT	900
	GCGGATGACT	TGACTGACCC	GTCTCCGGCA	ACCACCTTTG	CGCACCTTGA	950
	CGCAACCGTG	GTACTGAGCC	GTCAGATCGC	GTCTCTGGGT	ATCTACCCGG	1000
35	CCGTTGACCC	GCTGGACTCC	ACCAGCCGTC	AGCTGGACCC	GCTGGTGTT	1050
	GGTCAGGAAC	ACTACGACAC	CGCGCGTGCC	GTTCAAGTCCA	TCCTGCAACG	1100
	TTATCAGGAA	CTGAAAGACA	TCATCGCCAT	CCTGGGTATG	GATGAACTGT	1150
	CTGAAGAAGA	CAAACCTGGT	GTCAGCGGTG	CTCGTAAGAT	CCAGCGCTTC	1200
	CTGTCCCAGC	CGTTCTTCGT	GGCAGAAGTA	TTACCCGGTT	CTCCGGGTAA	1250
40	ATACGTCTCC	CTGAAAGACA	CCATCCGTGG	CTTTAAAGGC	ATCATGGAAG	1300
	GCGAATACGA	TCACCTGCCG	GAGCAGGCGT	TCTACATGGT	CGGTTCCATC	1350
	GAAGAAGCTG	TGGAAAAAGC	CAAAAAACTT	TAA		1383

2) INFORMATION FOR SEQ ID NO: 670

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1410 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
(A) ORGANISM: *Helicobacter pylori*
(B) STRAIN: NCTC 11638
(C) ACCESSION NUMBER: extracted from AF004014

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 670

	ATGAAAGCGA	TGGAAGGTAA	AATCATTCAG	GTTTATAGGCC	CGGTGGTAGA	50
	TGTGGAGTTT	GAATCCTATC	TGCCGGCGAT	TTTTGAAGCA	CTAGACATTA	100
5	ATTTTGAAGT	TAATGGCGTT	CAAAAATCTT	TAGTTTTAGA	GGTGGCAGCC	150
	CATTTGGGTG	GTAATCGGGT	GCGAGCGATT	GCTATGGATA	TGACAGAAGG	200
	CTTAGTGCCT	AACCAAGCCG	TCAAAGCTCG	TGGCAAAATG	ATTGAAGTGC	250
	CTGTGGGCGA	AGAAGTGTTA	GGGCGTATTT	TTAATGTTGT	GGGCGAGAGC	300
	ATTGATAATT	TAGAGCCGCT	TAAGCCGTCC	TTAACTTGGC	CCATTCACAG	350
10	AAAAGCCCCCT	AGTTTTGAGC	AGCAAAGCAC	TAAAACAGAA	ATGTTTGAAA	400
	CCGGTATTAA	AGTCATTGAC	TTGCTCGCGC	CTTATTCTAA	GGGCGGTAAA	450
	GTAGGCTTGT	TTGGTGGGGC	TGGCGTAGGC	AAAACGGTGA	TCATTATGGA	500
	GCTTATCCAC	AATGTGGCTT	ATAAGCATAA	CGGGTATTCT	GTGTTTGCAG	550
	GTGTGGGGGA	GCGCACCAGA	GAAGGGAACG	ATCTGTATTT	TGAGATGAAA	600
15	GAAGGGGGCG	TTTTAGACAA	AGTTGCGTTG	TGCTATGGGC	AAATGAATGA	650
	GCCACCAGGT	GCAAGGAATC	GCATCGCATT	CACCGGCTTG	ACGATGGCGG	700
	AGTATTTCCG	TGATGAAAAG	GGCTTAGATG	TGTTGATGTT	TATTGATAAC	750
	ATCTTTAGAT	ACGCTCAAAG	CGGTGCGGAA	ATGAGCGCGC	TATTAGGCCG	800
	TATCCCTTCA	GCGGTGGGGT	ATCAGCCAC	GCTAGCCGGG	GAAATGGGGA	850
20	AACTTCAAGA	GCGTATCGCT	TCCACTAAAA	ATGGCTCTAT	CACTTCGGTT	900
	CAAGCGGTGT	ATGTGCCAGC	AGACGACTTG	ACTGACCCAG	CCCCTGCTTC	950
	GGTGTTTGCG	CATTTAGATG	CGACTACGGT	GTTGAATAGA	AAGATCGCTG	1000
	AAAAAGGGAT	TTATCCGGCG	GTGGATCCTT	TGGATTCCAC	TTCAAGGATT	1050
	TTAAGCCCTC	AAATGATTGG	CGAGAAGCAC	TATGAAATCG	CCACCGGTAT	1100
25	CCAGCAAGTT	TTGCAAAAAT	ACAAGGATTT	GCAAGATATT	ATTGCGATTT	1150
	TGGGATTGGA	CGAATTGAGC	GAAGAGGATA	AAAAAACGGT	TGAAAGGGCC	1200
	AGAAAAATTG	AGAAGTTTTT	ATCCAGCCG	TTTTTTGTGG	CTGAAGTGTT	1250
	TACAGGAAGT	CCCGGTAAGT	ATGTGACTCT	CCAAGAGACT	TTAGAGGGCT	1300
	TTGGAGGGAT	TTTAGAGGGC	AAATACGATC	ACATTCCTGA	AAACGCGTTT	1350
30	TACATGGTGG	GCAGCATTC	AGAGGTTTTA	GAAAAAGCTA	AAAACATGAA	1400
	AAATTCCTAA					1410

35 2) INFORMATION FOR SEQ ID NO: 671

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1401 bases
 (B) TYPE: Nucleic acid
 40 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

45 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Clostridium acetobutylicum*
 (B) STRAIN: DSM 792
 (C) ACCESSION NUMBER: extracted from AF101055

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 671

	ATGCCAGAAC	ATGTAGGTAA	AATTGTTCAG	GTAATAGGAC	CTGTTGTGGA	50
	TATTAAATTT	GATGCAGAGA	ACCTTCCTGA	CATCTATAAT	TCCATAGAAA	100
	TAGATATGGG	AGATAATAAA	AAACTCATTG	CTGAAGTTGA	ACAACATGTA	150
55	GGAGATGACA	TAGTAAGAAC	AATAGCAATG	GAAGGTACTG	ACGGATTAAA	200
	AAGAGGAATG	GAAGCAGTTA	ACACTGGTAA	ACCAATATCT	GTACCAGTTG	250
	GAGAAAATGT	TTTAGGACGT	CTTTTAAATG	TTTTAGGTCA	GACAATAGAT	300
	GAAGCAGGAG	ACATGAATGC	TGATAAGTAT	TATCCAATTC	ATAGACCAGC	350
	TCCAACCTTT	GAAGAACAAT	CAGTTCAACC	AGAAATGTTT	GAAACAGGTA	400
60	TTAAGGTTAT	AGATTTACTT	GCTCCATATC	AAAAGGGTGG	AAAAATCGGT	450

	TTGTTTCGGTG	GTGCCGGTGT	TGGTAAAACA	GTTCTTATTC	AGGAACTTAT	500
	AAATAATATA	GCAAAAAGAAC	ACGGTGGATT	ATCAGTATTC	ACAGGTGTTG	550
	GAGAAAGAAC	AAGAGAAGGT	AATGACCTTT	ATTATGAAAT	GAAAGATTCA	600
	GGAGTTATAA	ATAAAACAGC	TCTAGTATTT	GGTCAGATGA	ATGAACCACC	650
5	TGGCGCTAGA	ATGAGAGTTG	CTTTAACAGG	ACTTACAATG	GCTGAATATT	700
	TTAGAGACAA	AGGTCAAGAT	GTGCTTCTAT	TTATAGATAA	TATATTCAGA	750
	TTTACACAAG	CTGGTTCAGA	GGTTTCAGCT	TTACTTGGTA	GAATACCTAG	800
	TGCCGTTGGT	TATCAGCCAA	CACCTTGCAA	TGAAATGGGT	GCTCTTCAAG	850
	AGAGAATAAC	ATCAACAAAA	CAGGGTTCAA	TCACATCCGT	TCAGGCTGTA	900
10	TATGTTCTTG	CTGATGACCT	TACAGACCCA	GCTCCAGCAA	CAACATTTAC	950
	GCATCTTGAT	GCAACAACAG	TTCTTTCAAG	AGAAATATCA	AACTTAGGAA	1000
	TATATCCTGC	AGTTAGTCCT	CTTGAATCAA	CTTCAAGAAT	ACTTGATCCA	1050
	AGAATTGTTG	GAGAAGAGCA	TTATGAAGTT	GCTAACAAGG	TTAAACATAT	1100
	ACTTGAAAGA	TATCAAGAAC	TTCAAGATAT	CATAGCTATA	CTTGGTGTG	1150
15	ATGAACCTTC	AGATGAGGAT	AGATTGTTAG	TTGGAAGAGC	AAGAAGAGTA	1200
	CAGAGATTCT	TATCTCAAGC	TTTTAGTGTT	GCTGAACAAT	TTACAGGAAT	1250
	GAAAGGTCAG	TTTGTACCTG	TAAAAGATAC	TATAAGAAGT	TTTAAAGAAA	1300
	TATTAGATGG	TAAGTGTGAT	GATCTTCCAG	AAGCTGCATT	TTTATTTGCA	1350
	GGAACAATAG	AAGATGTAAA	AGAAAAAGCT	AAAAAAATGA	TGGAAAGCTA	1400
20	A					1401

2) INFORMATION FOR SEQ ID NO: 672

25

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1509 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

30

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Cytophaga lytica*
 (B) STRAIN: DSM 2039
 (C) ACCESSION NUMBER: M22535

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 672

40

	ATGTCTAAAG	TTACAGGTAA	AGTTTCCCAA	ATTATTGGCC	CAGTTATAGA	50
	TGTGGAGTTC	CAAGCAGGGG	TAGATCTTCC	AAAAATTTAT	GATTCATTAG	100
	AAATTAAAAA	AGCAGATGGA	TCAATTTTGG	TTTTGGAAGT	ACAATCACAC	150
	ATTGGTGAGA	ACACAGTAAG	AACTATATCT	ATGGATTCTT	CTGATGGTTT	200
45	AAGTCGTGGA	GCAGAGGTTA	ATGCAACAGG	AAGCGCTATA	CAAATGCCAG	250
	TTGGAGATGA	CGTTTACGGA	CGTTTATTTA	ACGTAATTGG	AGACGCTATT	300
	GATGGTCTTG	GGAATTTACC	AAAATCTGGT	AAAGATGGTT	TGCCAATACA	350
	CAGAGAGGCA	CCAAAATTTG	AAGACTTATC	TACTTCTACA	GAAGTATTAT	400
	TTACAGGTAT	TAAAGTAATT	GACCTTATTG	AGCCTTATGC	AAAAGGTGGT	450
50	AAGATTGGTT	TATTTGGAGG	TGCCGGAGTA	GGTAAAACAG	TATTAATTCA	500
	GGAATTAATT	AACAACATTG	CAAAAGGTCA	CGGTGGACTT	TCTGTATTTG	550
	CTGGTGTAGG	TGAGCGTACT	CGTGAGGGTA	ACGATTTACT	ACGTGAGATG	600
	TTAGAGTCTG	GTATTATTAA	ATACGGAGAT	GACTTTATGC	ACTCTATGGA	650
	AGAAGGTGGT	TGGGATTTAT	CTAAAGTTGA	TAAATCTGTA	ATGAAAGATT	700
55	CTAAAGCAAC	CTTTGTATTT	GGACAAATGA	ATGAGCCACC	AGGAGCACGT	750
	GCACGTGTTG	CATTATCTGG	TTTAACTATT	GCAGAATATT	TCCGTGATGG	800
	AGCAGGTGAA	GGTCAAGGTA	AAGATGTACT	TTTCTTTGTG	GATAACATTT	850
	TCCGTTTTTAC	ACAAGCTGGT	TCTGAGGTAT	CTGCATTACT	TGGTCGTATG	900
	CCATCTGCGG	TAGGTTACCA	ACCAACATTA	GCAACAGAAA	TGGGTGCTAT	950
60	GCAAGAGCGT	ATTACATCAA	CAAAAAGAGG	TTCTATTACA	TCTGTACAGG	1000

	CGGTTTACGT	ACCTGCGGAT	GATTTAACGG	ATCCAGCACC	GGCAACTACC	1050
	TTTGCTCACT	TAGATGCAAC	AACGGTATTG	TCTCGTAAAA	TTGCAGAGTT	1100
	AGGTATTTAC	CCAGCGGTAG	ATCCATTAGA	TTCTACTTCT	AGAATCTTAG	1150
	CTCCAGAAAT	TTTAGGAAAA	GATCACTACT	CTTGTGCACA	ACGTGTAAAA	1200
5	GAGTTGTTAC	AACGTTATAA	AGAATTACAA	GATATTATTG	CTATCCTTGG	1250
	TATGGAAGAA	TTATCTGAGG	AAGATAAAAT	GGCAGTTGGT	AGAGCAAGAC	1300
	GTGTACAACG	TTTCTTATCT	CAGCCTTTCC	ACGTAGCAGA	GCAATTTACA	1350
	GGTCTTAAAG	GTGTTTTAGT	AGATATCAAG	GATACTATTA	AAGGATTTAA	1400
	TATGATTATG	GATGGTGAAT	TAGATCACTT	ACCAGAATCT	GCATTTAACC	1450
10	TTAAAGGTAC	TATTGAAGAA	GCTATAGAAG	CAGGAGAAAA	AATGCTTGCT	1500
	GAAGCATAA					1509

15 2) INFORMATION FOR SEQ ID NO: 673

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 819 bases
 (B) TYPE: Nucleic acid
 20 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

25 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Ehrlichia risticii*
 (B) STRAIN: HRC-IL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 673

30	CCTAAAATAT	ATGATGCATT	ATATGTAAAA	CTAGATAATG	AAAATTTGTG	50
	TTTAGAAGTT	TCACAAATTA	TTGGAGATAA	TGTTGTTAGA	TGTATTGCAA	100
	TGGGAGCTAC	TTATGGATTA	AATCGTGGTT	TAGAAGTAGT	TTGTTTCAGGA	150
	AATCCAATTC	AGGTTCCCTGT	AGGTGAACAA	GTTTTAGGTA	GAATGTTTAA	200
35	TGTTGTTGGT	AAAACAATTG	ACAATCTTGA	ATCTTTAGAT	GATAAAAATA	250
	TAAAAATGAT	GCCAATTCAT	CGAAATCCAC	CATCATTTGA	AGAGCAATCC	300
	AATGAAATTG	AAATTTTGA	AACAGGCATT	AAAGTTATTG	ATTTATTAAT	350
	TCCATATGCT	AAAGGTGGTA	AGATTGGATT	ATTTGGTGGA	GCAGGGGTTG	400
	GGAAAACGGT	TCTTGTTCAA	GAATTAATTC	ACAATATCGC	AAAAGGTCAT	450
40	GGTGCTCTAT	CTGTTTTTGC	TGGAGTTGGT	GAAAGAACTC	GTGAAGGTAA	500
	TGACTTGCTAT	TATGAAATGA	TTGAAGGTGG	AGTTATAGAT	AAAACAGCCT	550
	TAGTGTTTGG	GCAAATGAAT	GAACCTCCTG	GCGCAAGAAT	GCGCGTAGCA	600
	TTAACTGCTT	TAACAATGGC	TGAATATTTT	CGTGATGTTC	AAAACCAAGA	650
	TGTTTTGTGA	TTTATTGATA	ATATCTTTAG	ATTTACACAA	GCTGGTAGTG	700
45	AAGTTTCAGC	ATTATTAGGA	AGAATGCCAT	CTGCTGTTGG	TTATCAACCA	750
	ACTTTGGCAT	ATGAAATGGG	ATTGTTACAA	GAAAGAATCA	CTTCCACTAA	800
	AAGTGGTTCT	ATAACATCT				819

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2) INFORMATION FOR SEQ ID NO: 674

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 840 bases
 55 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

60

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Vibrio cholerae*
 (B) STRAIN: ATCC 25870

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 674

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AGAGCGAAGT ACCAAGTGTT TACGATGCTC TGAATGTTGT GGATTCCAAA      50
GAACGTCTGG TTCTGGAAGT TCAACAGCAG CTAGGCGGTG GCGTGATTCTG     100
CGCTATCGTT ATGGGTAGCT CGGATGGTTT ACGTCGTGGA ATGACAGTAC      150
10 AAAACACTGG CGCTCCAATT TCAGTACCAG TAGGTACTAA AACCCTAGGT      200
CGTATCATGA ACGTGCTTGG TGATGCGATT GACGAACGTG GCGACATTGG      250
CGCAGAAGAG GTGTACTCGA TTCACCGTCC TGCTCCAAGC TAGGAAGAAC      300
AGTCTAGTGC AACTGAACTT TTGGAAACGG GTGTTAAGGT TATCGACCTG      350
ATCTGTCCGT TTGCGAAAGG CGGTAAAATC GGTCTGTTCG GTGGTGCGGG      400
15 TGTAGGTAAG ACCGTTAACA TGATGGAAC TATCAACAAC ATCGCGCTAC      450
AGCACTCAGG TTTGTCAGTA TTTGCTGGGG TAGGTGAGCG TACTCGTGAG      500
GGTAACGACT TCTACCACGA AATGCAGGAA GCGGGCGTTG TAAACGTTGA      550
ACAACCAGAA CTGTCGAAAG TAGCGATGGT TTACGGTCAG ATGAACGAGC      600
CACCAGGCAA CCGTCTGCGT GTAGCACTGA CTGGTCTGAC TATGGCGGAA      650
20 AAGTTCCGTG ATGAAGGCCG TGACGTACTG CTGTTTATCG ACAACATCTA      700
CCGTTACACC CTAGCGGGAA CGGAAGTATC TGCTCTGCTT GGCCGTATGC      750
CTTCAGCGGT AGGTTACCAA CCAACACTGG CTGAAGAGAT GGGTGTTCCTG      800
CAAGAACGTA TCACGTCAAC CAAAAAAGGT TCTATCACCT      840

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25

2) INFORMATION FOR SEQ ID NO: 675

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 828 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

35 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Vibrio cholerae*
 (B) STRAIN: ATCC 25870

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 675

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CGGCGGTATC CTAGTTGTAG CGGCAACTGA CGGTCCAATG CCACAAACTC      50
GTGAGCACAT CCTGCTGGGT CGCCAAGTAG GTATTCCTTA CATCATCGTA     100
45 TTCATGAACA AGTGTGACAT GGTGACGAT GAAGAGCTTC TAGAGCTGGT     150
AGAGATGGAA GTTCGTGAGC TGCTGTCTGA GTACGATTTC CCAGGTGATG     200
ACCTGCCAGT AATCCAAGGT TCAGCACTAG GCGCGCTAAA CGGCGAAGCA     250
CAGTGGGAAG CGAAGATTGT TGAGCTAGCA GAAGCACTGG ATACTTAYAT     300
TCCAGAGCCA GAGCGTGCAG TAGACATGGC ATTCCTGATG CCAATCGAAG     350
50 ACGTATTCTC AATCCAAGGT CGTGGTACAG TAGTAACTGG CCGTATCGAG     400
CGCGGCATCC TGAAAGTGGG TGACGAAGTA GCGATCGTTG GTATCAAAGA     450
GACAGTAAAA ACGACCTGTA CAGGTGTAGA GATGTTCCGT AAGCTGCTTG     500
ACGAAGGTCG TGCAGGTGAG AACGTAGGTG CACTRCTACG TGGTACTAAG     550
CGTGAAGAAG TAGAGCGTGG TCAAGTACTG GCGAAGCCAG GTTCAATCAC     600
55 ACCACACACT AAGTTCGAAT CAGAAGTATA CGTACTGTCA AAAGATGAAG     650
GTGGCCGTC TACTCCATTC TTCAAAGGTT ACCGTCCACA GTTCTACTTC     700
CGTACAACCTG ACGTAACAGG CAGCATTGAG CTACCAGARG GCGTAGAAAT     750
GGTAATGCCA GCGACAACG TGAAGATGGT TGTAGACCTG ATTGACACAA     800
TCGCGATGGA CGAAGGTCTA CGCTTCGC      828

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60.

2) INFORMATION FOR SEQ ID NO: 676

- 5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1298 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

10

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 15 (A) ORGANISM: *Leishmania enriettii*
 (B) STRAIN: ATCC 50120

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 676

CTTCTCGGAT GGCCTGCCGC CGGTGCTGAC GGCCTGGAC GTGACGGAGG 50
 20 AACTCGGGCG CGACGAGCCG CTGACGCTAG AGATCGTGCA AACTTTGGAC 100
 GCGCACACCG GCCGCTGCAT TCGATGCAG ACCACGGACC TACTGAAGCT 150
 GAAGTCGAAG GTCGTGTCGA CCGGCGGGAA CATCTCTGTG CCTGTGGGCC 200
 GCGAGACGCT TGGCCGCATC TTCAACGTAC TGGGCGACGC GATTGACCAG 250
 CGCGGCCCCG TGGGCGAGAA GATGCGCATG GCGATCCACG CGGAGGCGCC 300
 25 GAAGCTGGCG GACCAGGCGG CGGAGGACAC GATCCTGACG ACCGGCATCA 350
 AAGTGATCGA TCTGATCCTG CCGTACTGCA AGGGCGGCAA GATCGGTCTG 400
 TTCGGCGGTG CCGGTGTGGG GAAGACTGTG ATCATCATGG AGCTGATCAA 450
 CAACGTCGCG AAGGGCCACG GTGGCTTCTC CGTGTTCCGC GCGTTGGGG 500
 AGCGCACCCG CGAGGGGACG GATCTGTACC TGGAGATGAT GCAATCGAAG 550
 30 GTGATCGACC TGAAAGGTGA GTCGAAGTGT GTGCTTGTGT ACGGGCAGAT 600
 GAACGAGCCC CCGGGTGCGC GCGCGCGCGT TCGCAGTCT GCGCTGACGA 650
 TGGCCGAGTA CTTCCGCGAC GTGGAGGGCC AGAACGTGCT GCTGTTCATC 700
 GACAACATCT TCCGCTTCAC GCAGGCGAAC TCCGAGGTGT CAGCGCTGCT 750
 GGGCCGCATC CCCGCCGCTG TGGGCTACCA ACCGACGCTT GCGGAGGATC 800
 35 TCGGCATGTT GCAGGAGCGC ATCACGTCGA CGACGAAGGG GTCGATCACG 850
 TCTGTGCAGG CCGTGTACGT GCCTGCGGAT GATATCACGG ATCCCGCGCC 900
 GCGGACGACA TTCTCGCACC TGGACGCGAC GACGGTGCTG GACCGCGCGG 950
 TGGCGGAGTC TGGCATCTAC CCCGCGGTCA ACCCACTGGA GTGCGCGTGC 1000
 CGTATCATGG ACCCTGATGT GATCGACGTG GATCACTACA ACGTTGCGCA 1050
 40 GGACATTGTT CAGATGCTGA CCAAGTACAA GGAGCTGCAG GATATCATTG 1100
 CCGTGCTTGG TATCGACGAG CTGACGAGG AGGACAAGGT TGTGGTGGAC 1150
 CGTGCGCGCA AGGTGACCCG GTTCTGTGTA CAGCCGTTCC AGGTTGCGGA 1200
 GGTGTTTACT GGCATGACAG GCCATTACGT ACAGCTGAGC GACACGGTGG 1250
 AGTCGTTCTC CGGTTTGCTG ATGGGGTCGT ACGACCAGAT TCCGGAGA 1298

45

2) INFORMATION FOR SEQ ID NO: 677

- 50 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1083 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

55

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 60 (A) ORGANISM: *Babesia microtti*
 (B) STRAIN: Persing-1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 677

5	CAAGCTCAAG	TCTGAGCGTG	AGAGAGGTAT	TACTATTGAC	ATTACTCTCT	50
	GGAAATTTGA	GACCCAGAAA	TACGAGTACA	CTGTCATAGA	CGCACCTGGT	100
	CATCGTGACT	TTATCAAAAA	TATGATTACT	GGGACTTCAC	AAGCCGACGT	150
	TGCTATGCTT	GTCGTTCCCTG	CTGAATCTGG	CGGATTCGAG	GCTGCTTTTT	200
	CCAAAGAAGG	TCAGACCCGT	GAACACGCCT	TACTAGCCTT	CACACTTGGC	250
	GTCAAACAGA	TGATTGTTGC	TATTAACAAA	ATGGATTCTT	GTCAGTACAA	300
10	GGAGGATCGT	TATATGGAAA	TTTTCAAGGA	AGTACAGCAG	TACTTGAAGA	350
	AGGTGGGTTA	CAAAGTTGAA	AGCGTGCCGT	TTGTTGCTAT	TTCAGGATTC	400
	CACGGTGACA	ACATGGTTGA	AAAATCTACT	AACATGCCTT	GGTATAAGGG	450
	TAAGACCCTC	GTAGAGGCAC	TTGATCAAAT	GGAGCCTCCA	AAACGTCCGG	500
	TCGAAAAACC	TCTTAGATTG	CCCCTGCACT	CAGTCTATAA	AATTGGAGGT	550
15	ATTGGTACGG	TACCAGTCGG	AAGGGTCGAA	ACAGGACAAC	TGAAAGCAGG	600
	AATGATCATT	ACTTTTGCCC	CCACTGGTTT	GACCACTGAA	TGTAAATCTG	650
	TTGAAATGCA	TCACGAGGTT	GTGGAAGTGG	CTAGCCCCGG	TGATAACGTT	700
	GGATTTAATG	TCAAGAATGT	GTCTGTTAAG	GATATTAAGA	GAGGAAATGT	750
	GGCTTCGGAT	TCGAAAAATG	ACCCAGCCAA	GGAAGCTACC	TCTTTCTCTG	800
20	CACAAGTCAT	TGTACTCAAT	CACCCTGGTA	CCATCAAGGC	CGGTTACTCA	850
	CCTGTGGTTG	ATTGCCATAC	TGCCCACATT	GCTTGCAAAT	TCGAATCTCT	900
	AGACACTAGG	ATTGACAAGC	GTACTGGCAA	GACTTTGGAA	GAAAATCCTA	950
	AGACTATTAA	GAATGGTGAC	GCTGCCATGG	TGACTATGAA	ACCAAATAAA	1000
	CCCATGGTTG	TGGAAACTTT	CACCGACTAC	GCCCCGTTGG	GCCGGTTCGC	1050
25	CGTGCGTGAT	ATGCGCCAAA	CCGTTGCCGT	CGG		1083

2) INFORMATION FOR SEQ ID NO: 678

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 551 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 35 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 40 (A) ORGANISM: *Cryptococcus neoformans*
 (B) STRAIN: Lev-12

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 678

45	TGTGCTCATT	CAGGAGCTCA	TTAACAACAT	TGCCAAGGCT	CACGGTGGTT	50
	ACTCTGTCTT	CACTGGTGTC	GGTGAGCGAA	CTCGTGAGGG	TAACGACTTG	100
	TACCACGAAA	TGAGGGAGAC	TGGTGTTATC	AACCTTGAGG	GTGACTCCAA	150
	GGTCGCTCTT	GGTGAGTTCT	TTTTTTTCTT	CAGGCTAATT	AGTCGATGAC	200
	GTGGGGCCCTG	ACTAAAACTG	TTTCTTCCAG	TCTTCGGTCA	GATGAACGAG	250
50	CCCCCTGGAG	CCCGTGCCCG	AGTTGCCCTT	ACTGGTTTGA	CCATTGCCGA	300
	GTAATTCCGT	GACGAGGAAG	GCCAGGATGT	GTTGCTTTTC	ATTGACAACA	350
	TTTTCGGATT	CACCCAGGCC	GGTTCGGAGG	TGTCTGCCTT	GCTCGGTCGT	400
	ATCCCCTCTG	CCGTCGGTTA	CCAGCCCACT	CTTTCCACCG	ACATGGGTGG	450
	TATGCAGGAG	CGAATGTAGG	TTGCATTCTC	TGTGATTTTA	CGGCAAGCCT	500
55	TGACTTTTTT	TTTCTAGTAC	CACCACCAAG	AAGGGTTCCA	TTACCTCCGT	550
	C					551

60 2) INFORMATION FOR SEQ ID NO: 679

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 552 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Cryptococcus neoformans*
 (B) STRAIN: ATCC 44104

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 679

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15  TGTGCTCATT CAGGAGCTCA TTAACAACAT TGCCAAGGCC CACGGTGGTT      50
    ACTCCGTCTT CACCGGTGTC GGTGAGCGAA CTCGTGAGGG TAACGACTTG      100
    TACCACGAAA TGAGGGAGAC TGGTGTATC AACCTTGAGG GTGACTCCAA      150
    GGTGCTCTTT GGTGAGTTCT TTTTGTGGG AGCTAATTAG TCGATGACGT      200
20  GGGCCCTGAC CAAAACCGTT TCTTTCAGTC TTCGGTCAGA TGAACGAGCC      250
    CCCTGGAGCC CGTGCCCGAG TTGCTCTTAC TGGTTTGACC ATTGCCGAGT      300
    ACTTCCGTGA CGAGGAAGGC CAGGATGTGT TGCTTTTCAT TGACAACATT      350
    TTCCGATTCA CCCAGGCCCG TTCCGAGGTG TCTGCCTTGC TCGGTCGTAT      400
    CCCCTCTGCC GTCGGTTACC AGCCCACTCT TTCCACCGAT ATGGGTGGTA      450
25  TGCAAGAGCG AATGTAAGTT GCATTTTGTG TGATTTTACG GCAAGTCTTG      500
    ACTTACATTT TTTTCTAGCA CCACCACCAA GAAGGGTTCC ATTACCTCCG      550
    TC                                                                552
  
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2) INFORMATION FOR SEQ ID NO: 680

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1018 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

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(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Cunninghamella bertholletiae*
 (B) STRAIN: ATCC 42115

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 680

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    TCTCCCTGCT ATTTTAAACG CTCTTGAAGT TAAGGATCAT GCTGGTGGTC      50
    GTCTTGTCTT TGAAGTTGCT CAACACTTGG GTGAAAACAC TGTACGTACT      100
    ATTGCTATGG ATGGTACTGA AGGTAAGTTT ATTTTGTAGT GATCATAAAT      150
50  AATTGATCAT AATGATAAAA AAAAAAGAAG AAGAAGAACA GGATGTATAT      200
    AATGGTTAAT AAATAATATT TTCATATTGK ATATAACTAT TTAATCTGTT      250
    TTTTTTCTT CATGATTATA TATATATATG TMCTAATATC TAATATGAAC      300
    CTTTTTTTATA AAATTAATCA GGTCTTGTCC GTGGTCAAAA GGTGTTGTGAT      350
    ACTGGTGCTC CTATTACCAT TCCTGTTGGT AAGGAAGTTC TTGGTCGTAT      400
55  CATCAACGTT ATTGGTGAAC CCATTGATGA ACGTGGTCCT ATTAAGGCCA      450
    AGTCTCACCG TGCTATTCAC GCTGAAGCTC CAGAATTCGT TGATCAATCT      500
    CCTACTCCCG AAATTCTTGA AACTGGTATT AAGGTTGTCG ATTTATTAGC      550
    TCCTTATGCT CGTGGTGGTA AGATTGGTCT TTTCGGTGGT GCTGGTGTAG      600
    GTAAACTGT CTTGATTCAA GAACTATTA ACAACATTGC TAAAGCCCAT      650
60  GGTGGTTACT CTATTTCTG TGGTGTGGT GAACGTACTC GTGAAGGTAA      700
  
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385

	CGATTTATAC	CACGAAATGA	TGGAAACTGG	TGTCATTAAA	CTTGAAGGTG	750
	ACTCCAAGTG	TGCTCTTGTA	TTCGGTCAAA	TGAACGAACC	TCCTGGTGCT	800
	CGTGCCCGTG	TTGCTTTAAC	TGGTTTAACC	ATTGCTGAAT	ACTTCCGTGA	850
	TGAAGAAGGT	CAAGATGTGT	TACTTTTCAT	TGATAACATT	TTCCGTTTCA	900
5	CTCAAGCTGG	TTCTGAAGTA	TCTGCCCTTT	TAGGTCGTAT	TCCATCTGCT	950
	GTAGGTTACC	AACCCACTTT	ATCTACTGAT	ATGGGTGGTA	TGCAAGAACG	1000
	TATTACTACT	ACCAAGAA				1018

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2) INFORMATION FOR SEQ ID NO: 681

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 23 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: DNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 681

GGISSITTYG GIISIGGIAA RAC 23

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2) INFORMATION FOR SEQ ID NO: 682

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 26 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: DNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 682

GTIACIGGYT CYTCRAARTT ICCICC 26

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2) INFORMATION FOR SEQ ID NO: 683

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 26 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: DNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 683

GTIACIGGIT CISWIAWRTC ICCICC 26

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2) INFORMATION FOR SEQ ID NO: 684

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3267 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 5 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 10 (A) ORGANISM: *Candida tropicalis*
 (C) ACCESSION NUMBER: M64984

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 684

15	ATGGCTGGTG	CTTTAGAAAA	CGCAAGAAAA	GAAATTAAAC	GTCTTTCATT	50
	AGATGACACC	AATGAATCCC	AATATGGTCA	AATCTATTCT	GTTTCCGGTC	100
	CGGTTGTTAT	TGCCGAAAAC	ATGATTGGAT	GTGCCATGTA	CGAATTGGTT	150
	AAAGTTGGTC	ATGATAATTT	AGTTGGGGAA	GTTATTAGAA	TTAATGGTGA	200
	TAAAGCAACC	ATTCAAGTTT	ATGAAGAAAC	TGCAGGGGTC	ACTGTTGGTG	250
20	ATCCAGTTTT	AAGAACTGGT	AAACCATTAT	CTGTTGAATT	AGGTCCTGGT	300
	TTAATGGAAA	CTATTTATGA	TGGTATTCAA	AGACCTTTAA	AAGCCATTAA	350
	AGATGAATCC	CAATCTATTT	ATATCCCAAG	AGGTATTGAT	GTTCTGCTT	400
	TATCAAGAAC	TGTTCAATAT	GATTTCACCT	CAGGTCAATT	GAAAGTTGGT	450
	GATCATATCA	CTGGTGGGGA	CATTTTGGT	TCTATTTATG	AAAACCTCTT	500
25	ATTGGATGAC	CATAAGATTT	TGTTACCTCC	AAGAGCAAGA	GGTACTATTA	550
	CTTCTATTGC	TGAAGCCGGT	TCTTATAATG	TTGAAGAACC	AGTTTTGGAA	600
	GTTGAATTTG	ATGGTAAGAA	ACATAAATAC	TCTATGATGC	ATACATGGCC	650
	AGTTAGAGTT	CCAAGACCAG	TTGCTGAAAA	ATTGACTGCT	GATCATCCAT	700
	TGTTGACCGG	TCAAAGAGTC	TTGGATTCTT	TATTCCCATG	TGTTCAAGGT	750
30	GGTACTACTT	GTATCCCAGG	GGCTTTTGGT	TGTGGTAAAA	CTGTTATTTT	800
	TCAATCTTTG	TCCAAATTCT	CCAACCTCTG	TGTTATTATC	TATGTTGGTT	850
	GTTTCACTAA	AGGTACTCAA	GTCATGATGG	CTGATGGTGC	CGACAAATCT	900
	ATTGAATCTA	TTGAAGTTGG	TGACAAAGTC	ATGGGTAAAG	ATGGTATGCC	950
	AAGAGAAGTT	GTTGGCTTAC	CAAGAGGTTA	TGATGATATG	TACAAGGTTT	1000
35	GTCAACTTTC	TAGTACTAGA	CGTAATGCTA	AATCCGAAGG	CTTGATGGAT	1050
	TTCACTGTTT	CTGCTGATCA	TAAACTTATC	TTGAAAACTA	AACAAGATGT	1100
	CAAGATTGCT	ACACGTAAAA	TTGGTGGCAA	CACCTATACT	GGTGTACTTT	1150
	TCTATGTTTT	GGAAAAGACT	AAGACTGGTA	TTGAATTAGT	TAAAGCCAAG	1200
	ACTAAAGTTT	TCCGTCATCA	TATCCATGGT	CAAAATGGCG	CTGAAGAAAA	1250
40	AGCTGCTACT	TTTGCTGCTG	GCATTGACTC	TAAAGAATAC	ATTGATTGGA	1300
	TCATTGAAGC	TAGAGATTAT	GTACAAAGTT	ATGAAATTGT	CAAGACCAGC	1350
	ACCACTCAAA	TGATCAACCC	AGTTCATTTT	GAATCTGGTA	AACTCGGTAA	1400
	CTGGTTACAC	GAACACAAGC	AAAACAAATC	ACTTGCTCCA	CAATTGGGTT	1450
	ACTTGTTGGG	TACTTGGGCT	GGTATTGGAA	ATGTTAAATC	TTCTGCTTTC	1500
45	ACCATGAACT	CCAAAGATGA	TGTTAAATTA	GCTACAAGAA	TTATGAACTA	1550
	CTCTTCAAAA	TTGGGCATGA	CTTGTTCTTC	TACTGAATCC	GGTGAACTCA	1600
	ATGTCGCTGA	AAACGAAGAA	GAATTTTTCA	ATAACCTTGG	TGCTGAAAAG	1650
	GATGAAGCTG	GTGATTCAC	TTTTGATGAA	TTTACCGATG	CTATGGATGA	1700
	ATTGACTATC	AATGTTCATG	GTGCAGCTGC	AAGCAAGAAG	AACAATTTGT	1750
50	TGTGGAATGC	TTTGAAATCT	CTTGTTTCA	GAGCCAAGTC	TACTGATATT	1800
	GTCAAGAGTA	TTCCTCAACA	TATTGCTGTT	GATGATATTG	TTGTCAGAGA	1850
	ATCTTTGATT	GCCGGTTTAG	TTGATGCTGC	TGGTAATGTT	GAAACCAAAT	1900
	CCAATGGTTC	TATTGAAGCT	GTTGTTAGAA	CTTCTTTCAG	ACATGTCGCT	1950
	AGAGGTCTTG	TCAAGATTGC	TCATTCTTTG	GGTATTGAAT	CATCTATTAA	2000
55	TATTAAAGAT	ACTCACATTG	ATGCTGCTGG	TGTTAGACAA	GAATTTGCTT	2050
	GTATTGTCAA	TTTGACTGGT	GCTCCACTTG	CTGGTGTTCT	TTCTAAATGT	2100
	GCACTTGCAA	GAAACCAAAC	TCCAGTTGTC	AAATTTACCA	GAGACCCAGT	2150
	TTTGTTCAAC	TTTGATTTGA	TCAAATCTGC	AAAAGAAAAC	TATTATGGTA	2200
	TTACTTTGGC	TGAAGAAACT	GATCATCAAT	TCCTTTTATC	CAACATGGCC	2250
60	TTGGTGCACA	ACTGTGGTGA	ACGTGGTAAT	GAGATGGCTG	AAGTTTTGAT	2300

	GGAATTCCCA	GAATTGTTTA	CTGAAATTTTC	TGGTAGAAAA	GAACCAATTA	2350
	TGAAACGTAC	CACTTTGGTT	GCCAATACTT	CTAATATGCC	AGTCGCTGCC	2400
	AGAGAAGCTT	CTATTTATAC	TGGTATTACA	TTGGCTGAAT	ATTCAGAGA	2450
	TCAAGGTAAG	AATGTTTCTA	TGATTGCTGA	TTCTTCTTCA	CGTTGGGCTG	2500
5	AAGCTTTGAG	AGAAATTTCT	GGTAGATTGG	GTGAAATGCC	TGCTGATCAA	2550
	GGTTTCCCAG	CTTATTTGGG	TGCTAAATTG	GCTTCTTTCT	ATGAGCGTGC	2600
	CGGTAAAGCC	ACTGCTTTGG	GTTCAACCAGA	TAGAGTTGGT	TCAGTTTCTA	2650
	TTGTTGCTGC	TGTTTCTCCA	GCTGGTGGTG	ATTTCTCTGA	TCCAGTTACT	2700
	ACTTCTACTT	TGGGTATTAC	TCAAGTTTTC	TGGGGGTGG	ATAAGAAATT	2750
10	GGCCCAAAGA	AAACATTTCC	CATCTATTAA	CACCAGTGTT	TCTTATTCTA	2800
	AATACACCAA	TGTTTTGAAC	AAATACTATG	ATTCCAATA	TCCAGAATTC	2850
	CCACAATTGA	GAGACAAAAT	TAGAGAAATT	TTATCTAATG	CTGAAGAATT	2900
	GGAACAAGTT	GTTCAATTAG	TTGGTAAATC	TGCATTGTCT	GATTCTGATA	2950
	AGATTACTTT	AGATGTTGCT	ACCTTGATTA	AAGAAGATTT	CTTGCAACAA	3000
15	AATGGTTATT	CTTCATATGA	TGCATTCTGT	CCAATTGGA	AGACTTTTGA	3050
	TATGATGAGA	GCATTTATTT	CATATTATGA	TGAAGCACAA	AAAGCAATTG	3100
	CCAATGGTGC	TCAATGGTCT	AAATTAGCTG	AAAGTACTAG	TGATGTTAAA	3150
	CATGCTGTTT	CTTCAGCTAA	ATTCTTTGAA	CCATCAAGAG	GTCAAAAAGA	3200
	AGGTGAAAAA	GAATTTGGAG	ATTTATTAAC	CACTATCTCC	GAAAGATTTG	3250
20	CTGAAGCTTC	AGAATAA				3267

2) INFORMATION FOR SEQ ID NO: 685

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1782 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

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(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

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- (A) ORGANISM: *Enterococcus hirae*
 (B) STRAIN: ATCC 9790
 (C) ACCESSION NUMBER: D17462

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 685

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	TTGCAAATTG	GAAAAATCAT	AAAAGTCTCC	GGTCCTCTCG	TTATGGCAGA	50
	AAATATGTCA	GAAGCAAGTA	TTCAAGACAT	GTGTTTAGTG	GGAGATTTAG	100
	GAGTCATCGG	CGAAATCATT	GAGATGCGTC	AAGATGTGGC	GTCTATTCAA	150
	GTATATGAAG	AAACTTCAGG	AATTGGTCCC	GGAGAACCTG	TTCGTTCCAC	200
45	TGGGGAAGCA	CTATCTGTTG	AGCTAGGACC	AGGAATCATT	TCACAAATGT	250
	TTGACGGGAT	TCAAAGACCA	CTGGATACAT	TTATGGAAGT	GACTCAAAGT	300
	AACTTCTTAG	GACGTGGGGT	CCAATTACCA	GCTTTAGATC	ATGAGAAACA	350
	ATGGTGTTT	GAAGCGACAA	TCGAAGAAGG	AACAGAAGTA	AGTGCTGGAG	400
	ACATCATTGG	GTACGTGGAT	GAAACGAAGA	TCATTTCAGCA	CAAAATCATG	450
50	GTCCCTAATG	GTATCAAAGG	AACTGTACAA	AAAATTGAAT	CTGGATCATT	500
	TACGATCGAT	GATCCGATTT	GTGTGATCGA	AACGGAACAA	GGCTTAAAG	550
	AGCTGACGAT	GATGCAAAAA	TGGCCAGTAC	GTCGTGGTGC	ACCAATCAAA	600
	CAAAAATTAA	ATCCAGATGT	ACCGATGATC	ACCGGTCAAA	GGGTCATTGA	650
	CACGTTTTTC	CCAGTAACTA	AAGGAGGAGC	GGCAGCCGTT	CCAGGTCCGT	700
55	TTGGTGACAGG	GAAGACAGTT	GTGCAACACC	AGATTGCTAA	GTGGTCGGAC	750
	GTAGATCTAG	TGGTTTACGT	TGGTTGTGGG	GAACGAGGAA	ATGAAATGAC	800
	GGATGTCGTC	AATGAATTTC	CTGAACTGAT	CGATCCAAAT	ACAGGCGAGT	850
	CTTTGATGGA	ACGAACTGTG	TTGATCGCTA	ATACATCGAA	CATGCCAGTA	900
	GCTGCTCGAG	AAGCTTCTAT	TTATACGGGA	ATCACGATTG	CCGAGTACTT	950
60	CCGTGACATG	GGGTATGATG	TAGCAATCAT	GGCAGATTCC	ACTTCTCGTT	1000

	GGGCAGAAGC	ACTGCGTGAA	ATGAGCGGAC	GTTTAGAAGA	AATGCCCTGGT	1050
	GATGAAGGTT	ATCCCGCTTA	TCTGGGCTCT	CGTCTAGCTG	AATACTATGA	1100
	ACGTTTCAGGA	CGTGTCATTG	CTCTAGGCTC	TGACCAACGT	GAGGGCAGTA	1150
	TCACTGCCAT	CAGTGCGGTT	TCTCCTTCTG	GTGGAGATAT	CTCTGAACCA	1200
5	GTGACTCAAA	ATACCTTACG	TGTGGTGAAG	GTTTTCTGGG	GATTAGATTC	1250
	TAGTCTTGCT	CAAAAAAGAC	ATTTTCCATC	GATTAAGTGG	ATCCAAAGTT	1300
	ACTCATTATA	TTCAACAGAA	GTTGGCAGAT	ATATGGATCA	AATCTTACAA	1350
	CAGGATTGGT	CTGATATGGT	AACTGAAGGC	ATGCGGATCT	TGCAAGAAGA	1400
	AGAACAATTA	AATGAAATCG	TGCGCTTGGT	AGGGATCGAT	TCGCTTTCTG	1450
10	ATAACGATCG	CTTGACCCCTT	GAAGTAGCAA	AATCGATTCTG	AGAAGACTAT	1500
	TTACAACAAA	ATGCTTTTGA	TGATGTAGAT	ACGTTTACTT	CAAGAGAAAA	1550
	ACAATTCAAC	ATGTTGAAAG	TTATTTTGAC	TTTTGGGAAA	GAAGCTCGAA	1600
	AAGCCTTATC	GTTGGGAGCG	TACTTCAATG	AAATCATGGA	AGGTACAGTA	1650
	GCGGTCAGAG	AACGCATTAG	TCGGAGCAAG	TATATTCCAG	AAGAAGAGTT	1700
15	AGCCAAATT	AGTAGTATAA	ATGAAGAAAT	CAAAGAAACG	ATCCAATTGA	1750
	TTGTTTCAGA	AGGAGGGATG	ACCGATGATT	AA		1782

20 2) INFORMATION FOR SEQ ID NO: 686

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1781 bases
 (B) TYPE: Nucleic acid
 25 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

30 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Chlamydia pneumoniae*
 (B) STRAIN: CWL 029
 (C) ACCESSION NUMBER: Genome project

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 686

	CAGGGACATG	TTATAGAAGC	TTATGGAAAC	TTGTTACGTG	TACGCTTTGA	50
	CGGATATGTT	AGACAAGGTG	AAGTTGCATA	TGTCAACGTA	GATAATACCT	100
	GGTTAAAGC	AGAAGTGATT	GAAGTTGCTG	ATCAAGAAGT	CAAGGTTTCTG	150
40	GTATTTGAAG	ATACACAAGG	CGCGTGTCGA	GGAGCTCTTG	TTACGTTTTTC	200
	AGGACATCTT	TTAGAAGCCG	AGTTAGGGCC	TGGCTTGCTT	CAGGGCATTT	250
	TCGATGGACT	TCAAAATCGT	CTTGAGGTGC	TAGCTGAAGA	TAGTTCTTTTC	300
	TTGCAGAGAG	GCAAGCATGT	TAATGCTATT	TCTGATCATA	ATTTATGGAA	350
	TTATACTCCC	GTAGCTTCTG	TTGGGGATAC	TTTAAGACGA	GGAGATCTTC	400
45	TAGGAACAGT	ACCTGAAGGA	CGATTTACTC	ATAAGATTAT	GGTTCCTTTT	450
	TCTTGCTTTC	AAGAGGTTAC	CCTGACTTGG	GTAATTCTG	AAGGAACCTA	500
	TAATGCTCAT	ACTGTGGTCG	CAAAAGCTCG	AGATGCTCAG	GGTAAAGAAT	550
	GTGCCTTTAC	TATGGTGCAA	AGATGGCCGA	TCAAACAAGC	TTTTATTGAA	600
	GGAGAGAAGA	TCCCTGCGCA	TAAGATTATG	GATGTGGGTT	TGCGAATCTT	650
50	AGATACGCAA	ATTCCAGTAT	TGAAGGGGGG	AACCTTCTGT	ACCCAGGAC	700
	CTTTTGGTGC	AGGGAAAACA	GTCTTACAAC	ACCATCTTTC	TAAGTACGCT	750
	GCTGTAGATA	TTGTGATTTT	GTGTGCGTGC	GGAGAGCGTG	CTGGTGAAGT	800
	TGTTGAGGTA	TTACAAGAGT	TCCCTCATCT	TATCGACCCC	CATACCGGAA	850
	AGTCTTTAAT	GCACAGAACA	TGTATTATTT	GTAACACATC	ATCCATGCCT	900
55	GTGGCTGCCC	GAGAGTCTTC	GATCTATTTA	GGAGTGACGA	TTGCAGAATA	950
	CTATCGCCAG	ATGGGACTAG	ATATTCTGCT	TTTAGCTGAT	TCTACATCCC	1000
	GATGGGCACA	AGCCCTTAGA	GAGATTTTCG	GACGTCTTGA	AGAAATCCCT	1050
	GGAGAGGAAG	CATTTCTTGC	ATACCTGTCT	TCTAGAATAG	CTGCTTTTTTA	1100
	TGAGCGAGGA	GGAGCTATCA	CCACGAAAGA	TGGTTCTGAA	GGATCTTTAA	1150
60	CTATATGTGG	TGCGGTGTCT	CCTGCAGGAG	GAAACTTGA	AGAACCAGTC	1200

	ACTCAATCTA	CATTAGCTGT	AGTCGGAGCG	TTCTGTGGTC	TTTCAAAAGC	1250
	ACGAGCTGAC	GCACGTAGGT	ATCCTTCAAT	AGACCCTTTG	ATTTCTTGGT	1300
	CAAAATATTT	GAACCAGGTA	GGACAAATTT	TAGAAGAGAA	GGTTTCAGGC	1350
	TGGGGTGGTG	CTGTGAAAAA	AGCAGCACAG	TTTCTAGAGA	AAGGTTTCAGA	1400
5	AATCGGCAAG	CGTATGGAAG	TTGTCACTGA	AGAAGGGGTT	TCTATGGAAG	1450
	ACATGGAAAT	CTACTTAAAG	GCAGAACTTT	ATGATTTTTG	TkATCTCCAG	1500
	CAGAACGCAT	TCGATCCTGT	GGACTGTTAT	TGTCCTTTTG	AGAGACAGAT	1550
	AGAGTTATTT	TCATTAATCA	GTCGTATTTT	TGATGCTAAA	TTTGTTTTTG	1600
	ATAGTCCTGA	TGATGCAAGA	AGCTTTTTTC	TTGAGCTGCA	GAGCAAGATT	1650
10	AAGACATTAA	ATGGCCTGAA	ATTTCTTTCA	GAGGAATATC	ATGAGAGTAA	1700
	AGAGGTCATA	GTTAGACTGT	TGGAAAAAAC	AATGGTACAA	ATGGCGTAAG	1750
	GATATGCAAA	CAATCTACAC	AAAAATAACT	G		1781

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2) INFORMATION FOR SEQ ID NO: 687

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 1758 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

25

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Halobacterium salinarum*
(C) ACCESSION NUMBER: S56356

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 687

	ATGAGTCAAG	CTGAAGCAAT	CACTGACACC	GGCGAAATCG	AGAGCGTGAG	50
	CGGTCCGGTC	GTGACCGCCA	CGGGCCTCGA	CGCGCAGATG	AACGACGTGC	100
	TCTACGTGGG	CGACGAGGGT	CTGATGGGCG	AGGTCATCGA	GATCGAAGGC	150
35	GACGTAACCA	CCATCCAGGT	CTACGAGGAG	ACGTCCGGCA	TCGGGCCCGG	200
	CCAGCCCCGT	GACAACACGG	GCGAACCGCT	CACCGTGGAC	CTGGGCCCGG	250
	GGATGCTGGA	CTCCATCTAC	GATGGTGTGC	AGCGTCCACT	GGACGTCCTC	300
	GAAGACGAGA	TGGGGGCGTT	CCTCGATCGC	GGTGTTGACG	CACCCGGCAT	350
	CGACCTCGAC	ACCGACTGGG	AGTTCGAGCC	CACCGTCGAG	GCGGGCGACG	400
40	AGGTCGCGGC	CGGCGATGTC	GTCGGCACCG	TCGACGAAAC	GGTCAGCATC	450
	GAACACAAGG	TTCTGGTGCC	CCCCCGCAGT	GACGGCGGCG	AAGTCGTCGC	500
	CGTCGAATCC	GGCACGTTCA	CCGTCGACGA	CACGGTCGTC	GAGTTGGACA	550
	CCGGCGAGGA	GATCCAGATG	CACCAGGAGT	GGCCGGTCCG	CCGCCAGCGC	600
	CCCACCGTCG	ACAAGCAGAC	GCCGACGGAG	CCGCTGGTGT	CCGGCCAGCG	650
45	CATCCTCGAC	GGCCTGTTCC	CGATCGCGAA	AGGCGGGACG	GCCGCGATCC	700
	CGGGGCCGTT	CGGGTCCGGG	AAGACGGTCA	CCCAGCAGTC	CCTCGCGAAG	750
	TTCGCCGACG	CGGACATCGT	TGTCTACATC	GGCTGTGGTG	AGCGCGGCAA	800
	CGAGATGACG	GAAGTCATCG	AGGACTTCCC	GGAGCTGCCC	GACCCCCAGA	850
	CCGGGAACCC	GCTGATGGCC	CGCACCACGC	TCATCGCGAA	CACGTCGAAC	900
50	ATGCCGGTTG	CCGGGCCGTA	GTCCTGCATT	TACACGGGAA	TCACCATCGC	950
	GGAGTACTAC	CGCGACATGG	GCTACGACGT	GGCGCTGATG	GCCGACTCCA	1000
	CCTCGCGGTG	GGCGGAGGCC	ATGCGGGAGA	TCTCCTCGCG	ACTCGAGGAG	1050
	ATGCCCGGCG	AGGAGGGGTA	TCCCCGCTAC	CTGGCCGCCC	GCCTCTCGGA	1100
	GTTCTACGAG	CGCGCCGGCT	ACTTCGAGAA	CTTCAACGGG	ACCGAGGGCT	1150
55	CCATCTCGGT	CATCGGTGCG	GTGTCGCCGC	CCGGCGGGGA	CTTCTCCGAG	1200
	CCGGTCACCC	AGAACACGCT	GCGCATCGTG	AAGACGTTCT	GGGCGCTTGA	1250
	CTCGGACCTC	GCCGAGCGCC	GGCACTTCCC	GGCGATCAAC	TGGGACGAGT	1300
	CCTACAGCCT	CTACAAGGAC	CAACTCGACC	CGTGGTTTCA	GGACAACGTC	1350
	GTCGACGACT	GGGCCGAGCA	GCGCCAGTCG	GCGGTTCGACA	TCCTCGACGA	1400
60	GGAATCCGAA	CTCGAAGAGA	TCGTGCAGCT	CGTCGGGAAG	GACGCGCTGC	1450

	CCGAGGACCA	GCAGCTCAGC	CTGGAAGTCG	CGCGGTACAT	CCGCGAGGCG	1800
	TGGCTCCAGC	AGAACGCGCT	CCACGACGTG	GATCGCTACT	GCCCGCCCGA	1550
	GAAGACGTAC	GCCATCCTCT	CCGGCATCAA	GACGCTTCAC	GAGGAGTCCT	1600
	TTGAGGCGTT	GGACGCCGGT	GTGCCAGTCG	AGGAGATCAC	GTCGATCGAC	1650
5	GCCGCGCCGC	GCCTGAATCG	TCTCGGCACG	ACGCCCCGACG	ACGAGCACGA	1700
	GGCGGAGGTC	GCGGAGATCA	AACAGCAGAT	TACCGAGCAG	CTTCGGGAGC	1750
	TCTACTGA					1758

10

2) INFORMATION FOR SEQ ID NO: 688

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3118 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Human
 (C) ACCESSION NUMBER: L09234

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 688

	GAATTCCGGC	AGCTGACTAG	TCTTGTGATT	GGGGTCCTGG	GCTGATAAAA	50
	TCATTCCAAA	TGACGAGCAC	ATTGATAAAG	ACGTCCGATG	AGGACCGGGA	100
	GTCCAAATTC	GGCTTTGTTT	TTGCCGTATC	TGGACCTGTG	GTGACAGCTG	150
30	AACGAATGGC	CGGTTCTGCT	ATGTACGAAC	TGGTGCGTGT	CGGTTATTAT	200
	GAAGTGGTCG	GAGAGATCAT	CCGGTTGGAG	GGTGACATGG	CAACAATCCA	250
	AGTATACGAA	GACACCTCAG	GTGTGACAGT	AGGCGATCCC	GTGCTGCGCA	300
	CAGGCAAGCC	GCTGTCCGTG	GAAGTGGGAC	CCGGAATCAT	GGGCAGCATC	350
	TTCGACGGTA	TCCAGCGACC	GCTGAAGGAT	ATCAATGAAC	TGTCAAATAG	400
35	TATCTACATC	CCGAAAGGTG	TCAATGTGCC	TGCCCTGAGT	CGCACTGCAC	450
	AGTGGGACTT	CAGTCCCGTC	AGTGTC AAGG	TTGGAAGCCA	CATTACTGGT	500
	GGTGACCTGT	ACGGTTTGGT	CCACGAAAAT	ACTCTGGTGA	AACACAAGTT	550
	GCTGTGCGCC	CCCCGTGCCA	AGGGAACTGT	CACGTACATT	GCAGAACCTG	600
	GAAACTACAC	AGTTGATGAT	GTTGTCCCTGG	AGACAGAATT	TGACGGCGAG	650
40	CGATCAAAGT	TCACCATGCT	GCAAGTGTGG	CCTGTACGTC	AGCCCAGGCC	700
	TGTTACAGAA	AAGTTGCCAG	CTAACTACCC	CCTCCTTACT	GGCCAGCGTG	750
	TGCTCGACTC	CCTATTCCCG	TGTGTCCAGG	GTGGAACAAC	AGCTATTCTT	800
	GGGGCCTTCG	GATGTGGCAA	GACTGTAATA	TCACAGTCTT	TGTCAAATAA	850
	CTCAAATCC	GATGTAATTA	TCTATGTAGG	TTGTGGTGAG	CGAGGTAATG	900
45	AAATGTCAGA	AGTACTCAGG	GATTTCCCGC	AGTTGTCGTT	GGAGATTGAT	950
	GGTGTGACTG	AATCAATCAT	GAAGAGAACA	GCCCTGGTCG	CAAACACATC	1000
	AAACATGCCT	GTGGCTGCTC	GAGAAGCATC	TATCTACACA	GGTATTACAC	1050
	TGTCAGAATA	CTTCAGGGAC	ATGGGTTACA	ATGTATCCAT	GATGGCTGAC	1100
	TCAACTTCAC	GATGGGCCGA	AGCTCTTCGA	GAAATCTCAG	GTCGATTGGC	1150
50	TGAAATGCCT	GCCGACAGCG	GTTATCCCGC	CTACCTAGGT	GCACGACTTG	1200
	CCAGTTTCTA	CGAGCGTGCC	GGCCGTGTGA	AGTGCTTGGG	TAACCCAGAC	1250
	AGGGAGGGCT	CCGTGACTAT	AGTGGGCGCC	GTGTCGCCGC	CCGGTGGAGA	1300
	CTTCTCAGAT	CCCGTGACGA	CGGCCACACT	AGGTATCGTC	CAGGTGTTCT	1350
	GGGGTCTCGA	CAAGAACTT	GCCCAGCGAA	AGCACTTCCC	ATCCATCAAC	1400
55	TGGCTCATCT	CGTACAGTAA	ATACATGCGT	GCTCTGGATG	ACTTCTACGA	1450
	CAAGAATTTT	CCAGAGTTTG	TCCCACTGCG	TACAAAGGTG	AAGGAGATTT	1500
	TGCAGGAGGA	AGAAGACCTG	TCTGAAATTG	TGCAGTTGGT	CGGTAAAGCT	1550
	TCATTGGCAG	AAACTGACAA	GATCACACTT	GAGGTTGCCA	AACTATTAAA	1600
	GGATGATTTT	CTGCAACAGA	ACAGCTATTC	ACCATATGAC	CGTTTCTGCC	1650
60	CATTCTACAA	GACAGTAGGA	ATGCTGAAAA	ATATGATTGC	TTTCTACGAT	1700

	ATGTCTCGGC	ATGCAGTTGA	ATCTACTGCT	CAGAGCGAGA	ACAAATATCAC	1750
	TTGGAATGTT	ATTAGAGATT	CTATGGGCAA	TATTCTGTAT	CAGCTTTCCT	1800
	CCATGAAATT	CAAGGATCCA	GTCAAGGATG	GAGAAGCGAA	GATCAAGGCA	1850
	GACTTTGAGC	AGCTTCATGA	AGACATTCAG	CAAGCCTTCA	GGAACCTGGA	1900
5	GGATTAAAGT	GGTAGCTGCC	AGTGGTTCTC	TCGGTGCAGT	TGTCACATTT	1950
	GGCAAGCTCT	GTAGGGTTGC	CGAGTGGCAT	CGGTGCTAGA	CACCTGAGCA	2000
	TTCCTTTGCC	ACATAAAGAC	TAAAGCAGGT	GGAATTTTCAG	TTGTAAAAAG	2050
	CTGGTTCCAT	TGGTGCTAAG	ATTATGTTGT	GCCCTTTTCT	GCTTCTCACA	2100
	TTCCAACAGA	GGAATTTACT	TCCAGTTTTT	TTCCATTTTC	CTCCTCATTT	2150
10	TAAGTGTCGG	TACAGAGGCA	ATAATCTGAT	AACTCTGTAC	CGTCACTTAC	2200
	AAGCAGGGAG	AATTTGTAAT	TATTACAAAT	CCCATTATCT	CTGTGCACCA	2250
	CAGCCTTGTA	AATTCATTTG	TCCCAGGACT	CCCTCTTGTT	TGTAAGTGAG	2300
	ATTGCCGTCT	GTATGTATGT	ACACACCGTA	CTGCAGTATT	TGAAGTCAGT	2350
	CAGAAGGTGA	ATTACACCAC	TTACTCATTG	TGTCACGTAG	CAAGTGTGCA	2400
15	AACTGCCATC	CATTGTCCTA	TTTATTCACA	TAAGTAGTTT	TCTTTGCATT	2450
	TCCAGTGTTG	CAAATTGTGT	TTAGAAAATT	ATGCCATCGA	GACTGGTCGA	2500
	ACCTCACATT	GTAAGTCAGT	ATTTACACAC	ACGTTTACTT	GCTACAGAAA	2550
	TGTAGAAAAA	ATAATTGTTG	TATATTGAAA	GTACAAGTGA	CAAAGTTGCA	2600
	TTTAAAATGG	TGAATGTATT	TTATATTTCT	TTTGTAGACA	CAAGAGTTAA	2650
20	TGCATTTTGC	TTAATGGAGA	TGTATGTAAA	CCTAAAATAG	CAGTTTGTGC	2700
	ACAAATTATG	TATATGTGAA	ATGGAGATGG	TTTCTAATTT	GCTGATTGAT	2750
	TGCCAGTATT	AATTTAAACA	ACTGTAGTTG	TGGGATGTAG	TGGGAAGATT	2800
	TTTTTTTTTC	TATAAAATTG	GTGGATGTAT	GTGTCGGAGA	TTTTGATTGT	2850
	ATGTGTAAAA	TAGTGATCCC	AGTAACTGTA	AAGCTTTAGA	ATACAGTTAC	2900
25	TGACTGTATA	GTTGTACAGG	TGTTGTTACT	TTTAAGAATT	TATTGACACA	2950
	AAGGTGAAAG	TCTATTATTG	TATTGTAATG	TTTAAAGCAT	TTAAGGTTTA	3000
	AAAATCCTAC	TTCTGTGTAT	AAATGTTACC	ATTCTTCATA	TAACATAACT	3050
	GTGTAGAAAT	ACAGTCAACT	TCATGTTTAT	TAGCATTTCA	CTGTTGTAC	3100
	ATAAATTATG	CCCGGAAT				3118
30						

2) INFORMATION FOR SEQ ID NO: 689

- 35 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1836 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Double
 - (D) TOPOLOGY: Linear
- 40 (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Plasmodium falciparum*
 - (B) STRAIN: 3D7
 - (C) ACCESSION NUMBER: L08200
- 45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 689

50	ATGACAAAAG	TTGCTGTTGA	AAAAGAGGAA	CCAGGAGTTG	TTTATAAGGT	50
	GGCTGGTTCA	TTAGTTATTG	CTGAGAATAT	GAGTGGAAT	CGTATGTACG	100
	AGTTAGCTAA	AGTAGGATGG	AATAAATTGG	TTGGAGAAAT	TATTAGATTA	150
	GAAGGGAATT	ATGCATATAT	ACAAGTTTAT	GAAGATACTT	CAGGTTTATC	200
	TGTAGGAGAC	CCTGTTATAA	AAACAGGAAA	TGCTTTATCA	GTCGAATTGG	250
55	GTCCTGGTAT	TTTAGATAAT	ATTTATGATG	GTATTCAAAG	ACCATTAGAA	300
	AGAATAGCAA	ATGTGTGTGG	TGATGTATAT	ATATATAAAG	GTATTGATAT	350
	GACATCTTTA	GATCATGATA	AACAATGGCA	ATTTTATGCT	GATAAGAAAT	400
	TAAAATTAAA	TGATATTGTT	ACTGGTGGAG	ATATCTTTGG	ATTTGTTGAT	450
	GAAAATAAAT	TATTTAAAGA	ACACAAAATT	ATGGCTCCAC	CTAATGCTAA	500
60	AGGGAGGCTT	ACATATATTG	CTCCAGATGG	ATCATATACT	TTAAAAGATA	550

	AAATATTTGA	ATTAGAATAT	CAAGGAAAAA	AATATACATA	TGGTTTATCT	600
	CATTTATGGC	CTGTTCTGTA	TCCTAGACCT	GTTTATAGAA	AGGTAACAGG	650
	GGATACTTTA	TTATTAACAG	GGCAAAGAGT	TTTAGATTCTG	TTATTTCCAA	700
	CAGTTCAAGG	AGGTACTTGT	GCTATTCCTG	GTGCATTTGG	TTGTGGAAAA	750
5	ACTTGTGTTT	CTCAGGCCTT	ATCAAAAATAT	TCTAATAGTG	AAGTTATTAT	800
	ATATGTAGGA	TGTGGTGAAA	GAGGTAATGA	AATGGCTGAA	ATTTTATCCG	850
	ACTTTCTCTGA	ATTAACACT	AAAGTAGATA	ATGAAGATGT	AGGTATTATG	900
	CAAAGAACGT	GTTTAGTTGC	TAATACTTCT	AACATGCCTG	TCGCTGCAAG	950
	AGAAGCTAGT	ATTTATACAG	GTATTACTTT	ATGTGAATAT	TTCCGTGATA	1000
10	TGGGTTATAA	TGCTACCATG	ATGGCTGATA	GTACAAGTAG	ATGGGCAGAA	1050
	GCCTTAAGAG	AAATTTTCAGG	ACGTTTTCAGT	GAAATGCCTG	CAGATAGTGG	1100
	TTATCCAGCT	TATTTAGGTG	CTAGATTAGC	TTCTTTTAT	GAACGTGCAG	1150
	GAAAAGTCAA	ATGTATTGGT	TCTCCATCTC	GTATAGGATC	CATTACAATT	1200
	GTGGGTGCTG	TGTCTCCACC	AGGTGGTGAT	TTCTCTGACC	CTGTAACACT	1250
15	AGCAACCATG	TCTATTGTTT	AAGCATTTTG	GGGGTTAGAT	AAAAAACTAG	1300
	CTCAAAGAAA	ACATTTCCCT	TCTGTTAATT	GGTCTACATC	CTTTTCAAAG	1350
	TATGTCAGAC	AATTAGAACA	ATACTTTGAT	AATTTTGATC	AAGATTTCTT	1400
	ATCTTTAAGA	CAAAAAATTA	GTGATATTTT	ACAACAAGAA	AGTGACTTGA	1450
	ATGATATTGT	TCAACTAGTA	GGAAAGGATT	CATTATCAGA	AGACCAAAAA	1500
20	GTTGTTATGG	AAGTAGCCAA	AATTATTAGA	GAAGATTTTC	TTCAACAAAA	1550
	TGCATTTAGC	GATTATGATT	ATATGTGCC	ATTACAAAAA	ACAGTTGGTA	1600
	TGATGAGAAT	TATTTGCCAC	TTTTATGCTC	AATGCTTAAG	AACATTACAA	1650
	GAATATGACT	CAAGAGAAAG	AAAAATTGGT	TGGGGATCTA	TATATAATAC	1700
	ATTAAGACCA	ACTATAAATA	AAATTACACA	TATGAAATTT	GAAAACCCAA	1750
25	AAAATTCAGA	TGAATATTTT	AAAAAGTATT	TTAAGGCACT	TGAAGAAGAA	1800
	ATAACAGTAG	GTTTAAGAAA	CTTGATGGAA	AAATGA		1836

30 2) INFORMATION FOR SEQ ID NO: 690

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3216 bases
 (B) TYPE: Nucleic acid
 35 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

40 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Saccharomyces cerevisiae*
 (B) STRAIN: X2180-1A
 (C) ACCESSION NUMBER: J05409

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 690

	ATGGCTGGTG	CAATTGAAAA	CGCTCGTAAG	GAAATAAAAA	GAATCTCATT	50
	AGAAGACCAT	GCTGAATCTG	AATATGGTGC	CATCTATTCT	GTCTCTGGTC	100
	CGGTCGTCAT	TGCTGAAAAT	ATGATTGGTT	GTGCCATGTA	CGAATTGGTC	150
50	AAGGTCGGTC	ACGATAACCT	GGTGGGTGAA	GTCATTAGAA	TTGACGGTGA	200
	CAAGGCCACC	ATCCAAGTTT	ACGAAGAAAC	TGCAGGCCTT	ACGGTCGGTG	250
	ACCCTGTTTT	GAGAACAGGT	AAGCCTCTGT	CGGTAGAATT	GGGTCCTGGT	300
	CTGATGGAAG	CCATTTACGA	TGGTATTCAA	AGACCTTTGA	AAGCCATTAA	350
	GGAAGAATCG	CAATCGATTT	ATATCCCAAG	AGGTATTGAC	ACTCCAGCTT	400
55	TGGATAGGAC	TATCAAGTGG	CAATTTACTC	CGGGAAAGTT	TCAAGTCGGC	450
	GATCATATTT	CCGGTGGTGA	TATTTACGGT	TCCGTTTTTG	AGAATTCGCT	500
	AATTTCAAGC	CATAAGATTC	TTTTGCCACC	AAGATCAAGA	GGTACAATCA	550
	CTTGGATTGC	TCCAGCTGGT	GAGTACACTT	TGGATGAGAA	GATTTTGGAA	600
	GTTGAATTTG	ATGGCAAGAA	GTCTGATTTT	ACTCTTTACC	ATACTTGGCC	650
60	TGTTCTGTGT	CCAAGACCAG	TTACTGAAAA	GTTATCTGCT	GAATATCCTT	700

	TGTTAACAGG	TCAAAGAGTT	TTGGATGCTT	TGTTTCCTTG	TGTTCAAGGT	750
	GGTACGACAT	GTATTCCAGG	TGCTTTTGGT	TGTGGTAAGA	CCGTTATCTC	800
	TCAATCTTTG	TCCAAGTACT	CCAATTCTGA	CGCCATTATC	TATGTCGGGT	850
	GCTTTGCCAA	GGGTACCAAT	GTTTTAATGG	CGGATGGGTC	TATTGAATGT	900
5	ATTGAAAACA	TTGAGGTTGG	TAATAAGGTC	ATGGGTAAAG	ATGGCAGACC	950
	TCGTGAGGTA	ATTAAATTGC	CCAGAGGAAG	AGAAACTATG	TACAGCGTCG	1000
	TGCAGAAAAG	TCAGCACAGA	GCCCACAAAA	GTGACTCAAG	TCGTGAAGTG	1050
	CCAGAATTAC	TCAAGTTTAC	GTGTAATGCG	ACCCATGAGT	TGGTTGTTAG	1100
	AACACCTCGT	AGTGTCCGCC	GTTTGTCTCG	TACCATTAAG	GGTGTGCAAT	1150
10	ATTTTGAAGT	TATTACTTTT	GAGATGGGCC	AAAAGAAAGC	CCCCGACGGT	1200
	AGAATTGTTG	AGCTTGTCAA	GGAAGTTTCA	AAGAGCTACC	CAATATCTGA	1250
	GGGGCCTGAG	AGAGCCAACG	AATTAGTAGA	ATCCTATAGA	AAGGCTTCAA	1300
	ATAAAGCTTA	TTTTGAGTGG	ACTATTGAGG	CCAGAGATCT	TTCTCTGTTG	1350
	GGTTCCCATG	TTCGTAAAGC	TACCTACCAG	ACTTACGCTC	CAATTCTTTA	1400
15	TGAGAATGAC	CACTTTTTCG	ACTACATGCA	AAAAAGTAAG	TTTCATCTCA	1450
	CCATTGAAGG	TCCAAAAGTA	CTTGCTTATT	TACTTGGTTT	ATGGATTGGT	1500
	GATGGATTGT	CTGACAGGGC	AACTTTTTTCG	GTTGATTCCA	GAGATACTTC	1550
	TTTGATGGAA	CGTGTTACTG	AATATGCTGA	AAAGTTGAAT	TTGTGCGCCG	1600
	AGTATAAGGA	CAGAAAAGAA	CCACAAGTTG	CCAAAAGTGT	TAATTTGTAC	1650
20	TCTAAAGTTG	TCAGAGCTAA	TGGTATTCGC	AATAATCTTA	ATACTGAGAA	1700
	TCCATTATGG	GACGCTATTG	TTGGCTTAGG	ATTCTTGAAG	GACGGTGTCA	1750
	AAAATATTCC	TTCTTTCTTG	TCTACGGACA	ATATCGGTAC	TCGTGAAACA	1800
	TTTCTTGCTG	GTCTAATTGA	TTCTGATGGC	TATGTTACTG	ATGAGCATGG	1850
	TATTAAAGCA	ACAATAAAGA	CAATTCATAC	TTCTGTCAGA	GATGGTTTGG	1900
25	TTTCCCTTGC	TCGTTCCTTA	GGCTTAGTAG	TCTCGGTAA	CGCAGAACCT	1950
	GCTAAGGTTG	ACATGAATGG	CACCAAACAT	AAAATTAGTT	ATGCTATTTA	2000
	TATGTCTGGT	GGAGATGTTT	TGCTTAACGT	TCTTTCGAAG	TGTGCCGGCT	2050
	CTAAAAAATT	CAGGCCTGCT	CCCGCCGCTG	CTTTTGCACG	TGAGTGCCGC	2100
	GGATTTTATT	TCGAGTTACA	AGAATTGAAG	GAAGACGATT	ATTATGGGAT	2150
30	TACTTTATCT	GATGATTCTG	ATCATCAGTT	TTTGCTTGCC	AACCAGGTTG	2200
	TCGTCCATAA	TTGCGGAGAA	AGAGGTAATG	AAATGGCAGA	AGTCTTGATG	2250
	GAATTCCCAG	AGTTATATAC	TGAAATGAGC	GGTACTAAAG	AACCAATTAT	2300
	GAAGCGTACT	ACTTTGGTCG	CTAATACATC	TAACATGCCG	GTTGCAGCCA	2350
	GAGAAGCTTC	TATTTACACT	GGTATCACTC	TTGCAGAATA	CTTCAGAGAT	2400
35	CAAGGTAAAA	ATGTTTCTAT	GATTGCAGAC	TCTTCTTCAA	GATGGGCTGA	2450
	AGCTTTGAGA	GAAATTTCTG	GTCGTTTGGG	TGAGATGCCT	GCTGATCAAG	2500
	GTTTCCCAGC	TTATTTGGGT	GCTAAGTTGG	CCTCCTTTTA	CGAAAGAGCC	2550
	GGTAAAGCTG	TTGCTTTAGG	TTCCCAGAT	CGTACTGGTT	CCGTTTCCAT	2600
	CGTTGTGCCC	GTTTCGCCAG	CCGGTGGTGA	TTTCTCAGAT	CCTGTTACTA	2650
40	CTGCTACATT	GGGTATCACT	CAAGTCTTTT	GGGGTTTAGA	CAAGAAATTG	2700
	GCTCAAAGAA	AGCATTTCCC	ATCTATCAAC	ACATCTGTTT	CTTACTCCAA	2750
	ATACACTAAT	GTCTTGAACA	AGTTTTATGA	TTCCAATTAC	CCTGAATTTT	2800
	CTGTTTTAAG	AGATCGTATG	AAGGAAATTC	TATCAAACGC	TGAAGAATTA	2850
	GAACAAGTTG	TTCAATTAGT	TGGTAAATCG	GCCTTGTCTG	ATAGTGATAA	2900
45	GATTACTTTG	GATGTTGCCA	CTTTAATCAA	GGAAGATTTT	TTGCAACAAA	2950
	ATGGTTACTC	CACCTATGAT	GCTTCTGTCT	CAATTTGGAA	GACATTTGAT	3000
	ATGATGAGAG	CCTTCATCTC	GTATCATGAC	GAAGCTCAAA	AAGCTGTTGC	3050
	TAATGGTGCC	AACTGGTCAA	AACTAGCTGA	CTCTACTGGT	GACGTTAAGC	3100
	ATGCCGTTTC	TTCATCTAAA	TTTTTTGAAC	CAAGCAGGGG	TGAAAAGGAA	3150
50	GTCCATGGCG	AATTCGAAAA	ATTGTTGAGC	ACTATGCAAG	AAAGATTTGC	3200
	TGAATCTACC	GATTAA				3216

55 2) INFORMATION FOR SEQ ID NO: 691

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1860 bases

(B) TYPE: Nucleic acid

60 (C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

5 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Schizosaccharomyces pombe*

(B) STRAIN: 972 h-

(C) ACCESSION NUMBER: S47814

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 691

	ATGGCGGGAG	GAATTGAACT	GGCCAAGAAG	GCTATCAGGA	GCCTCAAAAA	50
	TTACGACGAG	CATGAAAACC	GATATGGATC	TATTTTCAGC	GTTTCTGGTC	100
	CTGTCGTTGT	TGCAGCCAAT	ATGCTTGGAT	GTTTCGATGTA	CGAACTCGTT	150
15	CGCGTTGGTC	ATGAAGAACT	AGTTGGTGAA	GTAATTCGTA	TCCATCAAGA	200
	TAAATGTACT	ATTCAAGTAT	ACGAAGAGAC	GTCCGGTCTC	ACTGTTGGTG	250
	ATCCTGTCCA	ACGCACTGGA	AAGCCATTAT	CTGTTGAATT	AGGTCCTGGT	300
	TTAGCTGAGA	CTATTTATGA	TGGTATCCAA	CGTCCGTAA	AGCAAATTTT	350
	CGACAAATCT	CAAAGTATTT	ATATTCCTAG	AGGTATTAAT	ACAGAATCAC	400
20	TTAATCGTGA	GCATAAGTGG	GATTTACAC	CAAATAAGGA	TTTACGCATT	450
	GGCGATCATG	TATCCGGTGG	TGATGTTTTC	GGTTCTGTAT	TTGAAAACCTC	500
	TCTTTTCAAT	GATCATAAAA	TTATGTTACC	CCCTAGAGCC	CGTGGTACCG	550
	TCACATATAT	TGCTGAAGCT	GGATCATACC	ATGTTGATGA	AAAACCTTCTT	600
	GAAGTCGAGT	TTAATGGCAA	GAAACATTCT	TTTAGTATGT	TGCATACTTG	650
25	GCCTGTCCGT	GCTGCTCGTC	CAGTTGCGGA	CAACTTAACT	GCTAATCAAC	700
	CTTTATTGAC	TGGTCAACGT	GTTTTGGATG	CGTTATACCC	CTGTGTTCAA	750
	GGTGGCACTA	CTGCTATCCC	CGGTGCCTTT	GGTTGTGGTA	AAACAGTTAT	800
	TTCACAATCT	CTTTCTAAGT	ACTCTAATTC	TGATTTGATT	GTTTACGTCG	850
	GTTGTGGTGA	ACGTGGAAAC	GAAATGGCAG	AAGTGTTAAT	GGATTTCCCA	900
30	GAACATAACAA	TTGATATTAA	TGGTAAACCA	GAGCCCATTA	TGAAGCGTAC	950
	TACATTGGTA	GCCAACACTT	CTAACATGCC	TGTCGCTGCT	CGTGAAGCTT	1000
	CCATTTATAC	CGGTATTACA	CTTGCTGAAT	ATTATCGTGA	TCAAGGTAAG	1050
	AACGTTTCAA	TGATGGCTGA	TTCTACATCT	CGTTGGGCTG	AAGCTTTGCG	1100
	TGAAATTTCT	GGTCGTTTGG	CTGAGATGCC	TGCCGATTCT	GGTTATCCCG	1150
35	CTTATTTGGG	TGCCAAATTG	GCTTCTTTTT	ACGAACGTGC	TGGTCGTGCT	1200
	CGTTGCTTGG	GAAGTCCTGA	CCGTGAAGGA	ACAGTTTCAA	TTGTTGGAGC	1250
	TGTTTCTCCT	CCGGGTGGTG	ATTTTTCTGA	TCCTGTTACT	AGTGCAACCT	1300
	TGGGAATTTG	TCAAGTCTTC	TGGGGTTTGG	ACAAGAAATT	GGCCCAACGT	1350
	AAACACTTTC	CCTCAATCAA	CACCTCTCTT	TCCTATTCTA	AATACATCAA	1400
40	TGCTTTGCAA	CCTTGGTATG	AGGAAAGAGT	TCCAGGCTTT	AATACTCTTC	1450
	GTGATCAAAT	CAAACAGATC	ATTCAACAAG	AAGATTCCAT	GTTGGAAATT	1500
	ATTCAAGTTGG	TTGGTAAGTC	GGCTCTTTCT	GAAACGGATA	AAGTTACTTT	1550
	GGACATAGCC	GGTATTATTA	AGAATGACTT	CTTACAACAA	AACGGTTATT	1600
	CTGATTACGA	TCGCTGTTGC	CCTCTTTACA	AGACTTATCA	TATGATGCGA	1650
45	AACATGATTG	CTTACTACAC	AAAGGCTAAA	AGTGCCGTTG	AAACTGGTAG	1700
	CGTTCCTTGG	TCAAAGATTA	AAGAAAGTAC	TTCAGATATC	TTTTATGAGT	1750
	TAACCTCGAT	GAAATTCGAA	AACCCTAATG	AAGGCGAGAA	GGAAATAGTC	1800
	GAACACTATG	AAACTCTGCA	CAAGAAGATT	GAGGACAAGT	TTCACACTCT	1850
	GACTGAGTAA					1860

50

2) INFORMATION FOR SEQ ID NO: 692

55 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1833 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

60

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 5 (A) ORGANISM: *Trypanosoma congolense*
 (B) STRAIN: IL3000
 (C) ACCESSION NUMBER: Z25814

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 692

```

10  ATGACGAGCG ATAAAAACCC TTACAAAACA GAGCAGCGCA TGGGGGCCGT      50
    GAAGGCCGTC TCCGGGCCAG TTGTCATTGC TGAAAACATG GGCGGTAGCG      100
    CTATGTATGA GCTTGTGCAG GTAGGTTCTT TCCGGTTAGT GGGCGAGATC      150
    ATTCGTCTAG AGGGCGATAC CGCCACTATT CAGGTCTATG AGGAAACAGG      200
    TGGCCTCACT GTCGGAGACC CGGTGTACTG TACGGGTAAG CCTCTTTTCGC      250
15  TTGAGCTTGG ACCTGGAATC ATGTCTGAAA TATTTGACGG TATCCAGCGG      300
    CCTCTTGACA CCATCTACCG CATGGTGGAA AACGTGTTTA TCCCCAGGGG      350
    CGTTCAGGTG AAGTCACTCA ATGACCAGAA ACAGTGGGAC TTTAAGCCAT      400
    GCCTGAAGGT TGGAGATCTT GTGTCTGGTG GTGATATCAT TGGCTCAGTG      450
    GTGGAGAACT CTCTCATGTA CAATCACAGC ATTATGATTC CGCCAATGT      500
20  GCGGGGCCGT GTTACTTCCA TTGTTCTTTC AGGAAATTAC ACCCTCCAAG      550
    ATGACATTAT TGAATTGGAA TATAATGGGA CAGTGAAATC ACTAAAACCT      600
    ATGCATCGCT GGCCAGTACG GACCCCGCGT CCTGTGGCGT CAAAAGAATC      650
    CGGCAATCAT CCGCTTCTCA CCGGACAGCG TGTGCTCGAT GCTCTCTTTC      700
    CATCCGTCCA GGGTGGAAAC TGCGCCATCC CTGGCGCGTT TGGATGCGGA      750
25  AAGACGGTTA TCAGTCAGGC TCTTTCGAAG TTCTCCAACA GCGACGCTGT      800
    TATCTATGTC GGCTGCGGCG AGCGTGGGAA TGAGATGGCA GAGGTGCTCA      850
    TGGACTTCCC CACACTCACC ACCGTTATTG ATGGTCGTGA GGAGTCCATC      900
    ATGAAGCGTA CCTGCCTGGT GGCAAACACC TCAAATATGC CTGTCGCTGC      950
    TCGTGAGGCG TCTATTTACA CTGGCATCAC TTTAGCTGAG TATTATCGTG     1000
30  ATATGGGCAA GCACATTGCT ATGATGGCCG ACTCTACCTC TCGATGGGCT     1050
    GAGGCTCTCC GTGAGATCTC TGGGCGTCTC GCTGAAATGC CCGCTGATGG     1100
    TGGTTACCCT GCGTACCTCA GTGCGCGTCT TGCTTCCTTC TACGAGCGTG     1150
    CGGGGCGCGT GACATGCATC GGTGGGCCAA AACGCGAGGG CTCAGTAACC     1200
    ATCGTTGGTG CCGTTTCTCC TCCTGGAGGT GACTTTTCTG ACCCAGTGAC     1250
35  GTCCGCTACG CTTGGTATTG TGCAAGTCTT TTGGGGTCTT GAGAAGCGTC     1300
    TTGCGCAACG TAAACACTTT CCTTCTGTTA ATTGGCTCAT TTCCTATTCA     1350
    AAATACCTTA ATGCTTTGGA GCCCTTCTTC AACACGCTTG ACCCTGACTA     1400
    CATGCGCCTG CGGTCAGTTG CTGCGGAGAT CCTTCAGCGT GAGGAAGAGT     1450
    TGCAAGAAAT TGTTCAACTT GTCGGTAAGG ACTCACTTTC GGAGTCTGAC     1500
40  AAAATTATTC TAGAAACGGC TAAGGTTATT CGTGAAGAGT TTCTCCAGCA     1550
    GAATGCCTTT ACGCCGTACG ACAAGTATTG CCCGCCGTAC AAGACCTGCT     1600
    GGATGCTACG TAACATTGTC GCGTTCTACG AGGAGAGCCA GCGCGTTGTA     1650
    GCTGAGTCCG CTGGGGAAC TAAAGATTAC TGGAAC TACA TTCGTGAAAT     1700
    GATTCTCAT ATTTACACGG GTTTAACTGA GATGAAGTTC CGTGATCCTC     1750
45  AGGAGGGTGA GGAGGCCAAC GTAGAATTCT ACAGAAAACA AAATGAGGAA     1800
    ATTGTCAGCG CATTCGCCTC GCTGCTGCAA TAA                      1833
  
```

50 2) INFORMATION FOR SEQ ID NO: 693

(i) SEQUENCE CHARACTERISTICS:

- 55 (A) LENGTH: 1758 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

60 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Thermus thermophilus*
 (B) STRAIN: HB8
 (C) ACCESSION NUMBER: D63799

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 693

```

      ATGATCCAAG GGGTGATCCA GAAGATCGCG GGCCCGGCGG TGATCGCCAA      50
      GGGCATGCTC GGGGCCCCGCA TGTACGACAT CTGCAAGGTG GGCGAAGAGG      100
      GCCTCGTGGG CGAGATCATC CGCCTGGACG GGGACACGGC CTTCGTCCAG      150
10    GTCTACGAGG ACACCTCGGG CCTAAAGGTG GGGGAGCCCG TGGTCTCCAC      200
      GGGCCTTCCC TTGGCGGTGG AGCTCGGCCC CGGGATGCTG AACGGCATCT      250
      ACGACGGCAT CCAGCGCCCC CTGGAGCGCA TCCGGGAGAA GACGGGGATC      300
      TACATCACCC GGGGCGTGGT GGTCCACGCC CTGGACCGGG AGAAGAAGTG      350
      GGCCTGGACG CCCATGGTCA AGCCCGGGGA CGAGGTGCGG GGGGGTATGG      400
15    TCCTGGGCAC GGTGCCCCGAG TTCGGCTTCA CCCACAAGAT CCTGGTACCC      450
      CCGGACGTGC GGGGCCGGGT CAAGGAGGTG AAGCCCGCCG GGGAGTACAC      500
      CGTGAGAGGAG CCGGTGGTGG TCCTCGAGGA CGGCACCGAG CTCAAGATGT      550
      ACCACACCTG GCCCGTTCGC CGGGCGAGGC CCGTGCAAAG GAAGCTTGAC      600
      CCCAACACCC CCTTCCTCAC GGGGATGCGC ATCCTGGACG TCCTCTTCCC      650
20    CGTGGCCATG GGGGGCACCG CCGCCATCCC TGGGCCCTTC GGCAGCGGCA      700
      AGACCGTGAC CCAGCAGTCC CTGGCCAAGT GGTCCAACGC CGACGTGGTG      750
      GTCTACGTGG GCTGCGGGGA GCGGGGGAAC GAGATGACCG ACGTGCTCGT      800
      GGAGTTCCCC GAGCTCACCG ACCCCAAGAC GGGTGGGCCC TTGATGCACC      850
      GCACCGTCTT CATCGCCAAC ACCTCCAACA TGCCCGTGGC CGCCCGCGAG      900
25    GCCAGCATCT ACGTGGGCGT GACCATCGCC GAGTACTTCC GCGACCAGGG      950
      CTTCTCCGTG GCCCTCATGG CCGACTCCAC GAGCCGCTGG GCCGAGGCTT      1000
      TGCGCGAGAT CTCTAGCCGC CTCGAGGAGA TGCCCGCCGA GGAGGGCTAC      1050
      CCGCCCTACC TCGCCGCCAG GCTCGCCGCC TTCTACGAGC GGGCGGGCAA      1100
      GGTTCATCACC CTGGGCGGCG AGGAGGGGGC GGTGACCATC GTGGGGGGCCG      1150
30    TCTCCCCGCC GGGCGGCGAC ATGTCCGAGC CCGTGACCCA GTCCACCTTG      1200
      AGGATCGTGG GGGCCTTCTG GCGGCTTGAC GCCTCCCTGG CCTTCCGCCG      1250
      CCACTTCCCC GCCATCAACT GGAACGGCTC CTACAGCCTC TTCACCTCCG      1300
      CCCTTGACCC CTGGTACCGG GAGAACGTGG CCGAGGACTA CCCCAGAGCTC      1350
      CGCGACGCCA TCTCCGAGCT TTTGCAGCGG GAGGCGGGCC TCCAGGAGAT      1400
35    CGTCCAGCTC GTGGGGCCCG ACGCCCTCCA GGACGCCGAG CGCCTCGTCA      1450
      TTGAGGTGGG CCGGATCATC CGCGAGGACT TCCTGCAGCA GAACGCCTAC      1500
      CACGAGGTGG ACGCCTACTG CTCCATGAAG AAGGCCTACG GGATCATGAA      1550
      GATGATCTTC GCCTTCTACA AGGAGGCGGA GCGGCGCATC AAGCGGGGGG      1600
      TTTCCATAGA CGAGATCCTG CAGCTCCCCG TTCTGGAGCG CATCGCCGC      1650
40    GCCCCGATAG TGAGCGAGGA GGAGTTCCCC GCCTACTTTG AGGAGGCCAT      1700
      GAAGGAGATC CAGGGGGCCT TCAAGGCTGG CCTAAAGGGG GAGAGATGGA      1750
      CTTTCTGA
  
```

45

2) INFORMATION FOR SEQ ID NO: 694

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 694

CGGCGCIATC YTS GTTGTG C

21

60

2) INFORMATION FOR SEQ ID NO: 695

- 5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

10 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 695

15 GTTTCACGTG ATGACGTACA 20

2) INFORMATION FOR SEQ ID NO: 696

- 20 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
25 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 696

30 ATIGGICAYR TIGAYCAYGG IAARAC 26

2) INFORMATION FOR SEQ ID NO: 697

- 35 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
40 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 697

45 CCIACIGTIC KICCRCCYTC RCG 23

50 2) INFORMATION FOR SEQ ID NO: 698

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1185 bases
(B) TYPE: Nucleic acid
55 (C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

60 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Escherichia coli*
(C) ACCESSION NUMBER: extracted from J01690

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 698

5
GTGTCTAAAG AAAAATTTGA ACGTACAAAA CCGCACGTTA ACGTTGGTAC 50
TATCGGCCAC GTTGACCACG GTAAAACTAC TCTGACCGCT GCAATCACCA 100
CCGTACTGGC TAAAACCTAC GGCGGTGCTG CTCGTGCATT CGACCAGATC 150
GATAACGCGC CGGAAGAAAA AGCTCGTGGT ATCACCATCA ACACCTTCTCA 200
10 CGTTGAATAC GACACCCCGA CCCGTCACTA CGCACACGTA GACTGCCCGG 250
GGCACGCCGA CTATGTTAAA AACATGATCA CCGGTGCTGC TCAGATGGAC 300
GGCGCGATCC TGGTAGTTGC TCGGACTGAC GGCCCGATGC CGCAGACTCG 350
TGAGCACATC CTGCTGGGTC GTCAGGTAGG CGTTCCGTAC ATCATCGTGT 400
TCCTGAACAA ATGCGACATG GTTGATGACG AAGAGCTGCT GGAAGTGGTT 450
15 GAAATGGAAG TTCGTGAACT TCTGTCTCAG TACGACTTCC CGGGCGACGA 500
CACTCCGATC GTTCGTGGTT CTGCTCTGAA AGCGCTGGAA GGCGACGCAG 550
AGTGGGAAGC GAAAATCCTG GAACTGGCTG GCTTCCTGGA TTCTTATATT 600
CCGGAACCAG AGCGTGCGAT TGACAAGCCG TTCCTGCTGC CGATCGAAGA 650
CGTATTCTCC ATCTCCGGTC GTGGTACCGT TGTTACCGGT CGTGTAAGAC 700
20 GCGGTATCAT CAAAGTTGGT GAAGAAGTTG AAATCGTTGG TATCAAAGAG 750
ACTCAGAAGT CTACCTGTAC TGGCGTTGAA ATGTTCCGCA AACTGCTGGA 800
CGAAGGCCGT GCTGGTGAGA ACGTAGGTGT TCTGCTGCGT GGTATCAAAC 850
GTGAAGAAAT CGAACGTGGT CAGGTAAGTG CTAAGCCGGG CACCATCAAG 900
CCGCACACCA AGTTCGAATC TGAAGTGTAC ATTCTGTCCA AAGATGAAGG 950
25 CGGCCGTCAT ACTCCGTTCT TCAAAGGCTA CCGTCCGCAG TTCTACTTCC 1000
GTACTACTGA CGTGACTGGT ACCATCGAAC TGCCGGAAGG CGTAGAGATG 1050
GTAATGCCGG GCGACAACAT CAAAATGGTT GTTACCCTGA TCCACCCGAT 1100
CGCGATGGAC GACGGTCTGC GTTTCGCAAT CCGTGAAGGC GGCCGTACCG 1150
TTGGCGCGGG CGTTGTTGCT AAAGTTCTGG GCTAA 1185
30

2) INFORMATION FOR SEQ ID NO: 699

35 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear
40

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 699

45 GTIACIGGYT CYTYRARRTT ICCICC

26

2) INFORMATION FOR SEQ ID NO: 700

50 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
55 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 700

60

5 2) INFORMATION FOR SEQ ID NO: 701

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 21 bases
 (B) TYPE: Nucleic acid
10 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 701

GTGTTACGA TCATCGATGC G 21

20 2) INFORMATION FOR SEQ ID NO: 702

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 bases
25 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 702

CTCTCGATAT CCGCGAAGCG 20

35 2) INFORMATION FOR SEQ ID NO: 703

- (i) SEQUENCE CHARACTERISTICS:
40 (A) LENGTH: 20 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

45 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 703

50 TATGGAAATT CGAAACATCT 20

2) INFORMATION FOR SEQ ID NO: 704

- 55 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
60 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 704

5 AGTGCTCCAA TTAATGTTGG 20

2) INFORMATION FOR SEQ ID NO: 705

10

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

15 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 705

20

GTACAGTTCC AATACCTGAA 20

25 2) INFORMATION FOR SEQ ID NO: 706

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 bases

(B) TYPE: Nucleic acid

30 (C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 706

TGAAATCTTC ACATCCAACA 20

40

2) INFORMATION FOR SEQ ID NO: 707

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 25 bases

45 (B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 707

TWACCATTTC AGTACCTTCT GGTA 25

55

2) INFORMATION FOR SEQ ID NO: 708

(i) SEQUENCE CHARACTERISTICS:

60 (A) LENGTH: 26 bases

401

- (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

5 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 708

TCRTCCATIC CIARIATIGC IATAT

26

10

2) INFORMATION FOR SEQ ID NO: 709

15 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1656 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Borrelia burgdorferi*
 25 (C) ACCESSION NUMBER: extracted from AE001122

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 709

	ATGAATGAAG	TTTTATTTGT	AAAGACTGCT	GGTAGGAATT	TAAAAGCAGA	50
30	AGTAATTCGT	ATTAGGGGCA	ATGAAGTTGA	TGCACAGGTT	TTTGAATTGA	100
	CAAAAGGGAT	ATCTGTTGGA	GACCTAGTTG	AATTTACAGA	CAAACCTTTA	150
	ACAGTTGAAC	TCGGACCAGG	GCTTTTAACT	CAAGTATATG	ATGGGCTTCA	200
	AAATCCTTTG	CCTGAATTGG	CTATTCAATG	TGGATTTTTT	TTAGAAAGGG	250
	GAGTATATTT	AAGGCCCTTG	AATAAAGATA	AAAAGTGGA	TTTTAAAAAA	300
35	ACCTCCAAAG	TTGGAGATAT	CGTTATTGCA	GGAGATTTTT	TAGGTTTGT	350
	AATTGAGGGA	ACTGTTCAAC	ATCAAATAAT	GATTCCATTT	TATAAAAGGG	400
	ATTCTTATAA	AATTGTGGAG	ATTGTAAGTG	ATGGCGACTA	TTCGATTGAT	450
	GAGCAAATTG	CTGTAATTGA	AGATGATTCT	GGTATGAGGC	ATAATATTAC	500
	AATGTCTTTT	CATTGGCCTG	TTAAAGTTCC	TATTACTAAT	TATAAGGAAC	550
40	GCCTTATTCC	TAGTGAACCT	ATGTTGACTC	AAACTAGAAT	TATAGATACA	600
	TTTTTCCCAG	TTGCCAAAGG	TGGAACTTTT	TGCATTCCGG	GTCCTTTTGG	650
	AGCAGGAAAA	ACGGTTCTTC	AGCAGGTTAC	AAGTCGAAAT	GCTGATGTTG	700
	ATGTAGTGAT	TATTGCAGCT	TGTGGTGAGC	GAGCAGGAGA	AGTGGTAGAA	750
	ACTCTTAAAG	AATTTCCCGA	ATTAATGGAT	CCAAAAACCG	GCAAATCTTT	800
45	AATGGACAGG	ACTTGTATTA	TTTGTAAATAC	ATCTTCAATG	CCAGTTGCAG	850
	CTAGAGAAGC	TTCTGTTTAT	ACTGCTATTA	CTATTGGTGA	GTATTACAGG	900
	CAAATGGGCC	TTGATATTCT	TCTTTTGGCA	GATTCAACTT	CAAGATGGGC	950
	TCAAGCAATG	AGAGAAATGT	CTGGACGCCT	TGAGGAAATT	CCTGGCGAGG	1000
	AGGCTTTTCC	GGCATATCTT	GAGTCTGTTA	TTGCTTCCTT	TTATGAAAGG	1050
50	GCAGGTATTG	TAGTTCTTAA	TAATGGGGAT	ATTGGATCTG	TAACAGTTGG	1100
	TGGCTCTGTA	AGTCCTGCTG	GTGGTAATTT	TGAAGAGCCA	GTTACTCAAG	1150
	CAACTTTAAA	AGTTGTAGGA	GCATTTACAG	GGCTTACAAG	AGAAAGGTCT	1200
	GATGCTAGGA	AATTTCCAGC	TATTAGTCCT	CTTGAATCTT	GGAGTAAATA	1250
	TAAAGGCGTT	ATTGATCAAA	AAAAGACTGA	ATATGCAAGA	TCTTTTTTGG	1300
55	TGAAAGGTAA	TGAAATTAAT	CAAATGATGA	AAGTTGTTGG	AGAAGAAGGC	1350
	ATAAGTAACG	ATGATTTTTT	AATTTATTTA	AAATCCGAGC	TACTTGATTC	1400
	GTGCTATTTG	CAGCAAATTT	CATTTGATTC	TATTGATGCT	GCTGTTAGTT	1450
	CAGAGCGTCA	AAATTATATG	TTTGATATAG	TTTATAACAT	TCTTAAAACT	1500
	AACTTTGAGT	TTTCTGATAA	ACTTCAAGCA	AGAGATTTTA	TAAATGAGTT	1550
60	AAGGCAAAAT	CTTTTAGACA	TGAATCTTTC	TTCTTTTAAG	GATCATAAGT	1600

TTAATAAAATT GGAGCATGCT TTGGGTGAAT TGATAAAATTT TAAAAAGGTA 1650
ATTTAG 1656

5

2) INFORMATION FOR SEQ ID NO: 710

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1818 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

15

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Treponema pallidum*
(B) STRAIN: Nichols
(C) ACCESSION NUMBER: extracted from AE000520

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 710

GTGATCAAAG ACGATGTGGT TACAGGCCGT GTAGTGAGGG TGTCTGGTCC 50
CATTGTGTAT GCCGAGGGCC TCTCTGCGTG CAGCGTATAC GATGTTGTCTG 100
25 ACGTAGGGGA AGCATCGCTC ATCGGAGAAA TTATCCGGTT GGATGAGAGC 150
AAGGCGGTCG TGCAAGTATA CGAGGATGAC ACAGGTATGC GAGTCGGGGA 200
GAAGGTGACA AGCTTGCGTC GACCACTCTC AGTCCGCTTA GGGCCTGGAT 250
TAATCGGCAC CATTATGAC GGTATTCAGC GCCCACTTGA GCGCCTCTTC 300
CAAGAAGACG GCGCCTTCTT GCGTCCTGGT GCGCGTTCAC AACCGCTTGA 350
30 TGGCTCCGTA CGCTGGGATT TTCGTCCTCA TTGTAACGAG CGCGGTGAGG 400
CCCTGTGCGC GGGGATTCCG ATTGCACCTG GGTCACTGTT AGGGACCGTG 450
CAGGAGACTC CTTCTGTTGT GCACACTATC ATGGTTCCTC CTGACATCCG 500
GGGGAGCGTG CTATCTTCGT TCAAGGGCGC AGGTGCTTAC ACAATAGATG 550
AAGAAATTGG ACGCACTGAT CTTGGTGAGC CGCTTTTCT ATCCAGTAC 600
35 TGGCCAGTGC GTCGTGCGCG TCCTTTCAGC AAAAACTTG CAGTGTGTGA 650
GCCACTAGTT ACTGGACAGC GGGCGATTGA TGTTCCTTC CCCCTATCAA 700
AGGGAGGAAT GGCGCTATT CCAGGGGAT TTGGAAGTGG GAAGACAATG 750
ACGCAGCATG CCGTTGCCAA GTGGTGTGAT GCAGATATTA TCGTGTACAT 800
CGGCTGCGGA GAGCGGGGCA ACGAGATGAC AGACGTGCTC TCTGAATTTT 850
40 CCAAATCAT CGATCCGCGC ACAGGACGCT CTCTTATGGA GCGGACGATT 900
TTGATCGCAA ATACGTCAA TATGCCTGTG TCCGCACGCG AGGTGTCGCT 950
GTATTCAGGG ATTACCCTTG CGGAATACTA CCGTGATATG GGTATGCATG 1000
TGGCCATCAT GGCTGATTCT ACCAGCCGCT GGGCGGAGGC GCTGCGTGAA 1050
TTGTCTGGGC GCATGGAAGA AATGCCTGCG GAGGAGGGAT TCCCTGCGTA 1100
45 CCTTCCGACG CGTCTTGCA GAAATTTATGA GCGCGCAGGA CGCGTGGA 1150
CCTGTGTGGC GCGCGAGGGC TCTGTGAGCA TCATTGGTGC TGTTCCTCCC 1200
CTGGGTGGAG ATTTCTCTGA GCCGGTGACG CAGCACACAA AGCGCTTCAT 1250
CCGTTGCTTT TGGGCCTTGG ATCGTGAAC TGCACACGCG CGTCATTACC 1300
CTGCCATTGG GTGGATAGAT TCATACTCTG AATATGCGCA GGAAGTAAGT 1350
50 GCATGGTGGA GTAAGTATGA CCCGCGCGCA GGC GCGTTCG CCGCCGAGC 1400
CTTGGATTTG CTGAGAAAG AACAGCGGTT ACAGCAAATT GTCAGGCTTG 1450
TCGGTCCTGA TGCGCTGCCT GGAGAAGATC GTCTGGTGCT AATGGTGTGT 1500
GAAATGATCA AAGGTGGCTT TCTGCAGCAG AACGCTTTTG ATCCGACGGA 1550
TGTGTTCTCC TGTCCCGAAA AGCAGGTGCA GATCTTGCGT ACCATAGTGG 1600
55 ATTTTCACGA ACGTGCCGTG GTGCTGCTGC GTGCAGGTAT TTCGCTTTCT 1650
GCGCTGTCCC AGCTTTCGTG CCGGGAGCTC ATCGTACGTA TGA AAACTAC 1700
GTACGGGAAT GAGGATGTAC ACAAGATGCA GAAAGTGTAC GACACGATGT 1750
GCACTGAGTT TGACCAACTG AGTGTGTGTG CTGCCGCGCG CACACAAGGG 1800
GGGGAGAAAG TCGAATGA 1818

60

2) INFORMATION FOR SEQ ID NO: 711

5 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1779 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

10

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Chlamydia trachomatis*
 (B) STRAIN: MoPn

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 711

20 CAGGGCTATG TCGTAGAAGC TTACGGAAAT TTATTGCGGG TGCATTTTGA 50
 TGGGCATGTG CGTCAAGGAG AAGTGGCCTA TGTCAGCGTG GATGATACTT 100
 GGTGAAAGC GGAAATTATA GAAGTTGTGG GAGATGAGGT TAAAGTCCAA 150
 GTTTTTGAGG AAACCTCAAGG AATTCTCTCGA GCGCTTTTGG TAACTTTTTTC 200
 CGGGCATTTA TTAGAAGCGG AACTTGGGCC CGGTCTATTG CAAGGTATTT 250
 TTGACGGACT TCAGAATCGC TTAGAGGTAT TGGCAGATAC AAGCTTGTTT 300
 25 TTGAAAAGAG GGGAGTATGT TAATGCCATT TGTCGGGAAA CTGTATGGGC 350
 TTATACGCAA AAGGCTTCTG TCGGGGATGT TCTATCTCGG GGAGATGTGC 400
 TTGGTACAGT AAAGGAAGGG CGGTTTGATC ATAAAATCAT GGTTCCCTTT 450
 TCTTGTTTTG AGGAAGTGAC TATCACTTGG GTCATTTCTT CAGGAGATTA 500
 CACTGTTGAT ACCGTTATTG CTAAAGGACG TACTGCTTCA GGAGCCGAGC 550
 30 TTGAATTTAC AATGGTTCAG AAATGGCCCA TTAAACAGGC TTTTTTAGAA 600
 GGGGAAAAGG TACCGTCTCA TGAAATTATG GATGTTGGGT TACGAGTATT 650
 AGATACTCAG ATCCCCGTCT TAAAGGGAGG AACTTTTTGT ACTCCAGGGC 700
 CTTTTGGTGC AGGAAAGACC GTTTTACAGC ACCATTTATC TAAGTATGCA 750
 GCTGTAGATA TCGTAGTTTT GTGTGCTTGT GGAGAGCGAG CTGGAGAGGT 800
 35 TGTAGAAATT CTTCAGGAGT TCCCGCATTT GACAGATCCT CATACGGGGC 850
 AGTCTTTGAT GCATAGGACC TGTATTATTT GTAATACATC TTCCATGCCT 900
 GTAGCAGCTA GAGAGTCCTC CATTATTTTG GGTATTACTA TAGCAGAATA 950
 TTACCGTCAA ATGGGGTTGC ATGTTTTGTT ATTGGCTGAC TCGACATCTA 1000
 GATGGGCTCA AGCTTTAAGG GAAATTTTCA GCGGATTAGA AGAAATCCCT 1050
 40 GGAGAAGAAG CTTTCCCAGC CTATTTGCGG TCTCGAATAG CAGCTTTTTA 1100
 TGAGCGAGGC GGGGCTGTGA AAATGAAAGA TGGATCGGAA GGCTCCTTGA 1150
 CTATCTGTGG AGCGGTTTCT CCCGCAGGAG GAAATTTTGA AGAGCCTGTT 1200
 ACACAAGCAA CTTTATCTGT TGTTGGGGCT TTCTGTGGGC TTTCTAAGGC 1250
 TAGAGCAGAT GCTAGACGGT ATCCTTCTAT TGATCCGATG ATTTTCATGGT 1300
 45 CTAAGTACTT GGATTCTGTG GCGGAGATTT TAGAGAAAAA AGTTCCAGGA 1350
 TGGGGAGATT CCGTTAAAAA AGCTTCTCGT TTCTTAGAAG AAGGAGCAGA 1400
 AATTGGTAAG CGAATAGAAG TTGTTGGGGA AGAAGGGATT TCTATGGAAG 1450
 ATATAGAAAT CTTTTTGAAA TCAGAGTTGT ATGATTTCTG TTAATTACAG 1500
 CAAAACGCTT TCGATGCAGA GGAAGTTTAT TGTCTTTTGG ATCGTCAAAT 1550
 50 AGAGCTTTTT TCTTTAATGA GTCATATTTT TAGCTCTAGA TTCTGTTTTG 1600
 ATTGTCCAGA TAATGCTCGG AGTTTCTTTT TAGAGCTTCA AAGTAAATTT 1650
 AAAACGCTGA ATGGTCAAAA ATTCCTTTCT GAAGACTATC AGAAGGGGCT 1700
 AGAAGTGATC TATAAACTAT TAGAAAGCAA AATGGTGCAG ACGGCGTAGG 1750
 TATGCAAACA ATATATACAA GAATTACGG 1779

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2) INFORMATION FOR SEQ ID NO: 712

60 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 965 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

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(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus faecalis*
 (B) STRAIN: V583

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~~(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 712~~

	GTGCAAATTG	GAAAAATTGT	CAAAGTTTCA	GGTCCTTTGA	TTTTAGCTGA	50
15	AAACATGTCA	GATGCTAGTA	TCCAAGACAT	TTGTCATGTA	GGAGATTTAG	100
	GCGTTATCGG	AGAGATTATT	GAAATGCGAG	GCGACGTCGC	TTCGATTCAA	150
	GTATATGAAG	AAACAACAGG	CATTGGACCA	GGAGAACCAG	TTATTTCAAC	200
	AGGAGAACCA	TTATCTGTTG	AATTAGCCCC	AGGTTTAATT	GCCGAAATGT	250
	TTGATGGTAT	TCAACGACCA	TTGGATACAT	TTCAAGAAGT	AACCCACAGT	300
20	AACTTTTTAG	GCCGTGGCGT	TAAAATTGAT	GCGTTAGATC	GTGAGAAAAA	350
	ATGGACGTTT	GAACCAACTG	TGGCAGTTGG	TGAAGAAGTG	TCGGCAGGTG	400
	ACATCGTCGG	TGTGGTTCAA	GAAACACCGA	TTATTCAACA	TAAAATTATG	450
	GTGCCTTTTCG	GCGTTTCAGG	AACGATTGCC	GAAATTAAAG	CAGGTGACTT	500
	TGCCATTGAT	GAAACAGTTT	ACTCAGTGGA	AACGGCTAAA	GGAACGGAAA	550
25	GTTTTAGCAT	GATGCAAAAA	TGGCCCGTTC	GGCGGGGACG	TCCCATTTTA	600
	GAAAAACTAA	GTCCCAAAGT	ACCGATGGTG	ACCGGACAAC	GCGTAATTGA	650
	TACCTTTTTTC	CCAATTACGA	AAGGCGGAGC	GGCAGCAGTT	CCAGGACCAT	700
	TTGGCGCTGG	AAAAACAGTC	GTTTCAGCACC	AAATTGCTAA	GTGGGCCGAT	750
	GTCGACTTAG	TCGTTTACGT	TGGTTGTGGG	GAACGCGGGA	ATGAAATGAC	800
30	AGATGTTTTTA	AATGAATTTC	CAGAATTAAT	TGACCCAACA	ACTGGTGAGT	850
	CTTTGATGAA	TCGGACGATT	TTAATTGCGA	ATACGTCAA	TATGCCCGTA	900
	GCGGCACGGG	AAGCCTCGAT	TTATACAGGG	ATTACCATTG	CAGAATATTT	950
	CCGTGATATG	GGTTA				965

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2) INFORMATION FOR SEQ ID NO: 713

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1737 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

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(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Methanosarcina barkeri*
 (C) ACCESSION NUMBER: extracted from J04836

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 713

	GTGGAAGTAA	AAGGTGAAAT	TTATCGTGTG	TCTGGGCCTG	TCGTCACCGC	50
	CATCGGCTTG	CAGGCAAAAA	TGTATGACCT	GGTCAAAGTC	GGTAATGAAG	100
55	GTTTAATGGG	TGAAGTCATT	CAGATATTAG	GGCCCAAGAC	CATCATCCAG	150
	GTATATGAAG	AGACCGCAGG	TATCAAGCCA	GGGGAACCCT	GTGTATCTAC	200
	AGGGTCGTCT	CTGTCCGTAG	AAC TTGGTCC	GGGTCTTCTT	TCCAGTATTT	250
	ATGACGGGGT	TCAAAGGCCT	CTGCACGTCC	TGCTTGAAAA	AATGGGTAGC	300
	TTCATCCAGA	GAGGTGTCAG	CGCAGATGGG	CTTGATCATA	AGAAACTCTG	350
60	GGATTTCAAA	CCCATTGTCA	AGAAGGGCGA	TTCCGTAAAA	GGTGGAGACG	400

	TAATTGGTGT	TGTACAGGAA	ACCGTGAATA	TTGAACATAA	GATCATGGTG	450
	CCTCCTGATA	TCTCAGGTAC	AATTTCCGAC	ATAAAGAGCG	GAAACTTTAC	500
	GGTAGTAGAC	ACAATCTGTA	CTCTGACTGA	TGGGACCGAA	TTGCAGATGA	550
	TGCAGAGGTG	GCCTGTTCTGA	AGACCCAGAC	CTGTGAAGGC	AAAACTTACT	600
5	CCAACCAGGC	CTCTGGTTAC	AGGAATGAGA	ATCCTTGATG	GGCTTTTCCC	650
	TGTGGCAAAA	GGCGGAACAG	CTGCAATCCC	CGGACCTTTC	GGATCGGGAA	700
	AGACCGTAAC	TCAGCAGTCG	CTTGCAAAAT	GGAGTGATAC	CGAAATTGTG	750
	GTCTACATCG	GTTGTGGTGA	GCGTGGAAC	GAAATGGCAG	ATGTTCTGAG	800
	CGAATTCCT	GAATCGAAG	ATCCGCAGAC	CGGGCGCCCA	CTTATGGAGC	850
10	GTACTGTTCT	TATCGCTAAC	ACTTCAAACA	TGCCTGTGGC	CGCAAGAGAA	900
	GCATCTGTGT	ATACCGGAAT	CACCATTGCA	GAATACTACC	GTGACATGGG	950
	ATTAGATGTA	TECCTTATGG	CAGACTCCAC	CTCAAGGTGG	GCAGAAGCCA	1000
	TGAGAGAAAT	CTCTTCCCGT	CTGGAAGAAA	TGCCTGGTGA	AGAAGGTTAC	1050
	CCAGCATACC	TGTCTGCAAG	ACTGGCCGAA	TTCTACGAGC	GTGCCGGGGT	1100
15	TGCGGAGAGT	CTTTGCGGCG	AAACAGGTTC	CATTACTGTT	ATTGGAGCAG	1150
	TATCTCCACC	TGGCGGTGAC	TTCTCAGAGC	CTGTTACACA	GAATACCCTG	1200
	CGTATCGTAA	AAGTGTTCG	GGCTCTCGAT	GCCAAACTAT	CTCAGAGGCG	1250
	TCACTTCCCG	GCCATCAACT	GGCTGAACAG	TTACAGTCTG	TATAAGGACA	1300
	GTCTTAATGA	CTGGTTTGCA	GATAATGTGG	CTCCTGATTA	TGTGCCTTTG	1350
20	AGGGAAAGAG	CAATGGAAAT	GCTCCAGACA	GAATCTGAAC	TGCAGGAAAT	1400
	CGTGCAGCTT	GTAGGTTCCG	ATGCTCTGCC	AGACGACCAG	CAGCTTCTGC	1450
	TTGAAATCAC	CCGTATGCTT	AGGGAAATTT	TCCTGCAGCA	GAATGCATTC	1500
	CACCCAGTAG	ATGCATACAG	CCCGTTCGAT	CAGCAGTACA	AGATCCTTAA	1550
	GGCAATCATG	AAATGGGGAG	ACGCTGCGAT	GGATGCCTTG	AAATCAGGTG	1600
25	TTCCCGTAAC	TGAAATTATC	AAGCTTGAAT	CCAAAAATGT	GCTTGCTAAG	1650
	GTCAAGTACG	AAGAGAAGTT	TGATGAGTCT	ATGAATGCTG	TCCTGGCACA	1700
	GATGGATAAA	GAGTTTGCAT	CCCTGAGAGG	TAGGTAA		1737

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2) INFORMATION FOR SEQ ID NO: 714

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1785 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

40

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Methanosarcina jannaschii*
 (C) ACCESSION NUMBER: extracted from U67477

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 714

	ATGAAAAGAG	AGGTTGAGAA	TATGCCAGTT	GTTGGTAAGA	TTATTAAAAT	50
	CGCAGGGCCT	GTTGTAGTTG	CAGAGGGAAT	GAAAGGAGCT	CAGATGTATG	100
	AGGTCGTTAA	AGTAGGAGAA	GAGAAATTGA	CTGGAGAAAT	CATTCAGTTG	150
50	CACGATGATA	AAGCAGTTAT	TCAGGTTTAT	GAAGAAACAT	CTGGAATTAA	200
	ACCAGGAGAG	CCAGTTGTTG	GTAAGAGCT	ATGTATGATG	GTATTTCAGAG	250
	GGCCAGGGAT	GTTAAGAGCT	ATGTATGATG	GTATTTCAGAG	GCCTTTAACA	300
	GCAATTGAAG	AGAAAACAGG	TTCAATCTTT	ATCCCAAGAG	GAGTTGATGT	350
	CCCTGCATTA	CCAAGAGATA	TAAAATGGGA	ATTTAAACCA	GTGGTAAATG	400
55	AAGGAGATTA	TGTTGAAGAA	GGAGACATAA	TTGGAACCTG	TGATGAAACT	450
	CCTTCAATAG	TTCATAAAAT	CTTAGTTCCA	ATTGGTGTGA	AAGGAAAAAT	500
	TGTTGAAATA	AAAGAGGGTA	AATTTACAGT	TGAAGAGACA	GTTGCAGTTG	550
	TAGAAACAGA	AAATGGAGAA	AGGAAAGAAA	TTACAATGAT	GCAAAAATGG	600
	CCAGTAAGAA	AACCAAGACC	ATATAAAGAG	AAACTACCTC	CAGAAATTCC	650
60	ATTAATTACA	GGGCAAAGAG	TTGAAGACAC	TTTCTTTACA	TTAGCAAAAG	700

	GAGGAACAGC	AGCAATTCCA	GGTCCATTCTG	GTTTCAGGAAA	AACCGTTACT	750
	CAGCATCAGT	TGGCAAAGTG	GTCTGACGCT	GATGTCGTTG	TTTATATCGG	800
	ATGTGGAGAA	AGAGGAAACG	AGATGACAGA	GGTTATTGAA	GAGTTCCAC	850
	ACTTAGAAGA	TATTAGAACT	GGAAACAAAT	TAATGGATAG	AACTGTATTA	900
5	ATAGCCAACA	CATCAAACAT	GCCTGTCGCT	GCAAGGGAAG	CATCTGTCTA	950
	TACAGGAATT	ACAATTGCAG	AGTACTTCAG	AGATATGGGT	TATGGAGTTT	1000
	TATTAACAGC	AGATTCAACA	TCAAGATGGG	CAGAGGCAAT	GAGAGAAATT	1050
	TCAGGTAGAT	TGGAAGAAAT	GCCAGGGGAA	GAAGGGTATC	CAGCATACTT	1100
	AGCTTCAAGA	TTGGCTCAGT	TCTATGAAAG	AGCTGGAAGA	GTTATAACCT	1150
10	TAGGGAAAGA	TAACAGACAA	GGATTTCGTTT	GTATCGTTGG	AGCTGTTTCA	1200
	CCACCAGGAG	GGGACTTCTC	AGAACCAGTT	ACATCAAACA	CACTAAGGAT	1250
	AGTTAAGGTA	TTCTGGGCGT	TAGATGCAAA	CTTGGCAAGA	AGAAGACACT	1300
	TCCCAGCTAT	CAACTGGTTG	CAGAGTTATT	CATTATACAT	TGATGATGTT	1350
	ACAGAGTGGT	GGAACACAAA	TACTGGTCCA	GATTGGAGAC	AATTAAGAGA	1400
15	TGAAGCAATG	AGCTTATTAC	AAAAAGAGGC	AGAGTTGCAA	GAGATTGTTC	1450
	AGTTAGTTGG	GCCTGATGCA	TTGCCAGATA	GGGAGAGAGT	TATTTTAGAA	1500
	GTTGCAAGAA	TGTTGAGGGA	GGATTTCTTA	CAGCAAGATG	CGTTTGATGA	1550
	GGTAGATACC	TACTGTCCCTC	CAATGAAACA	GTACTTAATG	TTAAAGATAA	1600
	TTATGACATT	CTACCAAGAA	GCATTGAAGG	CAGTTGAAAG	AGGAGTTGAA	1650
20	CCAGCTAAGA	TTTTAGGAGT	TTCAGTTAAG	CAAGATATTG	CAAGAATGAA	1700
	ATACATCCCA	CACGATGAGT	TTATAAATGT	TAAATCAAAA	GAAATAATGG	1750
	AGAAAATTAA	GAATGAATTA	GGTTCATTAA	ACTAA		1785

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2) INFORMATION FOR SEQ ID NO: 715

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1354 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

- (ii) MOLECULE TYPE: Genomic DNA

- (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Porphyromonas gingivalis*
- (B) STRAIN: W83

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 715

	TGAGCGAGGT	GATCAAGGTG	ATCGGCAAAA	ATGCTTATGT	GCAGGTTTTTC	50
	GAAAGTACTC	GCGGTATGCA	CGTAGGAGAT	GAGGCAGAGT	TTACCGGCAG	100
	TATGCTTGAG	GTAACGCTCG	GCCCCGGTAT	GCTTTCGAAG	AACTACGACG	150
45	GTCTGCAACA	CGACTTGAC	AAGATGGACG	GGATCTTCCT	CAAACGAGGC	200
	GATTATACTC	CCGCTCTCGA	TGACGACAAG	CTGTGGGACT	TCAAGCCTTT	250
	GGCCAATGTG	AACGACAATG	TGATCGCAGG	CTCATGGCTC	GGAGAGGTGA	300
	CGGAAAATTT	CCAACCGCAC	AAGATCATGG	TACCTTTCGT	TTTCGAAGGC	350
	AATTACAAGG	TGAAGAGTCT	GGCCAAAGCC	GGTTCGTACA	AAGTGAACGA	400
50	TGTGATCGCT	GTGGTAACGG	ATCAGGACGG	GAAAGACCAC	AATGTAACCA	450
	TGGTGCAGAA	ATGGCCGGTG	AAACGTGCTA	TCACTTGCTA	TCGCGAGAAG	500
	CCGCGTCCTT	TCAAACGCT	CGAAACGGGT	ATCCGTATCA	TCGACACTTT	550
	CAACCCCATC	GTAAGGGGTG	GTACGGGATT	TATCCCCGGT	CCTTTCGGTA	600
	CGGGAAAGAC	GGTGCTCCAG	CATGCTATCT	CGAAGCAGGC	GGAAGCCGAT	650
55	ATCGTGATCA	TTGCAGCCTG	TGGCGAGCGT	GCAAACGAGG	TTGTGGAGAT	700
	CTTTGCGGAA	TTCCCCCACC	TGAATGACCC	CCACACGGGA	CGTAAATTGA	750
	TGGAACGTAC	CATTATTATT	GCTAATACGT	CGAATATGCC	TGTGGCTTCG	800
	CGTGAGGCAT	CCGTATATAC	GGCCATGACG	ATAGCCGAGT	ACTATCGCTC	850
	CATGGGCCTT	CGCGTGCTGA	TGATGGCAGA	CTCCACTTCG	CGTTGGGCAC	900
60	AGGCTCTGCG	TGAGATGTCT	AACCGTCTGG	AAGAGCTTCC	CGGACCCGAT	950

	GCTTTCCCGA	TGGACTTGTC	AGCTATCGTA	GCCAACTTCT	ACGCTCGTGC	1000
	AGGATACGTT	TACCTGAACA	ACGGTTCGGC	CGGTTCCGTA	ACGTTCATCG	1050
	GTACGGTATC	TCCCGCCGGT	GGTAACCTCA	AAGAGCCTGT	GACGGAAAAC	1100
	ACCAAGAAAG	TGGCTCGCTG	CTTCTATGCT	TTGGAGCAGA	ATCGTGCCGA	1150
5	CCGCAAACGT	TATCCGGCTG	TAAACCCCAT	CGATAGTTAC	TCGAAGTACA	1200
	TCGAATATCC	CGAATTCGAG	AGCTATATAT	CGAACCACAT	CAGTTTACTC	1250
	ATTATATTCA	ACAGAAGTTG	GCAGATATAT	GGATCAAATC	TTACAGCAGA	1300
	CTGGACTACT	AAGGTGAATG	AGCTGAAGAT	GCGCTTGCAT	CAGGGTAAAG	1350
	AAAT					1354
10						

2) INFORMATION FOR SEQ ID NO: 716

15 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1788 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

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(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
 (B) STRAIN: Type 4

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 716

	TTTGA	CTCAA	GGGA	AGATTA	TAAA	AGTATC	GGG	ACCTCTA	GTT	ATTG	GCAT	50
30	CAGG	TATG	CA	GGAG	GCTA	ATTC	AAGATA	TTT	GCCG	TGT	AGGT	100
	GGGT	TAA	TCG	GTGA	AATT	TAT	TGAA	ATG	AG	ATC	AGG	150
	AGT	CTAT	GAA	GAA	CAT	CTG	GTCT	TGG	TCC	GGG	AG	200
	CTGG	AG	AACC	TCT	CTC	GGT	GAAT	TAG	GGC	CAG	GAT	250
	TTTG	ATG	GCA	TACA	ACG	CCC	ATT	AG	TCG	CA	ATG	300
35	TGAT	TTT	CTA	GTTC	CGT	GGG	TAGA	AGT	TCC	AAG	TTT	350
	AGT	GGC	ATTT	TG	ATT	CCACT	ATAG	CA	ATTG	GT	CAAAA	400
	GAT	ATT	CTTG	GAA	CTGT	CAA	GGAA	ACG	AG	GTAG	TAA	450
	GGT	TC	CTT	TAT	GG	AGT	ATCT	G	GAGA	AGT	CGT	500
	TTAC	AATT	G	TGA	AGT	TGTA	TATG	AAATA	AA	AATT	GGA	550
40	TATA	AAG	GAA	CG	CTT	ATG	CA	AAA	TGG	CC	T	600
	TTCT	AA	ACG	TTA	ATT	CCAG	AAGA	ACC	ATT	AAT	CAG	650
	TTG	ATG	CATT	CTT	TCC	AGTA	ACCA	AAG	GGG	GAG	CTG	700
	CCG	TTT	G	GAG	CAG	GAA	AG	AC	AGT	TGT	ACAA	750
	CAAT	GTT	GAT	ATT	GTT	ATTT	ATGT	CG	GTTG	TGG	GAAC	800
45	TGAC	G	GAT	G	ACT	GAAT	GAG	TTT	CCT	GAGT	TG	850
	CAAT	CA	ATTA	TG	CA	ACG	GAC	AGT	TCT	GATT	GCTA	900
	TGTT	GCT	GCT	CGT	GAG	GCTT	CAAT	TT	TAT	AC	AGGA	950
	ATTT	TC	G	TGA	TAT	GGG	CTAC	TCT	GT	CG	CCA	1000
	CGT	TGG	G	CAG	AAG	CGT	ACG	TGAA	ATG	TCA	GGAC	1050
50	TGGT	GAT	GAG	GGT	TAT	CCTG	CTT	TAT	CTG	GG	AAGT	1100
	ATGA	AAG	AGC	AGG	ACG	TTCT	CAGG	TTCT	AG	GGCT	CCAG	1150
	ACG	ATT	ACTG	CTAT	TGG	AGC	TGT	ATC	GCCA	CCT	G	1200
	ACC	AGT	TACT	CAAA	AC	ACTT	TACG	GATT	G	T	TTT	1250
	ATG	CTC	CGT	T	GGC	ACAG	CGT	CA	TTT	CT	GCA	1300
55	TCT	TAT	T	CAC	TAT	ATAA	AGA	CAGT	GTG	GGC	ACTT	1350
	GAAG	AC	AGAT	TG	GA	ATAG	TAA	AA	TA	ACT	CG	1400
	GGGA	AT	CTAG	TTT	AG	AGG	AA	ATT	GTT	CGT	C	1450
	TCT	GATA	ATG	AAC	GACT	AA	C	GAT	G	AA	ATT	1500
	TTAT	TTG	CAA	CAG	AAC	GCTT	TTG	ATT	CGG	T	AGTA	1550
60	CAAA	ACA	AGA	AG	CA	ATG	CTA	AG	TA	AT	TTC	1600

AATCATGCTT	TAGAGTTGGG	TTCTTACTTT	ACAGAGATTA	TGGAAGGTAC	1650
CGTGGCAGTT	CGAGACCGTA	TGGCGAGAAG	TAAATATGTT	TCAGAAGATA	1700
GATTAGATGA	AATCAAAATT	ATATCAAATG	AGATTACACA	TCAAATTCAT	1750
TTGATATTAG	AAACAGGAGG	TCTATAAATG	AGTGTTAT		1788

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2) INFORMATION FOR SEQ ID NO: 717

10 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 823 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

15

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Burkholderia mallei*
 (B) STRAIN: GB8

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 717

CGATCCTGGT	GTGCTCGGCC	GCTGACGGCC	CGATGCCGCA	AACGCGTGAG	50
25 CACATCCTGC	TGGCGCGTCA	GGTCGGTGTG	CCGTACATCA	TCGTGTTCTT	100
GAACAAGTGC	GACATGGTGG	ACGACGCGGA	GCTGCTCGAG	CTGGTCGAAA	150
TGGAAGTGCG	CGAACTGCTG	TGGAAGTACG	ACTTCCCGGG	CGACGACACG	200
CCGATCATCA	AGGGTTCGGC	GAAGCTGGCG	CTGGAAGGCG	ACAAGGGCGA	250
GCTGGGCGAA	GTGGCGATCA	TGAACCTGGC	CGACGCGCTG	GACACGTACA	300
30 TCCCGACGCC	GGAGCGTGCG	GTCGACGGCG	CGTTCCTGAT	GCCGGTGGAA	350
GACGTGTTCT	CGATCTCGGG	CCGTGGTACG	GTGGTGACGG	GTCGTGTCTGA	400
GCGCGGCGTG	ATCAAGGTTG	GCGAGGAAAT	CGAAATCGTC	GGTATCAAGG	450
CGACGGCGAA	GACGACCTGC	ACGGGCGTGG	AAATGTTCCG	CAAGCTGCTG	500
GACCAGGGTC	AGGCGGGCGA	CAACGTCGGT	ATCCTGCTGC	GCGGCACAAA	550
35 GCGTGAAGAC	GTGGAGCGCG	GCCAGGTTCT	GGCGAAGCCG	GGTTCGATCA	600
CGCCGCACAC	GCACTTCACG	GCAGAAGTGT	ACGTGCTGAG	CAAGGACGAA	650
GGCGGCCGCC	ACACGCCGTT	CTTCAACAAC	TACCGTCCGC	AGTTCTACTT	700
CCGTACGACG	GACGTGACGG	GCTCGATCGA	CTGCCCAGAG	GACAAGGAAA	750
TGGTGATGCC	GGGCGACAAC	GTGTCGATCA	CGGTGAAGCT	GATCGCGCCG	800
40 ATCGCGATGG	AAGAAGGTCT	GCG			823

2) INFORMATION FOR SEQ ID NO: 718

45

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 824 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Burkholderia pseudomallei*
 (B) STRAIN: 1026B

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 718

60 GCGATCCTGG	TGTGCTCGGC	CGCTGACGGC	CCGATGCCGC	AAACGCGTGA	50
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	GCACATCCTG	CTGGCGCGTC	AGGTCGGTGT	GCCGTACATC	ATGGTGTTC	100
	TGAACAAGTG	CGACATGGTG	GACGACGCGG	AGCTGCTCGA	GCTGGTCGAA	150
	ATGGAAGTGC	GCGAACTGCT	GTCGAAGTAC	GACTTCCCGG	GCGACGACAC	200
	GCCGATCATC	AAGGGTTCGG	CGAAGCTGGC	GCTGGAAGGC	GACAAGGGCG	250
5	AGCTGGGCGA	AGTGGCGATC	ATGAACCTGG	CCGACGCGCT	GGACACGTAC	300
	ATCCCGACGC	CGGAGCGTGC	GGTCGATGGC	GCGTTCCTGA	TGCCGGTGGA	350
	AGACGTGTTC	TCGATCTCGG	GCCGTGGTAC	GGTGGTGACG	GGTCGTGTCTG	400
	AGCGCGGCGT	GATCAAGGTT	GGCGAGGAAA	TCGAAATCGT	CGGTATCAAG	450
	GCGACGGCGA	AGACGACCTG	CACGGGCGTG	GAAATGTTCC	GCAAGCTGCT	500
10	GGATCAGGGT	CAGGCGGGCG	ACAACGTCGG	TATCCTGCTG	CGCGGCACGA	550
	AGCGTGAAGA	CGTGGAGCGC	GGCCAGGTTT	TGGCGAAGCC	GGGTTCGATC	600
	ACGCCGCACA	CGCACTTCAC	GGCTGAAGTG	TACGTGCTGA	GCAAGGACGA	650
	AGGCGGCCGC	CACACGCCGT	TCTTCAACAA	CTACCGTCCG	CAGTTCTACT	700
	TCCGTACGAC	GGACGTGACG	GGCTCGATCG	AGCTGCCGAA	GGACAAGGAA	750
15	ATGGTGATGC	CGGGCGACAA	CGTGTCGATC	ACGGTGAAGC	TGATCGCGCC	800
	GATCGCGATG	GAAGAAGGTC	TGCG			824

20 2) INFORMATION FOR SEQ ID NO: 719

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 800 bases
 (B) TYPE: Nucleic acid
 25 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

30 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Clostridium beijerincki* (deposited as
Clostridium butyricum)
 (B) STRAIN: ATCC 8260

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 719

	TGTATCAGCA	GCAGATGGTC	CAATGCCACA	AACAAGAGAA	CATATACTAC	50
	TAGGATCAAG	AGTTGGTATC	CAATATATCG	TAGTATTCTT	AAATAAAGCA	100
	GATATGGTAG	ACGATCCAGA	ATTATTAGAA	TTAGTAGAAA	TGGAAGTAAG	150
40	AGAATTATTA	AGCGAATATG	ACTTCCCAGG	AGACGATATT	CCAGTAATAA	200
	CAGGATCAGC	ATTAAAAGCA	TTAGAAAATC	CAACAGATGA	AGAAGCAATT	250
	AAGCCAATCA	TGGATTTAAT	GGAAGCAGTA	GATAGCTATA	TCCCAACTCC	300
	AGAAAGAGCA	ACAGATAAGC	CATTCTTAAT	GCCAATCGAA	GATGTATTCA	350
	CAATTACAGG	AAGAGGAACA	GTTGCAACAG	GAAGAGTTGA	AGCTGGAGTA	400
45	CTTCATGTAG	GAGATGAAGT	AGAAATCGTT	GGATTAACAG	AAGAAAAGAA	450
	GAAAGTTGTA	GTAAGTGGAA	TCGAAATGTT	CAGAAAGTTA	TTGGATGAAG	500
	CACAAGCTGG	AGATAACATC	GGAGCATTAT	TAAGAGGAGT	TCAAAGAACT	550
	GATATTGAAA	GAGGTCAAGT	TTTATCAAAA	CCAAATTCAG	TACACCCTCA	600
	CACTAAATTT	GTAGGTCAAG	TATACGTACT	TAAAAAAGAA	GAAGGTGGAA	650
50	GACATACTCC	ATTCTTTGAT	GGATACAGAC	CACAATTCTA	TTTCAGAACA	700
	ACAGACGTTA	CAGGRTCAAT	CAAGTTACCA	GATGGAATGG	AAATGGTAAT	750
	GCCTGGAGAT	CACATTGATA	TGAATGTTGA	ATTAATCACT	CCAATCGCAA	800

55

2) INFORMATION FOR SEQ ID NO: 720

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 799 bases
 60 (B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

5

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Clostridium innocuum*
(B) STRAIN: ATCC 14501

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 720

	GGTGCTATCC	TGGTTGTTGC	TGCATCTGAT	GGTCCTATGC	CTCAGACTCG	50
	TGAGCACATC	CTGCTTGCTC	GTCAGGTAGG	TGTTCCCTTAC	ATCGTTGTAT	100
	TCCTGAACAA	ATGCGACATG	GTTGATGACG	AAGAACTGAT	CGACCTTGTT	150
15	GAAATGGAAG	TACGTGAGCT	GTTAAGCGAG	TACGGATTTCG	ACGGAGATAA	200
	CGCTCCGGTT	ATCCGTGGTT	CTGCACTGAA	GGCTCTGGAA	GGTGACGACA	250
	AATACGTTGG	CGCTATCAAA	GAAGTATGAG	ATGCAGTTGA	TGAATTCATC	300
	CCAGATCCAA	CTCGTGAAAC	TGACAAACCA	TTCCTGATGT	CTGTAGAAGA	350
	CGTTATGACA	ATCACAGGAC	GTGGTACAGT	TGCTACAGGA	CGTGTTGAGC	400
20	GTGGGGTAGT	AAAAGTGGGA	GAAGAAGTTG	AAATCGTTGG	TATCAAGGAT	450
	ACTCAGAAAA	CTGTTGTTAC	CGGACTGGAA	ATGTTCCGTA	AGCAGCTGGA	500
	CTTCGCAGAA	TCCGGAGACA	ACATCGGTGC	TCTGCTGCGT	GGTATCAACC	550
	GTGACCAGAT	TCAGCGTGGA	CAGGTTCTTG	CTAAACCAGG	ATCCGTACAT	600
	CCACACACAA	AGTTCAAGGC	TCAGGTTTAT	GTATTAACAA	AAGAAGAAGG	650
25	TGGACGTCAC	ACTCCATTCG	TTTCTAACTA	CCGTCCTCAG	TTCTACTTCC	700
	GTACAACTGA	CGTAACTGGT	GTTATTACAT	TACCGGAAGG	AACTGAAATG	750
	GTTATGCCTG	GTGACAACGT	TGAAATGAAC	GTTGAGCTGA	TTGCTCCAA	799

30

2) INFORMATION FOR SEQ ID NO: 721

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 789 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

40

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Clostridium novyi*
(B) STRAIN: ATCC 19402

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 721

	TTGTATCAGC	AGCAGATGGT	CCAATGCCAC	AAACAAGAGA	ACACATCCTA	50
	TTAGCATCAA	GAGTAGGAGT	TAACCACATA	GTAGTATTCT	TAAACAAAGC	100
	AGACCAAGTA	GATGATCCAG	AATTACTAGA	ATTAGTAGAA	ATGGAAGTAA	150
50	GAGAATTATT	AAGCGAATAC	GGATTTGACG	GAGACGAATG	TCCAGTAGTA	200
	GTAGGATCAG	CATTAAAAGC	AATCGAAGAA	GGGGATGACC	AATGCATCCT	250
	AGACTTAATG	AAAGCTGTAG	ATGAATATAT	CCCAACTCCA	GAAAGAGCAA	300
	CAGATCAACC	ATTCTTAATG	CCTGTAGAAG	ATGTATTTAC	AATTACAGGA	350
	AGAGGAACAG	TTGCAACAGG	AAGAGTTGAA	AGAGGAGTAC	TACACGTAGG	400
55	AGATGAAGTA	CAAATCGTAG	GAATGAAAGA	AGAAATCGGA	AAGACAACAA	450
	TCACAGGAGT	AGAAATGTTT	AGAAAGATGT	TAGATGAAGC	AATGGCTGGA	500
	GATAACATCG	GAGCATTATT	AAGAGGAGTA	CAAAGAGACG	AAATCGAAAG	550
	AGGTCAAGTA	CTAGCAAAAC	CAGGTTTCAGT	AACACCTCAC	AAAAAATTCG	600
	TAGGTCAAGT	TTACGTATTA	AAGAAAGAAG	AAGGTGGAAG	ACACACTCCA	650
60	TTCTTTAACG	GATACAGACC	ACAATTCTAC	TTCAGAACAA	CAGACGTAAC	700

AGGATCAATC GCTTTACCAG AAGGAGTAGA AATGGTAATG CCAGGAGACC 750
ATATAGACAT GAACGTAGAA TTAATCACAC CAGTAGCAA 789

5

2) INFORMATION FOR SEQ ID NO: 722

- (i) SEQUENCE CHARACTERISTICS:
10 (A) LENGTH: 798 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- 15 (vi) ORIGINAL SOURCE:
(A) ORGANISM: *Clostridium septicum*
(B) STRAIN: ATCC 12464

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 722

	GTTCAGCAGC	AGACGGTCCA	ATGCCACAAA	CAAGAGAACA	TATACTACTA	50
	GCATCAAGAG	TTGGTGTTGA	CTATATCGTA	GTATTCTTAA	ACAAGGCAGA	100
	TATGGTAGAT	GACGAAGAAT	TATTAGAATT	AGTAGAAATG	GAAGTTAGAG	150
25	AATTATTATC	AGAATACAAC	TTCCCAGGAG	ATGATATTCC	AGTAATCAAG	200
	GGATCAGCTT	TAGTAGCATT	AGAAAACCCA	ACAGATGAAA	AATCAATCGC	250
	TCCAATCTTA	GAATTAATGG	AAGCAGTAGA	TAGCTACATT	CCAACACCAG	300
	AAAGAGCAAC	AGATAAGCCA	TTCTTAATGC	CAGTAGAAGA	TGTATTCACA	350
	ATAACTGGTA	GAGGAACAGT	TGCAACAGGA	AGAGTTGAAA	GAGGAGTTCT	400
30	TCATGTAGGA	GACGAAGTAG	AAATCGTTGG	ATTATCAGAA	GAAAGCAGAA	450
	AAGTAGTAGT	AACAGGAATA	GAAATGTTCA	GAAAGTTACT	AGACGAAGCA	500
	CAAGCTGGAG	ATAATGTTGG	AGTACTTTTA	AGAGGTGTTC	AAAGAACAGA	550
	TATCGAAAGA	GGTCAAGTAT	TAGCAAAGAC	TGGATCAGTT	AAGCCACACA	600
	GCAAGTTCGT	AGGTCAAGTA	TACGTACTTA	AGAAAGAAGA	AGGTGGAAGA	650
35	CATACTCCAT	TCTTCGATGG	ATACAGACCA	CAATTCTACT	TCAGAACAAC	700
	AGACGTTACT	GGATCAATCA	AATTACCAGA	CGGAATGGAA	ATGGTTATGC	750
	CAGGAGACCA	CATTGATATG	AACGTTGAAT	TAATCACTCA	AGTAGCAA	798

40

2) INFORMATION FOR SEQ ID NO: 723

- (i) SEQUENCE CHARACTERISTICS:
45 (A) LENGTH: 799 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- 50 (vi) ORIGINAL SOURCE:
(A) ORGANISM: *Clostridium tertium*
(B) STRAIN: ATCC 14573

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 723

	GTTCAGCAGC	AGATGGTCCA	ATGCCTCAAA	CAAGAGAACA	CATACTACTA	50
	GCTTCAAGAG	TTGGTGTTGA	CTACATAGTT	GTTTTCTTAA	ACAAGGCAGA	100
	TATGGTAGAT	GACGAAGAAT	TATTAGAATT	AGTTGAAATG	GAAGTAAGAG	150
60	AATTATTATC	AGAATACAAC	TTCCCAGGAG	ATGATATTCC	AGTAATAAAG	200

	GGTTCAGCTT	TACAAGCATT	AGAAAAACCCA	ACAGATGAAA	AAGCAATCGC	250
	TCCAATCCTT	GAGTTAATGG	AAGCTGTAGA	TAGCTACATT	CCAACTCCAG	300
	AAAGAGCAAC	AGATAAGCCA	TTCTTAATGC	CAGTAGAAGA	TGTATTACACA	350
	ATCACTGGTA	GAGGAACAGT	TGCTACAGGA	AGAGTTGAAA	GAGGAGTTCT	400
5	TCACGTAGGA	GACGAAGTAG	AAATCGTTGG	ATTATCAGAA	GACAGCAGAA	450
	AAGTAGTAGT	AACAGGAATA	GAAATGTTCA	GAAAGTTACT	AGACGAAGCG	500
	CAAGCTGGAG	ACAACGTAGG	AGTTCTTTTA	AGAGGAGTTC	AAAGAACTGA	550
	CATCGAAAGA	GGTCAAGTTT	TAGCAAAAAGT	TGGATCAGTT	AAGCCACACA	600
	AGAAATTTGT	AGGTCAAGTA	TACGTACTTA	AAAAAGAAGA	AGGTGGAAGA	650
10	CATACTCCAT	TCTTCGATGG	ATACAGACCA	CAATTCTACT	TCAGAACAAC	700
	AGAYGTTACT	GGTTCAATCA	AGTTACCAGA	TGGAATGGAA	ATGGTTATGC	750
	CAGGAGACCA	CATTGATATG	AACGTTGAAT	TAATCACTCA	AGTAGCTAT	799

15

2) INFORMATION FOR SEQ ID NO: 724

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 801 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

25

(ii) MOLECULE TYPE: Genomic DNA

25

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Clostridium tetani*
- (B) STRAIN: ATCC 19406

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 724

	TAGTAAGTGC	AGCAGATGGT	CCAATGCCAC	AAACAAGAGA	ACACATACTA	50
	TTAGCATCCA	GAGTTGGAGT	TGAGCACATA	GTAGTATTCT	TAAATAAAGC	100
	AGACCAAGTA	GATGACGCAG	AGTTAATCGA	ATTAGTAGAA	ATGGAAGTAA	150
35	GGGAATTAAT	GAACGAATAC	GGATTCCCAG	GAGATGACGC	ACCAGTAGTA	200
	GTAGGATCCG	CATTAAAAGC	ATTAGAAAAT	CCAGAAGATG	ATGCAGCAAC	250
	ACAATGCATA	ATGGACTTAA	TGGCAGCAGT	AGATGAATAT	ATACCAACAC	300
	CAGAAAGAGC	AACAGATAAG	CCATTCTTAA	TGCCAGTAGA	AGATATCTTC	350
	ACAATCACAG	GAAGAGGAAC	AGTTGCAACA	GGAAGAGTAG	AAAGAGGAAT	400
40	TCTAAAAGTA	GGAGACGAAA	TAGAAATCGT	AGGATTAAGT	GATGAAAGCA	450
	AGAAATCAGT	AATCACAGGA	ATAGAAATGT	TCAGAAAAC	ATTAGATGAA	500
	GCACAAGCAG	GAGATAACAT	CGGAGCATTA	TTAAGAGGTG	TTCAAAGAGA	550
	TGAAATCCAA	AGAGGTCAAG	TATTAGCAGC	AACAGGATCA	GTAAAACCAC	600
	ATAAGAGTTT	TACAGGTCAA	GTATATGTAT	TAAAGAAAGA	AGAAGGAGGA	650
45	AGACACACTC	CATTCTTTAA	CGGATACAGA	CCACAATTCT	ACTTTAGAAC	700
	AACAGACGTA	ACAGGTTCAA	TCGCACTACC	AGAAGGAGTA	GAAATGGTAA	750
	TGCCAGGAGA	CCACATAGAC	ATGAAGGTAG	AATTAATAAC	AAGAGTAGCA	800
	A					801

50

2) INFORMATION FOR SEQ ID NO: 725

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 633 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

60

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Enterococcus malodoratus*

(B) STRAIN: ATCC 43197

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 725

	TATGCCTCAA	ACTCGTGAAC	ACATCTTGTT	ATCTCGTAAC	GTTGGTGTTT	50
	CTTACATCGT	TGTATTCTTA	AACAAAATGG	ATATGGTTGA	TGATGAAGAA	100
10	TTACTAGAAT	TAGTTGAAAT	GGAAGTTCGT	GACTTATTGT	CAGAATACGA	150
	CTTCCCAGGC	GACGACACTC	CAGTTATCGC	TGGTTCAGCT	TTGAAAGCTT	200
	TAGAAGGCGA	TGCTTCATAC	GAAGAAAAAA	TCTTAGAATT	AATGGCTGCT	250
	GTTGATGAAT	ATATCCCAAC	ACCAGTTCGT	GATACTGACA	AACCATTTCAT	300
	GATGCCAGTC	GAAGATGTAT	TCTCAATCAC	TGGTCGTGGA	ACTGTTGCAA	350
15	CTGGTCGTGT	TGAACGTGGA	CAAGTTCGCG	TTGGTGACGA	AGTTGAAATC	400
	GTTGGTATTG	CTGAAGCAAC	TGCTAAAACA	ACTGTTACAG	GTGTTGAAAT	450
	GTTCCGTAAA	TTGTTAGATT	ACGCTGAAGC	AGGCGATAAC	ATTGGTGCAT	500
	TGTTACGTGG	TGTTGCACGT	GAAGACATCC	AACGTGGACA	AGTATTGGCT	550
	AAACCAGCTT	CAATCACTCC	ACATACAAAA	TTCTCTGCAG	AAGTTTACGT	600
20	TTTAACTAAA	GAAGAAGGCG	GACGTCATAC	TCC		633

2) INFORMATION FOR SEQ ID NO: 726

25

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 623 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

30

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

35

(A) ORGANISM: *Enterococcus sulfureus*

(B) STRAIN: ATCC 49903

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 726

40	CACGTGAACA	CATCTTGTTA	TCTCGTAACG	TAGGTGTTCC	TTACATCGTT	50
	GTATTCTTAA	ACAAAATGGA	TATGGTTGAT	GACGAAGAAT	TATTAGAATT	100
	AGTAGAAATG	GAAGTTCGTG	ACTTATTATC	AGAATACGAT	TTCCCAGGCG	150
	ATGACACTCC	AGTTGTTGCA	GGTTCTGCTT	TGAAAGCTTT	AGAAGGCGAC	200
	GCTTCTTACG	AAGAAAAAAT	CATGGAATTA	ATGGCTGCAG	TTGACGAGTA	250
45	CATCCCAACT	CCAACCTCGT	ACACTGACAA	ACCATTTCATG	ATGCCAGTTG	300
	AGGATGTATT	CTCAATCACT	GGACGTGGTA	CTGTTGCTAC	AGGTCGTGTT	350
	GAACGTGGAC	AAGTTCGCGT	TGGTGACGTT	GATGATATCG	TTGGTATCGC	400
	TGACGAAACT	GCTCAAACAA	CTGTAACAGG	TGTTGAAATG	TTCCGTAAAT	450
	TATTAGACTA	CGCTGAAGCA	GGCGATAACA	TCGGTGCTTT	ATTACGTGGT	500
50	GTTGCTCGTG	AAGACATCCA	ACGTGGACAA	GTTTTAGCTA	AACCAGCTTC	550
	AATCACTCCA	CATACAAAAT	TCTCTGCTGA	AGTATACGTA	TTAAGCAAAG	600
	AAGAAGGTGG	ACGTCATACT	CCA			623

55

2) INFORMATION FOR SEQ ID NO: 727

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 646 bases

60

(B) TYPE: Nucleic acid

- (C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

5

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Lactococcus garvieae*
(B) STRAIN: ATCC 49156

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 727

	CGGTCCTATG	CCTCAAACCTC	GTGAACACAT	CTTGTTATCA	CGTAACGTTG	50
	GCGTACCATA	CATCGTTGTT	TTCTTGAACA	AAATGGATAT	GGTTGATGAC	100
	GAAGAATTGC	TAGAATTAGT	TGAAATGGAA	GTTTCGTGACC	TATTGTCTGA	150
15	ATATGACTTC	CCAGGCGACG	ATGTTCTGT	AATCGCTGGT	TCTGCTTTGA	200
	AAGCTCTTGA	AGGAGATCCT	TCATACGAAG	AAAAAATCAT	GGAATTGATG	250
	GCTGCAGTTG	ACGAATACGT	TCCAACCTCA	GAACGTGATA	CTGACAAACC	300
	ATTCATGATG	CCAGTCGAAG	ACGTATTCTC	AATCACTGGA	CGTGGTACTG	350
	TTGCTACAGG	CCGTGTTGAA	CGTGGACAAG	TTCGCGTTGG	TGATGAAGTA	400
20	GAAATCGTTG	GTATTGCTGA	CGAAACTGCT	AAAACAACTG	TAACAGGTGT	450
	TGAAATGTTC	CGTAAATTGT	TAGACTATGC	TGAAGCAGGG	GATAACATTG	500
	GTGCATTGCT	ACGTGGGGTT	GCTCGTGAAG	ACATCCAACG	TGGACAAGTA	550
	TTGGCTAAAG	CTGGTACAAT	CACACCTCAT	ACAAAATTCA	AAGCTGAAGT	600
	TTATGTTTTG	ACAAAAGAAG	AAGGTGGACG	TCACACTCCA	TTCTTC	646

25

2) INFORMATION FOR SEQ ID NO: 728

(i) SEQUENCE CHARACTERISTICS:

30

- (A) LENGTH: 823 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Mycoplasma pirum*
(B) STRAIN: ATCC 25960D

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 728

	GAGCAATTTT	AGTTGTTTCT	GCAACTGATG	GTCCAATGCC	TCAAACCTCGT	50
	GAACATATCT	TATTAGCACG	CCAAGTTGGT	GTTCCCTAAAA	TGGTTGTTTT	100
45	CTTAAACAAA	TGTGATGTTG	CTTCTGATCC	AGAAATGCAA	GAATTAGTTG	150
	CTGAAGAAGT	AAAAGACTTA	TTAAAATCTT	ATGGTTTTGA	TGGTGACAAT	200
	ACTCCAATTA	TTCGTGGTTC	AGCATTAGAA	GCATTAAATG	GTAAACCTGA	250
	ATGAGAAGAA	AAAATTAAAG	AATTAATGAA	GGCAGTGGAT	GACACTATTC	300
	CTGATCCAGT	TCGTGATACT	GAAAAGCCAT	TCTTGTTACC	AATTGAAGAC	350
50	GTAATGACAA	TTACAGGTCG	TGGTACTGTT	GTTACAGGTC	GTGTAGAACG	400
	TGGTACTCTA	AAATTAAATG	ATGAAGTTGA	AATTGTTGGT	TTAGGTGAAA	450
	CATTTAAATC	TGTTGTAACA	GGTATTGAAA	TGTTCCGTAA	AGAATTAGAT	500
	GAAGCTCGTG	CTGGTGACAA	TGCTGGTATT	TTACTTCGTG	GTGTTGACCG	550
	TGGTCAAGTA	CAACGTGGTC	AAGTTCTTGC	TAAACCAGGT	TCTATTACTC	600
55	CTCATACTAA	ATTTAAAGCT	GAAATTTATG	CTTTGAAAAA	AGAAGAAGGT	650
	GGTCGTCATA	CTGCTTTCTT	AAACGGTTAT	CGTCCTCAAT	TCTATTTTCAG	700
	AACAACTGAT	GTTACAGGTT	CTATTAAATT	AAAAGATGGA	ACTGAAATGG	750
	TTATGCCTGG	TGACAATACT	GAAATCACTG	TAGAATTAAT	TTCACCAATT	800
	GCTTGTAATA	AGGAAGTAAG	TTT			823

60

2) INFORMATION FOR SEQ ID NO: 729

5 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 826 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

10

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Mycoplasma salivarium*
 (B) STRAIN: ATCC 23064

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 729

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20 GGAGCAATCT TAGTTGTTGC TGCAACTGAT GGTGCGATGC CTCAAACTCG      50
   TGAACACGTT TTA CTTGCAA AACAAGTTGG TGTCCTAAA ATCGTTGTTT      100
   TCTTAAACAA AATCGATATG TTCAAGCCAG AAGAAAGAGC CGAAATGGTT      150
   GAAATGGTTG AAATGGACAT TCGTGACTTA TTAAACAAAT ACGACTTTGA      200
   TGGTGACAAT ACTCCTATTA TTGCTGGTTC AGCATTAAAA GCATTACAAG      250
   GTGATCCAGA ATATGAAAAG AATATTCTAG AACTTATGGA TGCAGTAGAC      300
25 ACATACATTG ATGAACCTAC TCGTGATAAA GATAAACCAT TCTTAATGGC      350
   TGTAGAAGAC GTATTTACAA TTACTGGTTCG TGGAACTGTT GCTACTGGTA      400
   GAGTAGAACG TGGTACATTA CATCTAAATG ATGAAGTTGA AATCGTTGGT      450
   CTACGTCCAA CAATTAAAAC TGTGTGTTACT GGAATTGAAA TGTTCGGTAA      500
   AAATTTAAAA GAAGCTCAAG CTGGAGATAA TGCAGGACTT TTACTACGTG      550
30 GAATTGATAG AGATCAAGTA GAACGTGGAC AAGTTTGGC CAAACCAAAA      600
   AGTATTATTC CTCACACAGA ATTTGAAGCT GCTGTGTATG TTCTAAAAGC      650
   TGAAGAAGGT GGACGTCACA CTCCATTCTT TGAACACTAT AAACCACAAT      700
   TTTACTTTTCG TACAACCGAC GTTACTGGTG GAATTAAATT CAAACCTGGA      750
   CGTGAAATGG TTATGCCTGG CGAAAATGTT GAATTTACAG TTACTTTAAT      800
35 TGCTCCTATT GCAGTTGAAG AAGGAA                                826

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2) INFORMATION FOR SEQ ID NO: 730

40

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 810 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

45

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Neisseria polysaccharea*
 (B) STRAIN: ATCC 43768

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 730

```

55 TGGTATGTTC CGCAGCYGAY GGYCCTATGC CTCAAACTCG CGAACACATC      50
   CTGYTGCTC GCCAAGTAGG YGTACCTTAC ATCATCGTRT TCATGAACAA      100
   ATGCGACATG GTTGACGATG CCGAGCTGTT GGAAGTGGTT GAAATGGAAA      150
   TCCGYGACCT GYTGTCMAGC TACGACTTCC CMGGCGACGA CTGCCCAATC      200
   GTACAAGGTT CTGCACTGAA AGCTTTGGAA GGYGAYGCTG GTTACGAAGA      250
60 GAAAATCTTC GAAYTGCTG CTGCTTTGGA CAGCTACATC CCAACTCCTG      300

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	AGCGTGCTGT	GGACAAACCK	TTCYTGYTGC	CTATCGAAGA	CGTRTTCTCT	350
	ATCTCTGGYC	GYGGTACMG	AGTAACYGGY	CGTGTAGAGC	GCGGTRTCAT	400
	CCACGTTGGT	GACGAGATYG	AAATCGTAGG	TCTGAAAGAA	ACCCAAAAAA	450
	CCACTTGATC	CGGCGTTGAA	ATGTTCCGCA	AACTGCTGGA	CGAAGGTCAA	500
5	GCWGGTGACA	ACGTAGGCGT	ATTGYTGCCT	GGTACCAARC	GTGAAGACGT	550
	AGAGCGTGGT	CAAGTATTGG	CYAAACCAGG	YACCATYACT	CCSCACACCA	600
	AATTCAAAGC	AGAAGTATAC	GTACTGAGCA	AAGAAGAGGG	TGGTCGYCAC	650
	ACTCCATTCT	TCGCYAACTA	CCGYCCMCAA	TTCTACTTCC	GTACYACTGA	700
	CGTAACYGGT	GCAGTTACTT	TGGAAGAAGG	TGTAGAAATG	GTAATGCCAG	750
10	GTGAGAACGT	AACCATTACY	GTAGAACTGA	TTGCGCCTAT	CGCTAGGAAG	800
	AAGGTCTGCG					810

15 2) INFORMATION FOR SEQ ID NO: 731

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 813 bases
 (B) TYPE: Nucleic acid
 20 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

25 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Salmonella choleraesuis* subsp. *choleraesuis*
 serotype Enteritidis
 (B) STRAIN: ATCC 13076

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 731

	CTGGTTGTTG	CTGCGACTGA	CGGCCCGATG	CCGCAGACCC	GTGAGCACAT	50
	CCTGCTGGGT	CGTCAGGTAG	GCGTTCCGTA	CATCATCGTG	TTCCTGAACA	100
	AATGCGACAT	GGTTGATGAC	GAAGAGCTGC	TGGAACGGT	TGAAATGGAA	150
35	GTTTCGYGAAC	TGCTGTCTCA	GTACGACTTC	CCGGGCGACG	ACACTCCGAT	200
	CGTTCGTGGT	TCTGCTCTGA	AAGCGCTGGA	AGGCGACGCA	GAGTGGGAAG	250
	CGAAATCAT	CGAACTGGCT	GGCTTCCTGG	ATTCTTACAT	CCCGGAACCA	300
	GAGCGTCCGA	TTGACAAGCC	GTTCTGCTG	CCGATCGAAG	ACGTATTCTC	350
	CATCTCCGGT	CGTGGTACCG	TTGTTACCGG	TCGTGTAGAA	CGCGGTATCA	400
40	TCAAAGTGGG	CGAAGAAGTT	GAAATCGTTG	GTATCAAAGA	GA CTCAGAAG	450
	TCTACCTGTA	CTGGCGTTGA	AATGTTCCGC	AAACTGCTGG	ACGAAGGCCG	500
	TGCCGGTGAG	AACGTAGGTG	TTCTGCTGCG	TGGTATCAAA	CGTGAAGAAA	550
	TCGAACGTGG	TCAGGTACTG	GCTAAGCCGG	GCACCATCAA	GCCGCACACC	600
	AAGTTCGAAT	CTGAAGTGTA	CATTCTGTCC	AAAGATGAAG	GCGGCCGTCA	650
45	CACTCCGTTT	TTCAAAGGCT	ACCGTCCGCA	GTTCTACTTC	CGTACTACTG	700
	ACGTGACTGG	CACCATCGAA	CTGCCGGAAG	GCGTAGAGAT	GGTAATGCCG	750
	GGCGACAACA	TCAAAATGGT	TGTTACCCTG	ATCCACCCGA	TCGCAATGGA	800
	CGACGGTCTG	CGT				813

50

2) INFORMATION FOR SEQ ID NO: 732

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 812 bases
 (B) TYPE: Nucleic acid
 55 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

60 (ii) MOLECULE TYPE: Genomic DNA

417

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Salmonella choleraesuis* subsp. *choleraesuis*
serotype Gallinarum
(B) STRAIN: ATCC 9184

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 732

	CTGGTTGTTG	CTGCGACTGA	CGGCCCGATG	CCGCAGACCC	GTGAGCACAT	50
10	CCTGCTGGGT	CGTCAGGTAG	GCGTTCCGTA	CATCATCGTG	TTCCTGAACA	100
	AATGCGACAT	GGTTGATGAC	GAAGAGCTGC	TGGAAGTGGT	TGAAATGGAA	150
	GTTTCGYGAAC	TGCTGTCTCA	GTACGACTTC	CCGGGCGACG	ACACTCCGAT	200
	CGTTCTGGT	TCTGCTCTGA	AAGCGCTGGA	AGGCGACGCA	GAGTGGGAAG	250
	CGAAAATCAT	CGAACTGGCT	GGCTTCCTGG	ATTCTTACAT	CCCGGAACCA	300
15	GAGCGTGCGA	TTGACAAGCC	GTTCCTGCTG	CCGATCGAAG	ACGTATTCTC	350
	CATCTCCGGT	CGTGGTACCG	TTGTTACCGG	TCGTGTAGAA	CGCGGTATCA	400
	TCAAAGTGGG	CGAAGAAGTT	GAAATCGTTG	GTATCAAAGA	GACTCAGAAG	450
	TCTACCTGTA	CTGGCGTTGA	AATGTTCCGC	AAACTGCTGG	ACGAAGGCCG	500
	TGCCGGTGAG	AACGTAGGTG	TTCTGCTGCG	TGGTATCAAA	CGTGAAGAAA	550
20	TCGAACGTGG	TCAGGTACTG	GCTAAGCCGG	GCACCATCAA	GCCGCACACC	600
	AAGTTCGAAT	CTGAAGTGTA	CATTCTGTCC	AAAGATGAAG	GCGGCCGTCA	650
	CACTCCGTTT	TTCAAAGGCT	ACCGTCCGCA	GTTCTACTTC	CGTACTACTG	700
	ACGTGACTGG	CACCATCGAA	CTGCCGGAAG	GCGTAGAGAT	GGTAATGCCG	750
	GGCGACAACA	TCAAATGGT	TGTTACCCTG	ATCCACCCGA	TCGCAATGGA	800
25	CGACGGTCTG	CG				812

2) INFORMATION FOR SEQ ID NO: 733

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 814 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Salmonella choleraesuis* subsp. *choleraesuis*
serotype Paratyphi B
(B) STRAIN: ATCC 8759

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 733

	TGGTTGTTGC	TGCGACTGAC	GGYCCGATGC	CGCAGACCCG	TGAGCACATC	50
	CTGCTGGGTC	GTCAGGTAGG	CGTTCCGTAC	ATCATCGTGT	TCCTGAACAA	100
	ATGCGACATG	GTTGATGACG	AAGAGCTGCT	GGAAGTGGTT	GAAATGGAAG	150
	TTCGYGAACT	GCTGTCTCAG	TACGACTTCC	CGGGCGACGA	CACTCCGATC	200
50	GTTCGTGGTT	CTGCTCTGAA	AGCGCTGGAA	GGCGACGCAG	AGTGGGAAGC	250
	GAAAATCATC	GAAGTGGCTG	GCTTCCTGGA	TTCTTACATT	CCGGAACCAG	300
	AGCGTGCGAT	TGACAAGCCG	TTCTGCTGTC	CGATCGAAGA	CGTATTCTCC	350
	ATCTCTGGTC	GTGGTACCGT	TGTTACCGGT	CGTGTAGAAC	GCGGTATCAT	400
	CAAAGTGGGC	GAAGAAGTTG	AAATCGTTGG	TATCAAAGAG	ACTCAGAAGT	450
55	CTACCTGTAC	TGGCGTTGAA	ATGTTCCGCA	AACTGCTGGA	CGAAGGCCGT	500
	GCTGGTGAGA	ACGTAGGTGT	TCTGCTGCGT	GGTATCAAAC	GTGAAGAAAT	550
	CGAACGTGGT	CAGGTACTGG	CTAAGCCGGG	CACCATCAAG	CCGCACACCA	600
	AGTTCGAATC	TGAAGTGATC	ATTCTGTCCA	AAGATGAAGG	CGGCCGTCAT	650
	ACTCCGTTCT	TCAAAGGCTA	CCGTCCGCAG	TTCTACTTCC	GTACTACTGA	700
60	CGTGACTGGC	ACCATCGAAC	TGCCGGAAGG	CGTAGAGATG	GTAATGCCGG	750

GCGACAACAT CAAAATGGTT GTTACCCTGA TCCACCCGAT CGCAATGGAC 806
 GACGGTCTGC GTTT 814

5

2) INFORMATION FOR SEQ ID NO: 734

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 828 bases
 10 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- 15 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Salmonella choleraesuis* subsp. *choleraesuis*
 serotype Virchow
 (B) STRAIN: ATCC 51955

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 734

GGCGCGATCC TGGTTGTTGC TGCGACTGAC GGCCCGATGC CGCAGACCCG 50
 TGAGCACATC CTGCTGGGTC GTCAGGTAGG CGTTCCGTAC ATCATCGTGT 100
 25 TCCTGAACAA ATGCGACATG GTTGATGACG AAGAGCTGCT GGAAGTGGTT 150
 GAAATGGAAG TTCGTGAACT TCTGTCTCAG TACGACTTCC CGGGCGACGA 200
 CACTCCGATC GTTCGTGGTT CTGCTCTGAA AGCGCTGGAA GGCGACGCAG 250
 AGTGGGAAGC GAAAATCATC GAACTGGCTG GCTTCCTGGA TTCTTACATT 300
 CCGGAACCAG AGCGTGCGAT TGACAAGCCG TTCCTGCTGC CGATCGAAGA 350
 30 CGTATTCTCC ATCTCCGGTC GTGGTACCGT TGTTACCGGT CGTGTAAGAAC 400
 GCGGTATCAT CAAAGTGGGC GAAGAAGTTG AAATCGTTGG TATCAAAGAG 450
 ACTCAGAAGT CTACCTGTAC TGGCGTTGAA ATGTTCCGCA AACTGCTGGA 500
 CGAAGGCCGT GCCGGTGAGA ACGTAGGTGT TCTGCTGCGT GGTATCAAAC 550
 GTGAAGAAAT CGAACGTGGT CAGGTACTGG CTAAGCCGGG CACCATCAAG 600
 35 CCGCACACCA AGTTCGAATC TGAAGTGATC ATTCTGTCCA AAGATGAAGG 650
 CGGCCGTCAT ACTCCGTTCT TCAAAGGCTA CCGTCCGCAG TTCTACTTCC 700
 GTACTATGA CGTGAATGCG ACCATCGAAC TGCCGGAAGG CGTAGAGATG 750
 GTAATGCCGG GCGACAACAT CAAAATGGTT GTTACCCTGA TCCACCCGAT 800
 CGCAATGGAC GACGGTCTGC GTTTCGCA 828

40

2) INFORMATION FOR SEQ ID NO: 735

- 45 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 825 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
- 50 (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Serratia grimesii*
 55 (B) STRAIN: ATCC 14460

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 735

GGCGCTATCC TGGTTGTTGC TGCGACTGAT GGCCCAATGC CACAGACCCG 50
 60 TGAGCACATC CTGCTGGGTC GTCAGGTTGG CGTTCCTTTC ATCATCGTAT 100

	TCATGAACAA	ATGCGACATG	GTTGATGATG	AAGAGCTGCT	GGAAC TGGT A	150,
	GAAATGGAAG	TTCGTGAACT	TCTGTCTGCT	TATGACTTCC	CTGGTGATGA	200
	CCTGCCAGTT	GTTTCGTGGTT	CAGCGCTGAA	AGCACTGGAA	GGCGAAGCTG	250
	AGTGGGAAGC	TAAAATCATC	GAAGTGGCTG	GCTACCTGGA	TTCTTACATC	300
5	CCAGAACCAG	AGCGTGCTAT	CGACAAGCCG	TTCTTGCTGC	CAATCGAAGA	350
	CGTATTCTCC	ATCTCCGGYC	GTGGTACYGT	AGTTACCGGT	CGTGTAAGC	400
	GCGGTATCGT	TAAAGTTGGC	GAAGAAGTTG	AAATCGTTGG	TATCAAAGAC	450
	ACCGTTAAGT	CTACCTGTAC	TGGCGTTGAA	ATGTTCCGCA	AACTGCTGGA	500
	CGAAGGCCGT	GCTGGTGAGA	ACGTAGGTGT	TCTGCTGCGT	GGTATCAAGC	550
10	GTGAAGACAT	CGAACGTGGT	CAGGTACTGG	CTAAACCAGG	TTCAATCAAG	600
	CCACACACCA	AATTCGACTC	AGAAGTTTAC	ATCCTGAGCA	AAGAAGAAGG	650
	TGGTCGTCAC	ACTCCATTCT	TCAAAGGCTA	CCGTCCACAG	TTCTACTTCC	700
	GTACAACTGA	CGTGACCGGT	ACCATCGAAC	TGCCAGAAGG	CGTAGAGATG	750
	GTAATGCCAG	GCGATAACGT	GAACATGGTT	GTAACCCTGA	TTACCCCAAT	800
15	CGCGATGGAC	GACGGTCTGC	GTTTC			825

2) INFORMATION FOR SEQ ID NO: 736

20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 798 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

25

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

30

- (A) ORGANISM: *Clostridium difficile*
- (B) STRAIN: ATCC 9689

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 736

35	TATTAGTTTG	TTCAGCAACA	GATGGACCAA	TGCCACAAAC	AAGAGAGCAT	50
	ATACTATTAT	CAAGACAAGT	TGGAGTACCA	TATATAGTAG	TATTCTTAAA	100
	CAAATGTGAC	ATGGTAGATG	ATGAAGAGTT	ATTAGAGTTA	GTAGAGATGG	150
	AAGTAAGAGA	TTTATTAACA	GAATATGATT	TCCCAGGAGA	TGACACTCCA	200
	ATAGTAAGAG	GTTTCAGCAT	AATGGCATT	GAAGATCCAA	AGAGYGAGTG	250
40	GGGAGATAAG	ATAGTAGAAT	TATTCGAGCA	AATAGATGAG	TATATACCAG	300
	CTCCAGAGAG	AGATACAGAT	AAACCATTTCT	TAATGCCAGT	AGAGGACGTA	350
	TTCTCAATCA	CAGGAAGAGG	AACAGTTGCA	ACAGGAAGAG	TGGAAAGAGG	400
	AGTACTAAAA	GTACAAGACG	AAGTAGAKTT	AGTAGGATTA	ACAGAAGCAC	450
	CAAGAAAAGT	AGTAGTAACA	GGAGTAGAGA	TGTTTCAGAA	ATTATTAGAC	500
45	CAAGCACAAG	CAGGGGATAA	TATAGGAGCA	TTATTAAGAG	GAGTACAAAG	550
	AAACGAGATA	GAAAGAGGAC	AAGTACTAGC	AAAGACTGGA	TCAGTAAAGG	600
	CACACACAAA	GTTTACAGCA	GAAGTATATG	TACTTAAAAA	AGAAGARGGT	650
	GGAAGACATA	CACCATTCTT	TGATGGATAT	AGACCACAAT	TCTATTTTCAG	700
	AACAACAGAC	GTAACAGGAG	CTTGTAAGTT	ACCAGAAGGA	ATAGAGATGG	750
50	TAATGCCTGG	AGATAACGTA	ACAATGGAAG	TAGACTTAAT	AAACTCAA	798

2) INFORMATION FOR SEQ ID NO: 737

55

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 411 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

60

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 5 (A) ORGANISM: *Burkholderia pseudomallei*
(B) STRAIN: 1026B

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 737

10	GTCAACATGA TGGAGCTCAT CAACAACATC GCGAAGGAGC ACGGCGGTTA	50
	CTCCGTGTTC GCGGGCGTGG GCGAGCGTAC CCGTGAAGGG AACGACTTCT	100
	ACCACGAAAT GAAGGACTCG AACGTTCTCG ACAAGGTGCG GCTGGTGTAC	150
	GGCCAGATGA ACGAGCCGCC GGGCAACCGT CTGCGCGTGG CGCTGACGGG	200
	CCTCACGATG GCCGAGCACT TCCGTGACGA AGGCCTCGAC GTGCTGTTCT	250
15	TCGTCGACAA CATCTACCGT TTCACGCTGG CCGGTACCGA AGTGTCGGCG	300
	CTGCTCGGCC GTATGCCGTC GGCAGTGGGC TATCAGCCGA CGCTGGCTGA	350
	AGAAATGGGC AAGCTGCAAG AGCGCATCAC GTCGACGAAG AAGGGCTCGA	400
	TCACGTCGGT T	411

20

2) INFORMATION FOR SEQ ID NO: 738

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 394 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

30 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Clostridium bifermentans*
35 (B) STRAIN: ATCC 638

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 738

	TACAAGAGCT TATTAACAAT ATAGCTACTC AACACGGTGG TATATCAGTA	50
	TTCGCAGGTG TTGGAGAGAG AACAAAGAGAA GGTAACGACT TATTCCATGA	100
40	GATGAGCGAT ACAGGAGTTA TAAATAAAAC AGCTCTAGTA TTCGGACAAA	150
	TGAATGAGCC ACCTGGAGCA AGAATGAGAG TTGCTTTAAC TGGTCTTACA	200
	ATGGCTGAAT ACTTCAGAGA TCAACAAGGG CAAGACGTTT TATTATTCGT	250
	AGATAATATA TTCCGTTTCA CTCAAGCAGG ATCTGAGGTT TCTGCACTTC	300
	TTGGACGTAC TCCATCAGCA GTTGGATACC AACCAACATT AGCAACAGAG	350
45	ATGGGTAGAT TACAAGAGAG AATAACATCT ACAAATAAAG GGTC	394

2) INFORMATION FOR SEQ ID NO: 739

50

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 394 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
55 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Clostridium beijerincki* (deposited as
Clostridium butyricum)
 (B) STRAIN: ATCC 8260

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 739

	TTAATAAACA	ACATAGCTAA	ACAACATGGT	GGTTTATCAG	TATTTACTGG	50
	AGTTGGTGAA	AGATCAAGAG	AAGGTAATGA	CTTATATCAT	GAAATGAGAG	100
	AGTCAGGAGT	TATTGATAAG	ACAGCATTAG	TATTTGGACA	AATGAATGAG	150
10	CCACCGGGTG	CCAGAATGAG	AGTTGCATTA	ACAGGTCTTA	CTATGGCAGA	200
	GTATTTTAGA	GATAAAGGTC	AAGATGTGTT	ACTATTCATA	GATAACATAT	250
	TCAGATATAC	TCAAGCAGGT	TCAGAGGTTT	CAGCATTACT	TGGAAGAACA	300
	CCTTCAGCGG	TTGGATATCA	GCCAACACTT	GCAACTGAAA	TGGGTGCACT	350
	TCAGGAAAGA	ATTACATCAA	CAGTTAATGG	TTCTATTACG	TCAG	394

15

2) INFORMATION FOR SEQ ID NO: 740

20 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 393 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

25

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Clostridium difficile*
 (B) STRAIN: ATCC 9689

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 740

	TTATAAACAA	TATTGCTAAG	CAACATGGTG	GTATTTCTGT	ATTTTCAGGA	50
35	GTAGGAGAAA	GAACAAGAGA	AGGTAACGAC	CTTTATGGCG	AAATGAGTGA	100
	GTCTGGAGTT	ATAAATAAAA	CAGCTCTAGT	ATTTGGTCAA	ATGAATGAAC	150
	CACCTGGAGC	GAGAATGAGA	GTTGCTTTAA	CTGGACTTAC	AATGGCAGAA	200
	CATTTTAGAG	ATGAGCAAGG	ACAAGACGTT	TTACTTTTCG	TTGATAATAT	250
	ATTCCGTTTC	ACACAAGCTG	GTTCAGAAGT	TTCAGCACTT	CTAGGACGTA	300
40	TGCCATCAGC	TGTTGGTTAT	CAGCCAACAT	TAGCTACTGA	AATGGGTGCA	350
	CTTCAAGAGA	GAATAACATC	AACTAAGAAA	GGTTCAATAA	CAT	393

45 2) INFORMATION FOR SEQ ID NO: 741

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 398 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Clostridium ramosum*
 (B) STRAIN: ATCC 25582

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 741

60

	TTGATTCAAG	AATTCATTAA	TAACATTGCT	ACAGAACATG	GTGGTTTATC	50
	AGTTTTTGGT	GGAGTTGGTG	AACGTAGCCG	TGAAGGTAAT	GATTTATATT	100
	ATGAAATGAA	GGAAAGTGGT	GTTTTATCTA	AAACAACACT	AGTATTTGGA	150
	CAGATGAATG	AACCCCCAGG	AGCTCGTTTA	AGAGTTGCTT	TAACGGGTCT	200
5	TACTATGGCA	GAAGAATTCC	GTGATGAACA	AGGTCAGGAT	GTCTTATTAT	250
	TCATCGATAA	TATTTTCCGT	TTTACTCAAG	CTGGATCTGA	AGTATCTGCC	300
	TTACTTGGAC	GGGTACCATC	ACAAGCTGGG	TATCAGCCAA	CTTTAGCAAC	350
	CGAAATGGGT	GCTTTACAAG	AACGGATTAC	ATCAACTAAA	AAAGGATC	398

10

2) INFORMATION FOR SEQ ID NO: 742

- (i) SEQUENCE CHARACTERISTICS:
- 15 (A) LENGTH: 380 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear
- 20 (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Clostridium septicum*
- (B) STRAIN: ATCC 12964
- 25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 742

	TAGCTAAGGA	ACACGGTGGA	CTTTCAGTAT	TCACAGGTGT	TGGAGAAAGA	50
	TCAAGAGAAG	GTAATGATTT	ATATTACGAA	ATGAAAGAAT	CAGGAGTTAT	100
30	AGACAAGACA	GCTCTAGTGT	TTGGACAAAT	GAATGAATCT	CCAGGAGCTA	150
	GAATGAGAGT	ATCTTTAACA	GGATTAACATA	TGGCTGAATA	TTTCAGAGAT	200
	CAAGGTCAAG	ATGTGCTTTT	ATTCATAGAT	AACATATTTA	GATTTACTCA	250
	AGCTGGATCA	GAAGTATCGG	CTTTACTTGG	AAGAATACCA	TCAGCAGTTG	300
	GTTATCAACC	AACACTAGCA	ACTGAAATGG	GTGCACTTCA	AGAAAGAATT	350
35	ACTTCAACTA	AAAATGGATC	AATAACTTCA			380

2) INFORMATION FOR SEQ ID NO: 743

- 40 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 389 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- 45 (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
- 50 (A) ORGANISM: *Clostridium tertium*
- (B) STRAIN: ATCC 14573
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 743

55	TTAATAAATA	ATATAGCAAA	AGAGCATGGT	GGTCTTTCTG	TATTTACAGG	50
	AGTTGGAGAA	AGGTCAAGAG	AAGGTAACGA	CTTATATTAT	GAAATGAAAG	100
	AGTCAGGGGT	TATAGATAAG	ACAGCTTTAG	TATTTGGACA	AATGAATGAA	150
	TCACCAGGAG	CAAGAATGAG	AGTTTCATTA	ACTGGATTAA	CTATGGCTGA	200
	ATATTTTAGA	GATCAAGGTC	AAGACGTTCT	TTTATTTATA	GATAATATAT	250
60	TTAGATTTAC	TCAAGCGGGA	TCAGAAGTTT	CTGCGTTATT	AGGAAGAATT	300

CCTTCAGCAG TTGGATATCA ACCAACTCTT GCAACTGAAA TGGGAGCACT 350
TCAAGAAAGA ATAACATCAA CAAAGAATGG ATCAATCAC 389

5

2) INFORMATION FOR SEQ ID NO: 744

(i) SEQUENCE CHARACTERISTICS:

10

- (A) LENGTH: 843 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

15

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Comamonas acidovorans*
(B) STRAIN: ATCC 15668

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 744

	TTCCCCGCA	CGCATGCCCA	AGGTGTTCGA	TGCCCTGAAG	CTCGACGGCT	50
	CGGCCCTGAC	GCTGGAAGTG	CAGCAACTGC	TGGGTGACGG	CGTTGTGCGT	100
	ACCATCGCCC	TGGGTTCGTC	CGACGGTCTG	CGTCGCGGCC	TGATGGTGTC	150
25	CAACACCGGC	AACCCCATCA	CCGTGCCCCG	GGGCAAGGCG	ACGCTGGGTC	200
	GCATCATGGA	CGTGCTGGGC	AATCCCATCG	ACGAACGTGG	TCCCGTGGAT	250
	CAGGCGCTGA	CGGCTCCCAT	CCACCGCAAG	GCACCGGCTT	ATGACGAGCT	300
	GTGCGCTTCG	CAGGAACTGC	TGGAAACCGG	CATCAAGGTG	ATCGACCTGA	350
	TCTCGCCCTT	CGCCAAGGGC	GGCAAGGTGG	GTCTGTTCGG	TGGCGCCGGT	400
30	GTGGGCAAGA	CCGTGAACAT	GATGGAATCT	ATCAACAACA	TCGCCAAGGG	450
	CCACGGTGGT	CTGTGCGGTG	TCGCCGGTGT	GGGTGAACGT	ACCCGCGAAG	500
	GCAATGACTT	CTATCACGAA	ATGTGCGACG	CCGGCGTGGT	CAACCAGGAG	550
	TCGCTGAACG	ACTCCAAGGT	GGCCATGGTC	TACGGCCAGA	TGAACGAACC	600
	CCCGGGCAAC	CGTCTGCGCG	TGGCGCTGAC	CGGCCTGACC	ATGGCCGAAG	650
35	CCTTCCGTGA	CGAAGGCAAG	GACGTGCTGT	TCTTCGTGGA	CAACATCTAC	700
	CGCTACACGC	TGGCCGGTAC	CGAAGTGTCC	GCTCTGCTGG	GTCGCATGCC	750
	TTCCGCCGTG	GGCTACCAGC	CCACGCTGGC	CGAGGAAATG	GGCCGCCTGC	800
	AAGAGCGCAT	CACCTCGACC	AAGGTCGGTT	CGATCACTTC	CAC	843

40

2) INFORMATION FOR SEQ ID NO: 745

(i) SEQUENCE CHARACTERISTICS:

45

- (A) LENGTH: 819 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Klebsiella pneumoniae* subsp.
rhinoscleromatis
(B) STRAIN: ATCC 13884

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 745

	GCCGTACCAC	GCGTGTACGA	AGCCCTTGAG	GTACAGAAATG	GTAATGAAGT	50
60	TCTGGTGCTG	GAAGTTCAGC	AGCAGCTGGG	CGGCGGTATC	GTACGTACCA	100

	TCGCCATGGG	TTCTTCTGAT	GGTCTGCGCC	GCGGTCTGGA	TGTAAAAGAC	150
	CTCGAGCACC	CGATCGAAGT	CCCGGTAGGT	AAAGCAACGC	TGGGTCGTAT	200
	CATGAACGTA	CTGGGTCAAC	CGGTTGACAT	GAAAGGCGAC	ATCGGCCGAAG	250
	AAGAGCGTTG	GGCTATCCAC	CGCGCGGCAC	CGTCCTATGA	AGAGCTGTCC	300
5	AGCTCTCAGG	AACTGCTGGA	AACCGGCATC	AAAGTTATCG	ACCTGATGTG	350
	TCCGTTTCGCC	AAGGGCGGTA	AAGTTGGTCT	GTTTCGGCGGT	GCGGGTGTAG	400
	GTAAGACTGT	AAACATGATG	GAGCTGATCC	GTAACATCGC	GATCGAGCAC	450
	TCCGGTTACT	CTGTGTTTGC	GGGCGTAGGT	GAGCGTACTC	GTGAGGGTAA	500
	CGACTTCTAC	CACGAAATGA	CCGACTCCAA	CGTTATCGAT	AAAGTATCCC	550
10	TGGTGTACGG	CCAGATGAAC	GAGCCGCCGG	GAAACCGTCT	GCGCGTTGCG	600
	CTGACCGGCC	TGACCATGGC	TGAGAAATTC	CGTGACGAAG	GTCGTGACGT	650
	ACTGCTGTTC	GTCGATAACA	TCTATCGTTA	CACCCTGGCC	GGTACTGAAG	700
	TATCCGCGCT	GCTGGGTCGT	ATGCCTTCAG	CGGTAGGTTA	TCAGCCGACC	750
	CTGGCGGAAG	AGATGGGCGT	TCTGCAGGAA	CGTATCACCT	CCACCAAAC	800
15	CGGTTCTATC	ACCTCCGTA				819

2) INFORMATION FOR SEQ ID NO: 746

20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 824 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

25

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

30

- (A) ORGANISM: *Neisseria canis*
- (B) STRAIN: ATCC 14687

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 746

35	GCGATTCTAT	TCCGCGCGTA	TATGATGCTC	TTAAACTAGT	GGATAGAGAA	50
	CTGACGCTTG	AAGTACAACA	ACAGTTGGGT	GATGGTGTCT	TTCGTACTAT	100
	TGCGATGGGT	AGTTCCGACG	GCCTCAAACG	AGGTTTGGCG	GTAAGTTAACA	150
	CCGGTGCTCC	AATTACAGTG	CCTGTGGGCA	AAGCAACATT	AGGCCGTATT	200
	ATGGACGTAT	TAGGTAATCC	GGTTGATGAA	GCTGGTCCGA	TTGGCTCCGA	250
40	GCAAACCCGA	GCAATCCACC	AACCTGCTCC	TAAGTTCGAC	GAGCTTTCTA	300
	GCGCCACAGA	GATTTTGGAA	ACAGGTATTA	AAGTAATTGA	TTTGCTTTGC	350
	CCGTTTGCCA	AAGGCGGTAA	AGTAGGTTTG	TTTGGTGGTG	CGGGAGTGGG	400
	CAAAACCGTA	AATATGATGG	AGTTGATTAA	CAACATCGCG	AAAGCACACA	450
	GCGGTTTGTC	TGTATTTGCC	GGTGTGGGTG	AACGGACGCG	TGAAGGTAAT	500
45	GACTTTTATC	ATGAGATGAA	AGATTCCAAT	GTATTAGATA	AAGTAGCCAT	550
	GGTTTACGGT	CAGATGAACG	AGCCTCCCGG	TAACCGTTTG	CGCGTTGCGC	600
	TAACTGGCTT	GTCTATGGCC	GAATTCTTCC	GTGACGAGAA	AGATGAAAAC	650
	GGTAAAGGCC	GTGATGTATT	GTTCTTTGTA	GACAATATTT	ACCGCTATAC	700
	CCTAGCCGGT	ACAGAAAGTAT	CTGCATTGCT	TGGCCGTATG	CCTTCGGCAG	750
50	TAGGTTATCA	GCCGACGTTG	GCAGAGGAAA	TGGGCCGCTT	GCAAGAGCGT	800
	ATTACYTCAM	CCCAAACAGG	CTCT			824

55 2) INFORMATION FOR SEQ ID NO: 747

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 831 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double

60

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

5 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Neisseria cinerea*

(B) STRAIN: ATCC 14685

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 747

10
 CGCGACGCTA TCCCGCATGT TTACGATGCC CTGAAATTGG ACGAGAACGG 50
 TCTGACTCTG GAGGTTCAAC AGCTTCTGGG CGACGGCGTT GTCCGTACTA 100
 TTGCAATGGG TAGTTCAGAC GGCCTTAAAC GCGGTATGTC TGTAAGCAAT 150
 ACTGGTGCGC CAATCACTGT GCCGGTAGGT AAAGGTACAT TGGGTCGTAT 200
 15 TGTCGACGTA TTGGGTACGC CTGTTGATGA AGCAGGTCCG ATCGATACCG 250
 ACAAAGCCG TGCCATTCAC CAACTGCTC CGAAATTCGA CGAGTTGTCT 300
 TCAGTACCG AATTGTTGGA AACCGGTATT AAAGTGATCG ACTTGCTGTG 350
 TCCGTTTGCT AAAGGCGGTA AAGTAGGTCT GTTCGGTGGT GCCGGTGTGG 400
 GCAAACCGT GAACATGATG GAATTGATCA ACAACATCGC CAAAGCGCAC 450
 20 AGCGGTCTGT CCGTGTTCGC AGGTGTGGGT GAGCGTACCC GTGAAGGTAA 500
 CGACTTCTAC CACGAGATGA AAGATTCCAA CGTATTGGAT AAAGTAGCCA 550
 TGGTGTATGG CCAAATGAAC GAACCTCCGG GCAACCGTCT GCGCGTTGCT 600
 TTGACCGGTT TGA CTATGGC CGAATACTTC CGTGACGAAA AAGACGAAAA 650
 CGGTAAAGGC CGCGACGTAT TGTTCTTCGT TGACAACATC TACCGTTACA 700
 25 CTTTGGCCGG TACTGAAGTA TCTGCACTGT TGGGCCGTAT GCCTTCTGCA 750
 GTGGGTTACC AACCGACATT GGCTGAAGAA ATGGGTCGTT TGCAAGAGCG 800
 TATTACCTCT ACCCAAACCG GTTCCATTAC T 831

30

2) INFORMATION FOR SEQ ID NO: 748

(i) SEQUENCE CHARACTERISTICS:

35 (A) LENGTH: 862 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

40 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Neisseria cuniculi*

(B) STRAIN: ATCC 14688

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 748

CCGTGGCCAA GTACCACAAA TTTATGACGC ACTGAGTGTT GATGGCACCG 50
 AAACAACCTT GGAAGTTCAA CAGCAGTTGG GTGATGGCGT GGTGCGTACC 100
 ATTGCGATGG GTTCAACCGA AGGCTTGAAG CGTGGTTTGA CTGTATCTAA 150
 50 CTCTGGTGCA CCGATTTCTG TGCCAGTGGG TCAAGCGACT TTGGGTCGTA 200
 TTATGGATGT GTTGGGTCGT CCAATCGACG AGGCAGGTCC TGTAATGCT 250
 CAAGAAAAAT GGTCAATTCA CCGTGAAGCA CCAAGCTATG ATGAGCAATC 300
 AAAGTCAACT GAGCTGCTAG AAACAGGCAT CAAAGTAATT GATTTGCTTT 350
 GCCCATTTGC TAAAGGTGGT AAAGTTGGCT TGTTCCGGTGG TGCAGGTGTG 400
 55 GGTAAAACCG TGAATATGAT GGAGCTGATT AATAATATCG CTCTGAAGCA 450
 TTCAGGTCTT TCTGTTTTTG CAGGTGTTGG TGAGCGTACT CGTGAGGGTA 500
 ACGATTTTTA TCACGAAATG CAAGAAGCAG GCGTTGTTAA TACCGAAGAC 550
 TTCACCAAGT CAAAAGTAGC GATGGTTTAT GGTCAGATGA ATGAGCCACC 600
 AGGAAACCGT TTGCGTGTG CATTGACAGG CTTGACGATG GCAGAATATT 650
 60 TCCGTGACGA AAAAGATGAA GCAACAGGCA AAGGGCGTGA TGTTCTATTG 700

TTCGTTGATA	ACATCTATCG	TTACACACTG	GCTGGTACGG	AAGTGT [~] CAGC	750
ACTTCTAGGT	CGTATGCCAT	CAGCAGTAGG	TTATCAACCG	ACTCTGGCTG	800
AAGAAATGGG	TGCGTTGCAA	GAGCGTATTA	CCTCAACGCA	ATCGGGTTTCG	850
ATCACTTCGG	GG				862

5

2) INFORMATION FOR SEQ ID NO: 749

10 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 844 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

15

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Neisseria elongata* subsp. *elongata*
 (B) STRAIN: ATCC 25295

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 749

	GGA	ACT	CCCA	CGT	GAC	GCTA	TCCC	GCA	TGT	TTTT	GAT	GCA	TTAA	AATT	AG	50	
25	TTG	AAA	ATGA	CCT	AAC	CTTA	GAAG	TTCA	AC	AACT	TTTG	GG	GGAT	GGT	GTA	100	
	GTG	CGT	ACCA	TTG	CGA	TGGG	TAGT	TCA	GAT	GGAT	TAA	AGC	GTGG	TAT	GGC	150	
	TGT	GAA	TAAT	ACC	GG	A	CTC	CGAT	TACT	GT	TCCT	GTT	G	CGT	GAA	ACTT	200
	TGG	GTC	GAT	CAT	GGA	TGTA	TTGG	GTA	ATC	CGGT	TGA	TGA	GGC	AGG	TCCG	250	
	GTAA	ATGC	AT	CCA	ATA	CACG	TGCG	ATCC	AT	CAAG	AGG	CTC	CTA	AGT	TTGA	300	
30	TGAG	CTTT	CT	TCA	ACA	ACGG	AATT	ATTAG	A	AACT	GGC	ATT	AAG	GTT	TATCG	350	
	ACT	TGTT	ATG	TCC	GTT	TGCC	AAAG	G	TGGTA	AAG	TAG	GTCT	GTT	TGG	TGGT	400	
	GCG	GGT	G	GTAA	AAC	CGT	AAAT	ATG	ATG	GAG	TAA	T	ACA	A	ATTGC	450	
	CAAG	G	CACAT	AGC	GGT	TTGT	CTGT	GTTT	G	AGG	CGT	G	GA	ACG	TACTC	500	
	GTGA	AGG	TAA	TGAC	TTCT	AT	CAC	GAG	ATGA	AAG	ATT	CCAA	CGT	ATT	G	550	
35	AAAG	TGG	CAA	TGG	TTT	ACGG	TCAG	ATGA	AC	GAAC	CTC	CAG	GCA	ACC	GTCT	600	
	GCG	CGT	TGCT	TTG	ACC	GGTT	TGAC	TAT	G	CGA	ATA	CTTC	CGT	GAC	G	650	
	AAG	ACG	AAAA	CGG	TAA	AGGT	CGCG	ACG	TAT	TGTT	CTT	CGT	GG	ACA	ACATT	700	
	TAC	CGT	TACA	CTTT	G	CCCG	TAC	GGA	AGTA	TCC	G	CATTGC	TGG	G	T	750	
	GCCT	T	CAGCA	G	TAG	GTACC	AACC	G	ACATT	GGCT	GAA	GAA	ATG	GGT	TCGTT	800	
40	TGCA	AAG	AGCG	TATT	ACCT	CT	ACCC	AG	ACAG	GCT	CTAT	TAC	TTCC			844	

2) INFORMATION FOR SEQ ID NO: 750

45

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 834 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Neisseria flavescens*
 (B) STRAIN: ATCC 13120

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 750

60	CGCG	ACGCTA	TTCC	GCA	TGT	TTAC	GATGCC	CTG	AAATTGG	ACG	AGA	ACGG	50
----	------	--------	------	-----	-----	------	--------	-----	---------	-----	-----	------	----

	TCTGACTCTG	GAAGTTCAAC	AGCTTCTGGG	TGACGGCGTT	GTCCGTACTA	100
	TTGCAATGGG	TAGTTCAGAC	GGCCTGAAAC	GCGGCATGTC	TGTAAGCAAT	150
	ACCGGTGCGC	CAATCACTGT	GCCGGTAGGT	AAAGGTACAT	TGGGCCGTAT	200
	TGTCGACGTA	TTGGGTACGC	CTGTTGATGA	AGCAGGTCCG	ATCGATACCG	250
5	ACAAGAGCCG	TGCCATTAC	CAAACGCTC	CGAAATTCGA	TGAGTTGTCT	300
	TCAACTACCG	AATTGTTGGA	AACCGGTATT	AAAGTGATCG	ACTTGCTGTG	350
	TCCGTTTGCT	AAGGGCGGTA	AAGTAGGTCT	GTTCCGGTGGT	GCCGGTGTGG	400
	GCAAAACCGT	GAACATGATG	GAATTGATCA	ACAACATCGC	CAAAGCGCAC	450
	AGCGGCCTGT	CCGTGTTCCG	AGGTGTGGGT	GAACGTACCC	GTGAAGGTAA	500
10	CGACTTCTAC	CACGAGATGA	AAGATTCCAA	CGTATTGGAT	AAAGTAGCCA	550
	TGGTGTATGG	TCAAATGAAC	GAACCTCCAG	GCAACCGTCT	GCGCGTTGCT	600
	TTGACCGGTT	TGACTATGGC	CGAATACTTC	CGTGACGAAA	AAGATGAAAA	650
	CGGTAAAGGT	CGCGACGTAT	TGTTCTTCGT	TGACAACATC	TACCGTTACA	700
	CTCTGGCCGG	TACCGAAGTA	TCCGCACTGT	TGGGTCGTAT	GCCTTCTGCA	750
15	GTGGGTTACC	AACCGACATT	GGCTGAAGAA	ATGGGTCGTT	TGCAGGAGCG	800
	TATTACTTCT	ACGCAAACCG	GTTCCATTAC	TTCC		834

20 2) INFORMATION FOR SEQ ID NO: 751

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 834 bases
 (B) TYPE: Nucleic acid
 25 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

30 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Neisseria gonorrhoeae*
 (B) STRAIN: ATCC 31426

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 751

35	CGCGACATGA	TTCCGCGCGT	TTACGACGCT	TTGAAATTAG	ACGAAAACGG	50
	TCTGACTTTG	GAAGTCCAAC	AGCTTTTGGG	TGATGGCGTA	GTCCGTACCA	100
	TCGCTATGGG	CAGCTCGGAC	GGTTTGAAAC	GCGGCATGAC	TGTGAGCAAT	150
	ACTGGTTTCG	CCATTACTGT	GCCGGTAGGT	AAAGGTACGT	TGGGACGCAT	200
40	TGTCGATGTA	TTGGGAACTC	CTGTTGACGA	GGCAGGTCCA	ATTGATACCG	250
	ACAAGAGTCG	TGCCATCCAC	CAAGCCGCTC	CTAAGTTTGA	CGAACTGTCT	300
	TCCACAACCG	AATTGCTCGA	AACGGGCATT	AAAGTGATTG	ACTTGCTGTG	350
	TCCGTTTGCC	AAAGGCGGTA	AAGTAGGTCT	GTTCCGGCGT	GCCGGTGTGG	400
	GTAAAACCGT	GAACATGATG	GAATTGATCA	ACAACATCGC	CAAAGCGCAC	450
45	AGCGGCTTGT	CCGTGTTCTC	AGGCGTGGGT	GAGCGTACCC	GCGAAGGTAA	500
	CGACTTCTAC	CACGAGATGA	AAGATTCCAA	CGTATTGGAT	AAAGTAGCCA	550
	TGGTGTATGG	CCAAATGAAC	GAACCTCCAG	GCAACCGTCT	GCGCGTTGCT	600
	TTGACCGGTT	TGACTATGGC	TGAATACTTC	CGTGACGAAA	AAGACGAAAA	650
	CGGTAAAGGT	CGTGACGTAT	TGTTCTTCGT	TGACAACATC	TACCGTTACA	700
50	CTCTGGCCGG	TACCGAAGTA	TCCGCACTGT	TGGGCCGTAT	GCCTTCTGCA	750
	GTGGGTTACC	AACCGACATT	GGCTGAAGAA	ATGGGTCGTT	TGCAAGAGCG	800
	TATTACCTCT	ACCAAACCG	GTTCCATTAC	TTCC		834

55

2) INFORMATION FOR SEQ ID NO: 752

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 825 bases
 60 (B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

5

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Neisseria gonorrhoeae*

(B) STRAIN: ATCC 27628

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 752

	ACATGATTCC	GCGCGTTTAC	GACGCTTTGA	AATTAGACGA	AAACGGTCTG	50
	ACTTTGGAAG	TCCAACAGCT	TTTGGGTGAT	GGCGTAGTCC	GTACCATCGC	100
	TATGGGCAGC	TCGGACGGTT	TGAAACGCGG	CATGACTGTG	AGCAATACTG	150
15	GTTTCGCCCAT	TACTGTGCCG	GTAGGTAAAG	GTACGTTGGG	ACGCATTGTC	200
	GATGTATTGG	GAACGCCTGT	TGACGAGGCA	GGTCCAATTG	ATACCGACAA	250
	GAGTCGTGCC	ATCCACCAAG	CCGCTCCTAA	GTTTGACGAA	CTGTCTTCCA	300
	CAACCGAATT	GCTCGAAACG	GGCATTAAG	TGATTGACTT	GCTGTGTCCG	350
	TTTGCCAAAG	GCGGTAAAGT	AGGTCTGTTT	GGCGGTGCCG	GTGTGGGTAA	400
20	AACCGTGAAC	ATGATGGAAT	TGATCAACAA	CATCGCCAAA	GCGCACAGCG	450
	GCTTGTCCGT	GTTCTCAGGC	GTAGGTGAGC	GTACCCGCGA	AGGTAACGAC	500
	TTCTACCACG	AGATGAAAGA	TTCCAACGTA	TTGGATAAAG	TAGCCATGGT	550
	GTATGGCCAA	ATGAACGAAC	CTCCAGGCAA	CCGTCTGCGC	GTTGCTTTGA	600
	CCGGTTTGAC	TATGGCTGAA	TACTTCCGTG	ACGAAAAAGA	CGAAAACGGT	650
25	AAAGGTCGTG	ACGTATTGTT	CTTCGTTGAC	AACATCTACC	GTTACACTCT	700
	GGCCGGTACC	GAAGTATCCG	CACTGTTGGG	CCGTATGCCT	TCTGCAGTGG	750
	GTTACCAACC	GACATTGGCT	GAAGAAATGG	GTCGTTTGCA	AGAGCGTATT	800
	ACCTCTACCC	AAACCGGTTC	CATTA			825

30

2) INFORMATION FOR SEQ ID NO: 753

(i) SEQUENCE CHARACTERISTICS:

35

(A) LENGTH: 831 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

40 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Neisseria lactamica*

(B) STRAIN: ATCC 23970

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 753

	GATGCGATTC	CGCATGTTTA	CGATGCCCTG	AAATTGGACG	AGAACGGTCT	50
	GACCCTGGAA	GTCCAACAGC	TTTTGGGTGA	CGGCGTTGTC	CGTACTATTG	100
50	CAATGGGTAG	TTCAGACGGC	CTGAAACGCG	GCATGTCTGT	CAGCAATACC	150
	GGTGCGCCAA	TCACTGTGCC	GGTAGGTAAA	GGTACGTTGG	GCCGTATTGT	200
	CGACGTATTG	GGTACACCTG	TTGACGAAGC	AGGTCCGATC	GATACCGACA	250
	AGAGCCGCGC	CATCCACCAA	ACCGCCCCGA	AATTCGACGA	GTTGTCTTCA	300
	ACTACCGAAT	TGTTGGAAC	CGGCATTAAA	GTGATCGATT	TGCTGTGTCC	350
55	GTTTGCTAAG	GGCGGTAAAG	TAGGTCTGTT	CGGTGGTGCC	GGTGTGGGCA	400
	AAACCGTGAA	CATGATGGAA	TTGATCAACA	ACATCGCCAA	AGCGCACAGC	450
	GGTCTGTCCG	TGTTTGCAAG	CGTGGGCGAG	CGTACCCGCG	AAGGTAACGA	500
	CTTCTACCAC	GAGATGAAAG	ATTCCAACGT	ATTGGATAAA	GTAGCCATGG	550
	TGTATGGTCA	GATGAACGAA	CCTCCGGGCA	ACCGTCTGCG	CGTTGCTTTG	600
60	ACCGGTTTGA	CGATGGCCGA	ATACTTCCGC	GACGAAAAAG	ACGAAAACGG	650

CAAAGGCCGC	GACGTATTGT	TCTTCGTGGA	CAACATCTAC	CGTTACACCC	700
TGGCCGGTAC	CGAAGTATCC	GCACTGTTGG	GCCGTATGCC	TTCCGCAGTG	750
GGTTACCAAC	CGACATTGGC	TGAAGAAATG	GGTCGTTTGC	AAGAGCGTAT	800
TACCTCTACC	CAAACCGGTT	CCATTACTTC	C		831

5

2) INFORMATION FOR SEQ ID NO: 754

10 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 836 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

15

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Neisseria meningitidis*
 (B) STRAIN: 2241C

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 754

CCACGCGACA	TGATTCCGCG	CGTTTACGAC	GCTTTGAAAT	TAGACGAAAA	50
25	CGGTCTGACT	TTGGAAGTCC	AACAGCTTTT	GGGCGACGGC	100
	CCATTGCGAT	GGGCAGCTCG	GACGGTTTGA	AACGCGGCAT	150
	AATACCGGTG	CGCCATTAC	TGTGCCGGTA	GGTAAAGGTA	200
	CATTGTCGAT	GTATTGGGAA	CGCCTGTTGA	CGAGGCAGGT	250
	CCGACAAGAG	CCGTGCCATC	CACCAAGCCG	CTCCTAAGTT	300
30	TCTTCCACAA	CCGAATTGCT	CGAAACGGGC	ATTAAAGTGA	350
	GTGTCCGTTT	GCCAAAGGCG	GTAAAGTAGG	TCTGTTCGGC	400
	TGGGTAAAAC	CGTGAACATG	ATGGAATTGA	TCAACAACAT	450
	CACAGCGGCT	TGTCCGTGTT	CGCAGGCGTG	GGTGAGCGTA	500
	TAACGACTTC	TACCACGAGA	TGAAAGATTC	CAACGTATTG	550
35	CAATGGTTTA	CGGTCAGATG	AACGAACCTC	CGGGCAACCG	600
	GCATTGACCG	GTTTGACCAT	GGCGGAATAC	TTCCGTGACG	650
	AAACCGCAAA	GGCCGCGACG	TATTGTTCTT	CGTGGACAAC	700
	ACACTCTAG	TGGTACCGAA	GTATCCGCAT	TGTTGGGCCG	750
	GCAGTGGGCT	ACCAACCGAC	ATTGGCAGAA	GAAATGGGTC	800
40	GCGTATTACC	TCTACCCAAA	CCGGTTCTAT	TACTTC	836

2) INFORMATION FOR SEQ ID NO: 755

45

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 837 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Neisseria mucosa*
 (B) STRAIN: ATCC 19696

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 755

60	CCGCGTGATG	CCATTCCGCG	TGTTTACGAC	GCCCTGAAAT	TGGATGCAAA	50
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430

	CGGCCTGACT	TTGGAAGTGC	AACAGCTTCT	GGGTGACGGC	GTAGTTCGTA	400
	CTATTGCAAT	GGGTAGTTCG	GATGGTTTGA	AACGCGGCAT	GACTGTAAGC	150
	AATACAGGTG	CGCCGATTAC	AGTACCGGTA	GGTAAAGGTA	CTTTGGGACG	200
	TATTGTGCGAT	GTATTGGGTA	CGCCTGTTGA	CGAAGCAGGT	CCGATTGATA	250
5	CCGACAAACA	CCGTGCCATC	CATCAGACAG	CTCCGAAATT	TGATGAACTG	300
	TCTGCGACTA	CTGAGCTGCT	GGAAACCGGC	ATTAAAGTGA	TTGACTTGCT	350
	GTGTCCGTTT	GCCAAAGGCG	GTAAAGTAGG	TCTGTTCGGT	GGTGCCGGTG	400
	TAGGCAAAAC	CGTCAACATG	ATGGAATTAA	TTAACAACAT	CGCCAAAGCA	450
	CATAGCGGTT	TGTCCGTGTT	TGCAGGTGTG	GGTGAGCGTA	CCCGTGAAGG	500
10	TAATGACTTC	TACCACGAGA	TGAAAGATTG	CAACGTATTG	GACAAAGTGG	550
	CGATGGTTTA	CGGTCAGATG	AACGAACCTC	CGGGTAACCG	TCTGCGTGTA	600
	GCCTTGACCG	GTTTGACGAT	GGCCGAATAC	TTCCCGTGATG	AAAAAGACGA	650
	AAGCGGCAAA	GGCCGTGACG	TATTGTTCTT	CGTGGACAAT	ATCTACCGTT	700
	ACACCCTGGC	CGGTACCGAA	GTATCCGCAT	TGTTGGGTCG	TATGCCTTCA	750
15	GCAGTAGGTT	ACCAACCGAC	ATTGGCTGAA	GAAATGGGTC	GTTTGCAAGA	800
	GCGTATTACC	TCTACCCAAA	CAGGCTCCAT	TACCTCC		837

20 2) INFORMATION FOR SEQ ID NO: 756

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 834 bases
 (B) TYPE: Nucleic acid
 25 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

30 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Neisseria subflava*
 (B) STRAIN: ATCC 14221

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 756

35	CGCGACGCTA	TCCCGCATGT	TTACGATGCC	CTGAAATTGG	ACGAGAACGG	50
	TCTGACTCTG	GAAGTTCAAC	AGCTTCTGGG	TGACGGCGTT	GTCCGTACTA	100
	TTGCAATGGG	TAGTTCAGAC	GGCCTGAAAC	GCGGCATGTC	TGTAAGCAAT	150
	ACTGGTGCGC	CAATCACTGT	GCCGGTAGGT	AAAGGTACAT	TGGGTCGTAT	200
40	TGTGCGACGTA	TTGGGTACGC	CTGTTGATGA	AGCAGGTCCG	ATCGATACCG	250
	ACAAGAGCCG	TGCCATTAC	CAAACCTGCTC	CGAAATTCTGA	CGAGTTGTCT	300
	TCAACTACCG	AATTGCTGGA	AACCGGTATT	AAAGTGATCG	ACTTGCTGTG	350
	TCCGTTTGCT	AAGGGCGGTA	AAGTAGGTCT	GTTCCGTGGT	GCCGGTGTGG	400
	GCAAAACCGT	GAACATGATG	GAATTGATCA	ACAACATCGC	CAAAGCGCAC	450
45	AGCGGTCTGT	CCGTGTTTCG	AGGTGTGGGT	GAACGTACCC	GTGAAGGTAA	500
	CGACTTCTAC	CACGAGATGA	AAGATTCCAA	CGTATTGGAT	AAAGTAGCCA	550
	TGGTGTATGG	CCAAATGAAC	GAACCTCCGG	GCAACCGTCT	GCGCGTTGCT	600
	TTGACCGGTT	TGACTATGGC	CGAATACTTC	CGTGACGAAA	AAGACGAAAA	650
	CGGTAAAGGT	CGCGACGTAT	TGTTCTTCGT	TGACAACATC	TACCGTTACA	700
50	CTCTGGCCCG	TACCGAAGTA	TCTGCACTGT	TGGGCCGTAT	GCCTTCTGCA	750
	GTGGGTTACC	AACCGACATT	GGCTGAAGAA	ATGGGTCGTT	TGCAAGAGCG	800
	TATTACCTCT	ACCCAAACTG	GTTCCATTAC	TTCC		834

55

2) INFORMATION FOR SEQ ID NO: 757

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 833 bases
 60 (B) TYPE: Nucleic acid

- (C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

5

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Neisseria weaveri*
(B) STRAIN: ATCC 51223

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 757

	CCCGTGATGC	TATTCCCATG	TATACGATGC	CCTGAAATTG	GTAGATAAAG	50
	ATCTGACCCT	GGAAGTGCAA	CAACTTTTAG	GTGATGGTGT	GGTTCGTACC	100
	ATTGCAATGG	GTAGTTCAGA	CGGCCTAAAA	CGTGGTATGG	CTGTTAACAA	150
15	TACCGGCGCT	CCGATTACTG	TTCCGGTGGG	GAAAGCCACC	TTGGGACGTA	200
	TTATGGATGT	GTTGGGTAAT	CCGGTTGATG	AAGCAGGTCC	TGTTGTATCA	250
	GAAGAAACTC	GCGCTATTCA	TCAAGCTGCC	CCTAAATTTG	ACGAACTGTC	300
	TTCAGCAACT	GAGTTGTTGG	AAACAGGCAT	TAAAGTAATT	GACTTGCTGT	350
	GCCCGTTTGC	CAAAGGTGGT	AAAGTAGGTT	TGTTTGGTGG	TGCCGGCGTG	400
20	GGTAAAACCG	TAAATATGAT	GGAGTTGATC	AACAACATCG	CGAAGGCACA	450
	TAGTGGTTTG	TCTGTATTCT	CCGGTGTAGG	TGAGCGTACC	CGTGAAGGTA	500
	ACGACTTCTA	CCATGAAATG	AAAGACTCTA	ACGTATTGGA	TAAAGTAGCC	550
	ATGGTTTATG	GCCAGATGAA	TGAACCTCCG	GGTAACCGTT	TGCGCGTTGC	600
	TTTGACTGGT	TTGACTATGG	CCGAATATTT	CCGTGACGAG	AAAGATGAAA	650
25	ACGGCAAAGG	TCGTGACGTC	TTGTTCTTTG	TGGATAATAT	CTATCGCTAT	700
	ACTCTGGCCG	GTACTGAAGT	GTCTGCACTG	TTAGGTCGTA	TGCCGTCTGC	750
	AGTAGGTTAT	CAGCCTACAT	TGGCAGAAGA	AATGGGTCGC	TTGCAGGAGC	800
	GTATTACTTC	TACTCAAACA	GGTTCGATTA	CTT		833

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2) INFORMATION FOR SEQ ID NO: 758

(i) SEQUENCE CHARACTERISTICS:

35

- (A) LENGTH: 833 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

40 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Neisseria animalis*
(B) STRAIN: ATCC 19573

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 758

	CGCGATGCCA	TTCCTCACGT	TTACGATGCC	CTGAAATTGG	ACGACACCGG	50
	TCTGACTTTG	GAAGTACAAC	AACTTCTGGG	CGACGGTGTG	GTACGTACCA	100
50	TTGCAATGGG	TAGTTCAGAC	GGCCTGAAAC	GGGGTTTGTC	TGTGAGCAAT	150
	ACCGGTTCTC	CGATTGCCGT	TCCTGTCCGT	AAAGCGACTT	TGGGTCGTAT	200
	TATGGACGTA	TTGGGCAATC	CGGTTGATGA	AGCCGGTCCG	GTTGCTACCG	250
	AAGAGAAACG	TGCTATTAC	CAAGCCGCAC	CGAAGTTTGA	TGAATTGTCA	300
	TCAGCTACCG	AGTTGTTGGA	AACCGGTATT	AAAGTAATCG	ACTTGCTGTG	350
55	TCCGTTTGCA	AAAGGCCGTA	AAGTAGGTCT	GTTCCGGCGGT	GCCGGTGTGG	400
	GCAAAACCGT	AAACATGATG	GAATTGATCA	ACAACATCGC	CAAAGCACAC	450
	AGCGGTCTGT	CTGTGTTTGC	CGGTGTAGGT	GAACGTACCC	GCGAAGGTAA	500
	CGACTTCTAC	CACGAGATGA	AAGATTCCAA	CGTGTTGGAT	AAAGTAGCCA	550
	TGGTGTACGG	TCAGATGAAT	GAGCCGCCCG	GCAACCGCTT	GCGCGTGGCT	600
60	TTGACCGGCC	TGACTATGGC	CGAATACTTC	GTGACGAAAA	AGACGAAAAC	650

GGCAAAGGTC	GTGACGTATT	GTTCTTCGTG	GACAAACATTT	ACCGCTACAC	700
ACTGGCCGGT	ACCGAAGTAT	CAGCATTGTT	GGGCCGTATG	CCGTCTGCAG	750
TAGGTTATCA	GCCGACATTG	GCAGAGGAAA	TGGGTCGCTT	GCAAGAGCGT	800
ATTACCTCTA	CCCAAACCGG	TTCGATTACC	TCT		833

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2) INFORMATION FOR SEQ ID NO: 759

10 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 819 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

15

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Proteus penneri*
 (B) STRAIN: ATCC 33519

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 759

AGCGTCCCTA	AAGTATACGA	CGCTCTTGAG	GTTATGAATG	GTAAAGAAAA	50
25 ACTGGTGCTG	GAAGTTCAGC	AACAGTTAGG	CGGTGGTATC	GTTCGTTGTA	100
TCGCAATGGG	TACATCAGAC	GGTTTAAGCC	GTGGCTTAAA	AGTTGAAGAT	150
TTAGGCCACC	CAATTGAAGT	ACCAGTAGGT	AAAGCAACAC	TGGGACGTAT	200
CATGAACGTT	CTGGGTACAC	CTATTGATAT	GAAAGGTGAT	ATTGCAACTG	250
AAGAACGTTG	GTCTATTAC	CGTGAAGCAC	CAACCTACGA	AGAGTTATCA	300
30 AACTCACAAG	AACTGCTTGA	AACCGGTATC	AAAGTAATGG	ACTTAATCTG	350
TCCGTTTGCT	AAAGGTGGTA	AAGTAGGTCT	GTTCCGGTGGT	GCGGGTGTGG	400
GTAACACAGT	TAACATGATG	GAATTGATCC	GTAATATCGC	GATCGAGCAC	450
TCAGGTTACT	CTGTATTTGC	TGGTGTTGGT	GAGCGTACTC	GTGAGGGTAA	500
CGACTTCTAT	CATGAAATGA	CAGATTCTAA	CGTTCTTGAC	AAAGTATCGT	550
35 TAGTTTATGG	TCAGATGAAT	GAGCCACCAG	GAAACCGTCT	GCGTGTAGCA	600
CTGACTGGTC	TGACTATGGC	TGAAAAATTC	CGTGATGAAG	GCCGTGACGT	650
ACTGTTATTC	GTCGATAACA	TTTATCGTTA	CACCTTAGCC	GGTACAGAAG	700
TATCAGCACT	GTTAGGTCGT	ATGCCATCAG	CGGTAGGTTA	CCAGCCAACA	750
TTGGCTGAAG	AGATGGGTGT	TCTGCAAGAA	CGTATCACTT	CAACCAAAAC	800
40 AGGTTCAATC	ACCTCTGTA				819

2) INFORMATION FOR SEQ ID NO: 760

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 819 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Salmonella choleraesuis* subsp. *choleraesuis*
 serotype Enteritidis
 (B) STRAIN: ATCC 13076

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 760

60

	GCCGTACCAC	GCGTGTACGA	TGCCCTTGAG	GTGCAGAATG	GTAATGAGAA	50
	GCTGGTGCTG	GAAGTTCAGC	AGCAGCTTGG	CGGCCGGTATC	GTGCGTACCA	100
	TCGCGATGGG	GTCTTCTGAC	GGTCTGCGTC	GCGGTCTGGA	TGTAAAAGAT	150
	CTCGAACACC	CGATCGAAGT	CCCGGTAGGT	AAAGCCACGC	TGGGTCGTAT	200
5	CATGAACGTC	CTGGGCGAAC	CGGTCGACAT	GAAAGGCGAG	ATCGGCCAAG	250
	AAGAGCGTTG	GGCGATTAC	CGCGCAGCAC	CTTCCTACGA	AGAGTTGTCA	300
	AACTCTCAGG	AACTGCTGGA	AACCGGTATC	AAAGTTATCG	ACCTGATGTG	350
	TCCGTTCCGG	AAGGGCGGTA	AAGTCGGTCT	GTTCCGGTGGT	GCGGGTGTAG	400
	GTAACACCGT	AAACATGATG	GAGCTTATTC	GTAACATCGC	GATCGAGCAC	450
10	TCCGGTTACT	CAGTGTTTGC	GGCGGTAGGG	GAACGTACTC	GTGAGGGTAA	500
	CGACTTCTAC	CACGAAATGA	CCGACTCCAA	CGTTATCGAT	AAAGTATCCC	550
	TGGTGTATGG	CCAGTGAAC	GAGCCGCCGG	GAAACCGTCT	GCGCGTTGCA	600
	CTGACCGGCC	TGACCATGGC	GGAGAAATTC	CGTGACGAAG	GTCGTGACGT	650
	ATGTCTGTTT	GTCGATAACA	TCTATCGTTA	CACCCTGGCC	GGTACGGAAG	700
15	TATCCGCACT	GCTGGGCCGT	ATGCCTTCCG	CAGTAGGTTA	CCAGCCGACT	750
	CTGGCGGAAG	AGATGGGCGT	TCTGCAGGAA	CGTATCACCT	CCACCAAAC	800
	CGGTTCTATC	ACCTCCGTA				819

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2) INFORMATION FOR SEQ ID NO: 761

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 812 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Yersinia pestis*
 (B) STRAIN: KIM D27

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 761

	ACCAAAAGTG	TACAACGCCC	TTGAGGTAGA	AGGTACAAC	GAAAAGTTAG	50
	TGCTGGAAGT	TCAGCAACAG	TTGGGCGGTG	GTGTTGTTTC	TTGTATCGCA	100
	ATGGGCTCTT	CCGATGGTCT	GAGCCGTGGG	TTGAAAGTAA	CCAACCTAGA	150
40	ACACCCGATC	GAAGTACCGG	TTGGTAAAGC	GACCCTTGGC	CGTATCATGA	200
	ACGTATTGGG	TGAACCAATC	GACATGAAAG	GTCCTATCGG	TGAAGAAGAG	250
	CGTTGGGCAA	TCCATCGCGA	AGCGCCTTCT	TATGAAGAGC	TTGCTAGCTC	300
	ACAAGTACTG	TTAGAAACCG	GTATCAAGGT	TATGGACCTG	ATTTGTCCGT	350
	TTGCTAAGGG	CGGTAAAGTC	GGTCTGTTTC	GTGGTGCGGG	TGTAGGTAAA	400
45	ACAGTAAACA	TGATGGAGCT	GATCCGTAAC	ATCGCGATCG	AGCACTCTGG	450
	GTATTCTGTA	TTTGCCGGTG	TAGGTGAGCG	TACCCGTGAG	GGTAATGACT	500
	TCTACCATGA	AATGACTGAC	TCCAACGTTT	TGGACAAAGT	ATCCTTGGTT	550
	TACGGCCAGA	TGAATGAGCC	ACCAGGTAAC	CGTCTACGCG	TTGCACTGAC	600
	CGGCCTGACC	ATGGCGGAGA	AATTCCGTGA	TGAAGGTCGT	GACGTAAGTC	650
50	TGTTTATCGA	TAATATCTAT	CGTTATACCC	TAGCTGGTAC	GGAAGTATCC	700
	GCATTGCTGG	GTCGTATGCC	ATCAGCGGTA	GGTTATCAGC	CAACACTGGC	750
	TGAAGAGATG	GGTGTGTTGC	AGGAACGTAT	TACTTCCACT	AAGACGGGTT	800
	CAATCACCTC	TG				812

55

2) INFORMATION FOR SEQ ID NO: 762

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 408 bases

- (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

5 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Burkholderia mallei*
 (B) STRAIN: GB8

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 762

	CGACGTGATC	GAGCCCTTCT	TCGTGACGT	GATGCGCTCT	TGCAGCTTGC	50
	CCATTTCTTC	AGCCAGCGTC	GGCTGATAGC	CCACTGCCGA	CGGCATACGG	100
15	CCGAGCAGCG	CCGACACTTC	GGTACCGGCC	AGCGTGAAAC	GGTAGATGTT	150
	GTCGACGAAG	AACAGCACGT	CGAGGCCCTT	GTCACGGAAG	TGCTCGGCCA	200
	TCGTGAGGCC	CGTCAGCGCC	ACGCGCAGAC	GGTTGCCCCG	CGGCTCGTTC	250
	ATCTGGCCGT	ACACCAGCGC	GACCTTGTCG	AGAACGTTTC	AGTCCTTCAT	300
	TTCGTGGTAG	AAGTCGTTCC	CTTCACGGGT	ACGCTCGCCC	ACGCCCCGCG	350
20	ACACGGAGTA	ACCGCCGTGC	TCCTTCGCGA	TGTTGTTGAT	GAGCTCCATC	400
	ATGTTGAC					408

25 2) INFORMATION FOR SEQ ID NO: 763

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 bases
 (B) TYPE: Nucleic acid
 30 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

35 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Clostridium sordellii*
 (B) STRAIN: ATCC 9714

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 763

40

	GAACTTATAA	ACAACATAGC	TACTCAACAT	GGTGGTATAT	CAGTATTTCG	50
	AGGTGTTGGA	GAGAGAACAA	GAGAAGGTAA	CGACCTTTAC	GGAGAAATGA	100
	GTGAGTCTGG	AGTTATAAAC	AAGACAGCTC	TAGTATTTCG	ACAAATGAAT	150
	GAGCCACCTG	GAGCAAGAAT	GAGAGTTGCT	TTAACTGGTC	TTACAATGGC	200
45	TGAATATTTT	AGAGATCAAG	AAGGACAAGA	CGTTTTATTA	TTCGTAGATA	250
	ATATATTCCG	TTTCACTCAA	GCAGGATCTG	AGGTTTCTGC	ACTTCTTGGA	300
	CGTACTCCAT	CAGCAGTTGG	ATACCAACCA	ACATTAGCTA	CAGAGATGGG	350
	TAGATTACAA	GAGAGAATAA	CATCTACAAA	TAAAGGGTCT	ATAACATCAG	400

50

2) INFORMATION FOR SEQ ID NO: 764

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 405 bases
 55 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

60 (ii) MOLECULE TYPE: Genomic DNA

435

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Clostridium novyi*
 (B) STRAIN: ATCC 19402

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 764

	TTAATTCAAG	AATTAATCAA	CAATATAGCG	AAGGAACACG	GTGGATTATC	50
	TGTATTTACA	GGAGTTGGAG	AAAGAACAAG	AGAAGGTAAT	GACCTTTACT	100
10	ATGAAATGAA	AGAATCTGGT	GTTATAAATA	AAACAGCACT	AGTATTTGGT	150
	CAAATGAATG	AGCCACCTGG	AGCAAGAATG	AGAGTTGCTC	TTACAGGACT	200
	TACTATGGCA	GAATATTTCA	GGGATCAAGG	ACAAAACGTA	CTTTTATTCA	250
	TAGACAACAT	ATTTAGATTTC	ACTCAAGCAG	G TTCAGAGGT	GTCAGCTTTA	300
	CTTGGAAGAA	TACCTAGTGC	CGTTGGATAC	CAACCAACAC	TAGCAACAGA	350
15	AATGGGTGCG	CTTCAAGAAA	GAATAACATC	TACAAAGCAT	GGTTCTATAA	400
	CATCA					405

20 2) INFORMATION FOR SEQ ID NO: 765

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 393 bases
 (B) TYPE: Nucleic acid
 25 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

30 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Clostridium botulinum*
 (B) STRAIN: 20:3.1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 765

35	AATTAATAAA	TAACATAGCT	AAAGAACATG	GTGGATTATC	AGTGTTTACT	50
	GGAGTTGGAG	AAAGATCTAG	AGAAGGTAAT	GATCTTTATC	ATGAAATGAG	100
	AGAATCAGGC	GTTATAGATA	AAACCGCATT	AGTATTTGGT	CAAATGAATG	150
	AGCCACCTGG	TGCTAGAATG	AGAGTTGCAT	TAACAGGGTT	AACTATGGCT	200
40	GAATATTTTA	GAGATAAAGG	TCAAGATGTA	TTACTATTTA	TAGATAATAT	250
	ATTTAGATTT	ACTCAAGCTG	GATCAGAAGT	TTCAGCATTA	CTTGGAAGAA	300
	TACCATCAGC	AGTTGGTTAC	CAACCAACTT	TAGCAACTGA	AATGGGTGCA	350
	CTTCAAGAGA	GAATTACATC	AACTAAGAAT	GGTTCTATAA	CAT	393

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2) INFORMATION FOR SEQ ID NO: 766

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 399 bases
 50 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

55 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Clostridium histolyticum*
 60 (B) STRAIN: ATCC 19401

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 766

	AGGA	ACTTAT	AAATAATATT	GCAAAACAAT	ATGGAGGTCT	ATCTGTATTT	50
	ACAGGTGTTG	GTGAAAGAAC	AAGAGAAGGT	AATGACCTAT	ATAATGAAAT		100
5	GAAAGATTCT	GGGGTTATAG	AGAAAACGTC	ACTAGTATTT	GGACAGATGA		150
	ATGAACCACC	AGGAGCGAGA	ATGAGAGTAG	CATTGACAGG	ACTTACTATG		200
	GCAGAATATT	TTAGAGATCA	AGGGCAAGAT	GTACTTTTAT	TTATAGATAA		250
	TATATTTAGA	TTTACGCAGG	CTGGTTCTGA	AGTTTCTGCA	TTGTTAGGAA		300
	GAATTCCAAG	TGCAGTTGGA	TATCAACCAA	CCCTTGCAAC	TGAAATGGGT		350
10	GCATTACAAG	AAAGAATAAC	ATCCACAAAA	AATGGATCAA	TTACTTCAG		399

2) INFORMATION FOR SEQ ID NO: 767

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 390 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 20 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 25 (A) ORGANISM: *Peptostreptococcus prevotii*
 (B) STRAIN: ATCC 9321

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 767

30	CATGATGGAA	CTGATCCGTA	ACATCGCCAT	CGAGCACAGC	GGTTATTCCG	50
	TGTTCCGCCG	TGTGGGTGAG	CGTACTCGTG	AGGGTAACGA	CTTCTACCAC	100
	GAGATGAAGG	ACTCCAACGT	TCTGGACAAA	GTGGCACTGG	TCTACGGTCA	150
	GATGAACGAG	CCGCCGGGTA	ACCGTCTGCG	CGTAGCACTG	ACTGGCCTGA	200
	CCATGGCCGA	GAAGTTCCGT	GACGAAGGTA	ACGACGTTCT	GTTGTTCTGTC	250
35	GACAACATCT	ACCGTTACAC	CCTGGCCGGT	ACTGAAGTAT	CCGCACTGCT	300
	GGGCCGTATG	CCTTCGGCAG	TAGGTTACCA	GCCGACCCTG	GCTGAAGAGA	350
	TGGGCGTTCT	GCAAGAACGT	ATCACTTCGA	CCAAGGAAGG		390

40

2) INFORMATION FOR SEQ ID NO: 768

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 953 bases
 45 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

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(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Absidia corymbifera*
 (B) STRAIN: ATCC 46775

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 768

	AGGTCTTGTT	CGTGGCAAAA	GGTCATTGAC	ACTGGTGCTC	CTATCACCAT	50
	TCCTGTTGGT	AACGAAGTCC	TTGGTCGTAT	CATTAACTGC	ATTGGTGAGC	100
	CCATTGATGA	GCGTGGTCCY	ATCAAGTCCA	AGGCCACTCG	TGCTATCCAC	150
60	GCTGATGCTC	CCGAGTTTCGT	TGATCAATCC	CCCACTCCCG	AGATTCTCGA	200

	GACTGGTATC	AAGGTTGTCTG	ATTTGCTTGC	TCCCTATGCT	CGTGGTGGTA	250
	AGATTGGTCT	TTTCGGTGGT	GCCGGTGTCTG	GCAAGACTGT	CTTGATTCAA	300
	GAATTGATCA	ACAACATTGC	CAAGGCTCAC	GGTGGTTACT	CTATCTTCTG	350
	TGGTGTCTGGT	GAACGTACTC	GTGAAGGCAA	CGATTTGTAC	CACGAAATGA	400
5	TTTCCACTGG	TGTCATCAAG	CTTGAAGGTG	AATCCAAGTG	TGCTCTTGTC	450
	TTTGGTCAAA	TGAACGAACC	CCCCGGAGCT	CGTGCCCGTG	TTGCCTTGAC	500
	TGGTTTGACC	ATTGCCGAAT	ACTTCCGTGA	TGAGGAAGGT	CAAGATGTGT	550
	TGCTCTTCAT	TGACAACATT	TTCCGTTTCA	CTCAAGCCGG	TTCTGAAGTG	600
	TCCGCTTTGC	TTGGTCGTAT	TCCCTCTGCT	GTCGGTTACC	AACCCACTCT	650
10	YTCCACTGAT	ATGGGTGGTA	TGCAAGAGCG	TATTACTACC	ACCAAGAACG	700
	GTTCCATTAC	CTCCGTGCAA	GCTGTCTACG	TCCCTGCTGA	CGATTTGACT	750
	GATCCTGCTC	CTGCTACTAC	TTTTGCTCAC	TTGGACGCCA	CCACTGTGTT	800
	GTCTCGTTCC	ATTGCTGAGT	TGGGTATCTA	CCCTGCTGTC	GATCCCCTTG	850
	ACTCCAAGTC	CCGTATCTTG	GATCCCCGTA	TCGTTGGTGA	TGAGCACTAC	900
15	TCTGTTGCCA	CTGGTGTCCA	ACAAATCCTT	CAAACTACA	AGTCGCTTCA	950
	AGA					953

20 2) INFORMATION FOR SEQ ID NO: 769

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1343 bases
 (B) TYPE: Nucleic acid
 25 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

30 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Alternaria alternata*
 (B) STRAIN: ATCC 62099

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 769

35	CGCGGTTCCA	AGGCCACCGA	CACCGGTGCC	CCCATCAAGA	TTCCCGTTGG	50
	TCACGGTACC	CTTGGTCGTA	TCATGAACGT	CACTGGTGAC	CCCATTGACG	100
	AGCGTGGTCC	CATCAAGGCC	ACCAAGTACG	CTCCCATCCA	CGCCGACCCC	150
	CCGGAGTTCA	CCGAGCAATC	CACCTCCGCT	GAGGTCCTCG	TTACCGGTAT	200
40	CAAGGTTGTC	GACCTGTTGG	CTCCTTACGC	TCGTGGTGGA	AAGATTGGTC	250
	TCTTCGGAGG	TGCTGGTGTC	GGAAAGACTG	TCTTCATTCA	GGAGCTGATT	300
	GTAAGGAGAC	ACACTGTCTA	CTGGCTGAGC	ATTAGCTAAC	GGCAGGCAGA	350
	ACAACATCGC	CAAGGCCAC	GGTGGTTTCT	CTGTCTTCAC	TGGTGTCTGGT	400
	GAGCGTACCC	GTGAGGGTAA	CGATCTGTAC	CACGAGATGC	AGGAGACTTC	450
45	CGTCATTAG	CTTGACGGTG	ACTCCAAGGT	CGCCCTCGTC	TTCGGTCAGA	500
	TGAACGAGCC	CCCGGGTGCC	CGTGCCCGTG	TCGCTCTTAC	TGGTCTTACT	550
	GTTGCTGAGT	AAGTCTTGAA	TTCATCTGTG	TGACAACGTC	GTGGCTAATG	600
	GGAAAAAGA	TACTTCCGTG	ACGAAGAGGG	ACAGGATGTG	CTTCTCTTCA	650
	TCGACAGTAA	GTGCTTGTA	GAAGTGCCTG	TGAGACATAC	ACTGACTTCG	700
50	GCAATAGACA	TTTTCCGTTT	CACCCAGGCC	GGTTCCGAGG	TGTCCGCTCT	750
	TCTTGGTCGT	ATCCCCCTCTG	CCGTCGGTTA	CCAGCCCACC	CTCGCCATTG	800
	ACATGGGTGT	CATGCAGGAG	CGTATTACCA	CCACCACCAA	GGGTTCACATC	850
	ACCTCCGTCC	AGGCCGTCTA	CGTGCCCGCT	GACGATTGTA	CTGACCCTGC	900
	CCCCGCCACC	ACCTTCGCCC	ATTTGGACGC	CACCACTGTC	TTGTCCCGTG	950
55	GTATCTCCGA	GTTGGGTATC	TACCCCGCCG	TCGACCCTCT	TGACTCCAAG	1000
	TCCCGTATGT	TGGACCCCGG	TGTCATTGGT	CAGGACCACT	ACGACACCGC	1050
	CACCCGCGTT	CAGCAGATTC	TCCAGGAGTA	CAAGTCGCTC	CAGGATATCA	1100
	TTGCCATTCT	CGGTATGGAC	GAGTTGTCTG	AAGCTGACAA	GCTTACCGTC	1150
	GAGCGTGCCC	GTAAGATCCA	GCGTTTCTTG	AGCCAGCCTT	TCGCTGTCTGC	1200
60	CCAGGTCTTC	ACTGGTATTG	AGGGCAAGCT	TGTCGACCTC	AAGGACACCA	1250

TCCGATCATT CAAGGCTATC TTGACTGGTG AGGGTGACGA CCTTCCCAG 1300
GGTGAGTCTC GACTATCTCC GCATTCATAG CGTATAACTG ACA 1343

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2) INFORMATION FOR SEQ ID NO: 770

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 480 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Aspergillus flavus*
(B) STRAIN: ATCC 26947

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 770

TTCAGGAGTT GATTGTATGT TCACCTGCAA CATAAGACTT CCCATTCTCC 50
ACTCTTTTCT AACTCTTCAC AGAACAACAT TGCCAAGGCT CACGGTGGTT 100
ACTCTGTCTT CACTGGTGTC GGTGAGCGTA CCCGTGAGGG TAACGATCTG 150
25 TACCACGAAA TGCAGGAGAC TGGTGTTCATT CAGCTCGAGG GTGAATCTAA 200
GGTCGCCCTT GTCTTCGGTC AGATGAACGA GCCCCCAGGT GCCCGTGCCC 250
GTGTCGCCCT TACCGGTCTG ACCATCGCCG AGTACTTCCG TGACGAGGAA 300
GGTCAGGATG TGCTGCTCTT CATTGACAAC ATTTTCCGTT TCACCCAGGC 350
CGGTTCTGAG GTGTCTGCCC TTCTTGGTCG TATCCCCTCC GCTGTCGGTT 400
30 ACCAGCCAC TCTGGCCGTC GACATGGGTG GTATGCAGGA GCGTATTACC 450
ACCACCACCA AGGGTTCCAT TACCTCCGTC 480

35 2) INFORMATION FOR SEQ ID NO: 771

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1174 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Mucor circinelloides*
(B) STRAIN: ATCC 38592

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 771

50 CTCGAACAAG AYAAGTTGCC YGCCATTTTG AACGCCCTTG AAGTCAAGGA 50
YACTCTGGT GGACGTCTCG TYCTCGAAGT CTCTCAACAT TTGGGTGAGA 100
AACTGTCCG TACTATTGCT ATGGATGGTA CTGAAGGTAA GTTATGTYCA 150
TCCCANNGGA TACAGTCARA CAGMAATGTC TAGTGGTTAT AGCAGYAGCA 200
55 GATGATTGAC CAATATGTTA GGTCTTGTC GGTGGTCAA AGGTGTTGA 250
CACTGGTGCT CCCATTACCA TCCCCGTTGG TAAGGAAGTC CTTGGTCGTA 300
TCATCAACGT TATTGGTGAA CCCATTGATG AACGTGGTCC CATTGACGCC 350
AAGACTCACC GTCCTATTCA CGCTGAAGCT CCCGAATTCTG TTGATCAATC 400
CCCCACTCCC GAAATCCTCG AGACTGGTAT CAAGGTYGTC GATTGTTGG 450
60 CTCCTTATGC TCGTGGTGGT AAGATTGGTC TCTTCGGTGG TGCTGGTGTC 500

	GGTAAGACTG	TCTTGATTCA	AGAATTGATT	AACAACATYG	CCAAGGCTCA	550
	CGGTGGTTAC	TCTATCTTCT	GTGGTGTCGG	TGAACGTACT	CGTGAGGGTA	600
	ACGATTTGTA	CCATGAAATG	ATTGAAACCG	GTGTCATTCA	ATTGGAAGGC	650
	GAGTCCAAGT	GTGCTCTCGT	CTTTGGTCAA	ATGAACGAAC	CCCCAGGTGC	700
5	TCGTGCCCCG	GTCGCTTTGA	CTGGTTTGAC	TATTGCTGAA	TACTTCCGTG	750
	ATGATGAGGG	TCAAGATGTC	TTGCTTTTCA	TTGATAACAT	TTTCAGATTG	800
	ACTCAAGCTG	GTTCTGAGGT	ATCTGCCCTT	TTGGGTCGTA	TTCTTCCGC	850
	TGTCGGTTAC	CAACCCACTC	TTTCCACYGA	TATGGGTGGT	ATGCAAGAGC	900
	GTATTACTAC	CACCAAGAAC	GGTTCATTG	CCTCCGTCCA	AGCTGTCTAC	950
10	GTCCCTGCTG	ATGATTTGAC	CGATCCTGCT	CCTGCCACCA	CTTTTGCTCA	1000
	CTTGGATGCC	ACCACTGTCT	TGTCTCGTTC	CATCGCTGAA	TTGGGTATCT	1050
	AYCCCGCTGT	CGATCCTCTT	GATTCCAAGT	CTCGTATCCT	CGATCCCCGT	1100
	ATTGTCGGTG	ATGAGCACTA	CAAGGTTGCC	ACTGAAGTTC	AACAAATCCT	1150
	CCAAACTAC	AAGTCTCTCC	AAGA			1174

2) INFORMATION FOR SEQ ID NO: 772

20 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 467 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

25

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Piedraia hortai*
- (B) STRAIN: ATCC 24292

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 772

	AGGAGCTTAT	CAACAACATC	GCCAAGGCTC	ACGGTGGTTA	CTCCGTCTTC	50
35	ACTGGTGTGCG	GTGAGCGTAC	TCGTGAGGGT	AACGATTTGT	ACCACGAGAT	100
	GCAAGAGACT	TCCGTCAATC	AGCTTGACSG	CGAGTCCAAG	GTCGCTCTCG	150
	TGTTGCGTCA	GATGAACGAG	CCCCCGGGTG	CCCGTGCCCCG	TGTTGCCCTG	200
	ACTGGTCTTA	CCATCGCTGA	GTACTTCCGT	GATGCCGAGG	GTCAGGATGG	250
	TAAGTTCTAT	AACTCTTGTC	GCAAAGGTTT	CATTCTGGTC	GCTAACTTGC	300
40	TCAGTGCTCC	TGTTCAATCGA	CAACATTTTC	CGTTTCACCC	AGGCTGGTAT	350
	GGAGGTGTCT	GCCCTCCTCG	GTCGTATTCC	TTCTGCCGTC	GGTTACCAAC	400
	CTACTCTCGC	CGTCGACATG	GGTGGTATGC	AAGAGCGTAT	TACCACTACC	450
	AAGAAGGGAT	CCATTAC				467

45

2) INFORMATION FOR SEQ ID NO: 773

50 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 578 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

55 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Pseudallescheria boydii*
- (B) STRAIN: ATCC 44331

60

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 773

	TTGCCAAGGC	CCACGGTGGT	TACTCTGTCT	TCACTGGTGT	CGGTGAGCGT	50
	ACCCGTGAGG	GTAACGATCT	GTACCACGAA	ATGCAGGAAA	CCTCCGTCAT	100
5	TCAGCTTGAT	GGCGAGTCCA	AGGTCGCGCT	TGTCTTCGGT	CAGATGAACG	150
	AGCCCCCTGG	TGCCCGTGCT	CGTGTCGCTC	TTACTGGTCT	TACCGTTGCC	200
	GAGTACTTCC	GTGATGAGGA	GGGTCAGGAT	GGTAAGTTAT	ATCGTTTTTA	250
	TTATCTTCTT	TGCCACCACC	CCTCTACGAA	TCCATGCCTC	CGTTGGTGAA	300
	GGCATCGTTT	GTAGGGCGGG	TCCGAGTTTG	CGGCAATTTT	TGCCGTCGGC	350
10	TTGAAGCCGC	GGATGCCCCG	TGTTTGACGC	GTATCGATGC	TAACAACAAT	400
	GACAACAGTG	CTTCTCTTCA	TTGACAACAT	TTTCCGATTG	ACCCAGGCCG	450
	GTTCCGAGGT	GTCTGCCCTT	CTCGGTCGTA	TTCCCTCTGC	CGTCGGTTAC	500
	CAGCCCACTC	TTGCCGTAGA	CATGGGTGCC	ATGCAGGAAC	GTATTACCAC	550
	CACCAAGAAG	GGTTCGATTA	CCTCCGTC			578

15

2) INFORMATION FOR SEQ ID NO: 774

20 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1123 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

25

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Rhizopus oryzae*
 (B) STRAIN: ATCC 56015

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 774

	AACTTACCYG	CTATCTTGAA	CGCTCTCGAA	GTCCAAGATC	ACTCTGGTGG	50
35	ACGTCTTGTC	CTTGAAGTTC	GCTCAACACT	TGGGTGAAAA	TACTGTCCGT	100
	ACTATTGCTA	TGGATGGTAC	TGAAGGTAAG	CTATACTATA	ACCGTKTTAT	150
	CCGAGTATGA	TATTAAGTTG	AAAAAAGGTC	TCGTTCGTGG	TCAAAAGGTT	200
	ATTGACACTG	GTGCTCCCAT	TACCAATCCT	GTYGTAAGG	AAGTTCTCGG	250
	TCGTATCATG	AACGTCATTG	GTGAACCCAT	CGATGAACGT	GGTCCTATCA	300
40	ACGCCAAGAG	CCAACGTCCC	ATTACGCGCG	AAGCTCCCGA	ATTCGTTGAC	350
	CAATCTCCTA	CTCCCGAAAT	TCTTGAAACT	GGTATCAAGG	TTGTCGACTT	400
	GTTGGCTCCT	TATGCTCGTG	GTGGTAAGAT	TGGTCTTTTC	GGTGGTGCTG	450
	GTGTCGGTAA	GACTGTGTTG	ATTCAAGAAT	TGATTAACAA	CATCGCCAAG	500
	GCTCACGGTG	GTTACTCTAT	TTTCTGTGGT	GTCGGTGAAC	GTACTCGTGA	550
45	AGGTAACGAT	CTTTACCACG	AAATGATTGA	AACTGGTGTC	ATCAAGCTCG	600
	ATGGTGAATC	CAAGTGTGCT	CTTGTCTTTG	GTCAAATGAA	CGAACCCCCA	650
	GGAGCTCGTG	CCCGTGTGTC	CTTGACTGGT	TTGACCATTG	CTGAATACTT	700
	CCGTGATGAT	GAAGGTCAAG	ATGTGTTGCT	TTTCATTGAT	AACATTTTCC	750
	GTTTCACCCA	AGCTGGTTCW	GAAGTATCTG	CCCTTTTGGG	TCGTATTCCC	800
50	TCCGCTGTGC	GTTACCAACC	CACTCTTTCT	ACTGATATGG	GTGGTATGCA	850
	AGAACGTATT	ACAACCACCA	AGAACGGTTC	CATTACATCC	GTCCAAGCTG	900
	TCTACGTCCC	TGCTGATGAT	TTGACCGATC	CTGCTCCCGC	CACCACTTTT	950
	GCTCACTTGG	ATGCCACCAC	TGTCTTGTCT	CGTTCCATTG	CCGAATTGGG	1000
	TATTTACCCT	GCCGTCGATC	CTCTTGAYTC	CAAGTCTCGT	ATCTTGGATC	1050
55	CTCGTATCGT	TGGTGACGAA	CACTACAAGG	TCGCTACCGA	AGTTCAACAA	1100
	ATCCTTCAAA	ACTACAAGTC	TCT			1123

60 2) INFORMATION FOR SEQ ID NO: 775

441

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 477 bases
 (B) TYPE: Nucleic acid
 5 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

10 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Scopulariopsis koningii*
 (B) STRAIN: ATCC 38745

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 775

15 ATTCAAGGAGC TCATCAACAA CATTGCCAAG GCTCACGGTG GTTACTCTGT 50
 GTTCACTGGT GTCGGTGAGC GTACCCGTGA GGGTAACGAT CTGTACCACG 100
 AAATGCAGGA GACTTCGGTC ATTCAAGCTCG AGGGCGAGTC CAAGGTCGCG 150
 CTTGTGTTCG GTCAGATGAA CGAGCCCCC GGTGCCCCGTG CCCGTGTTCG 200
 20 CCTTACCGGT CTGACCGTTG CCGAGTACTT CCGTGACGAG GAGGGCCAGG 250
 ATGGTGAGTA ACCGACGAAG TCTGAGATCT TGTCGGGCAT TATTCTAACG 300
 ACAACTAGTG CTTCTCTTCA TCGACAACAT TTTCCGCTTC ACCCAGGCCG 350
 GTTCCGAGGT GTCCGCGCTT CTCGGCCGTA TCCCCTCTGC CGTCGGTTAC 400
 CAGCCCACCC TGGCCGTCGA CATGGGAGGT ATGCAGGAGC GTATTACCAC 450
 25 GACTCAGAAG GGCTCGATTA CCTCGGT 477

2) INFORMATION FOR SEQ ID NO: 776

30 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 610 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 35 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 40 (A) ORGANISM: *Trichophyton mentagrophytes*
 (B) STRAIN: ATCC 8125

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 776

45 TCCGGAGTTG ATTGTAAGTC ATTTGAAACC CAGCCCCAAG AACAGAAGC 50
 TAGGCGAAAA TTGGACAATT GAGCAATTTA GCCATTGGAG AAAAGAAATT 100
 TCGAGTATTA ATTGTTTTTA TAGAACAACA TTGCCAAGGC TCACGGTGGT 150
 TACTCTGTCT TCACTGGTGT CGGAGAGCGT ACCCGTGAAG GAAACGATCT 200
 CTACCATGAA ATGCAGGAGA CCCGTGTCAT TCAGCTTGAT GGCGAGTCCA 250
 50 AGGTCGCCCC TGTCTTCGGC CAGATGAACG AGCCCCCAGG TGCCCGTGCC 300
 CGTGTGCTC TTAAGTGGTT GACCATTGCT GAGTACTTCC GTGATGAGGA 350
 AGGTCAAGAC GGTGAGTTTY TTATGGATAA AARATTTTTT TTTTTTTTTT 400
 TTTTTTMAAR AAATTCATGT TCTAACAAAG TATATCCTAG TGCTTCTCTT 450
 CATCGACAAC ATTTTCCGTT TCACTCAGGC TGGTTCCGAA GTGTCTGCCC 500
 55 TGCTTGGTCG TATCCCATCT GCCGTCCGTT ACCAACCAC TCTTGCCGTC 550
 GACATGGGTG GTATGCAGGA ACGTATTACC ACCACCAAGA AGGGATCCAT 600
 TACCTCCGTC 610

60

2) INFORMATION FOR SEQ ID NO: 777

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 593 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

10 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Trichophyton tonsurans*
(B) STRAIN: ATCC 56185

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 777

GGAGTTGATT GTAAGTCATT TGAAACCCAG CCCCAGAGAA CAGAAGCTAG 50
GTGAAAATTG GACAATTGAA CAATTTAGCC CTTGGAGAAA AGAAATTTTCG 100
AGTATTAATT ATTTTATAG AACACATTG CCAAGGCTCA CCGTG GTTAC 150
20 TCTGTCTTCA CTGGTGTCTG AGAGCGTACC CGTGAAGGAA ACGATCTCTA 200
CCATGAAATG CAGGAGACCC GTGTCATTCA GCTTGATGGC GAGTCCAAGG 250
TCGCCCTGGT CTTCCGCCAG ATGAACGAGC CCCCAGGTGC CCGTGCCCGT 300
GTTGCTCTTA CTGGTTTGAC CATTGCTGAG TACTTCCGTG ATGAGGAAGG 350
TCAAGACGGT GAGTTTCTTA TGGATGAAAG ATTTTTTTTT TTCAAGAAAT 400
25 TCATGTTCTA ACAAAGTGTA TTCTAGTGCT TCTCTTCATC GACAACATTT 450
TCCGTTTCAC TCAGGCTGGT TCCGAAGTGT CTGCCCTGCT TGGTCGTATC 500
CCATCTGCCG TCGGTTACCA ACCCACTCTT GCCGTCGACA TGGGTGGTAT 550
GCAGGAACGT ATTACCACCA CCAAGAAGGG ATCCATTACC TCC 593

30

2) INFORMATION FOR SEQ ID NO: 778

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 1141 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

40 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Trichosporon cutaneum*
(B) STRAIN: ATCC 62965

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 778

CCGTGGTCAA GAAGTTATTG AACTGGTGC CCAATTACC ATTCCTGTTG 50
GTCGTGGTAC TCTTGGTAGA ATTATCAACG TCATTGGTGA ACCAATTGAC 100
50 GAACGTGGCC CTATCAAGGC TTCTAAGTAT GCTCCTATCC ATACTGAACC 150
ACCAACCTTT GCTGAACAAT CTACTTCTGC TGAAGTTCTT GAAACCGGTA 200
TCAAGGTTGT CGATCTTCTT GCTCCTTACG CCCGTGGTGG TAAGATTGGT 250
CTTTTCGGTG GTGCTGGTGT CGGTAAGACT GTCTTCATTC AAGAACTTAT 300
TAACAACATT GCCAAGGCTC ACGGTGGTTT CTCTGTCTTC ACTGGTGTCTG 350
55 GTGAAAGAAC CCGTGAAGGT AACGATCTTT ACCGTGAAAT GAAGGAAACT 400
GGTGTTCATCA ACCTCGAAGG TGAATCCAAG GTCGCTCTCG TTTTCGGTCA 450
AATGAACGAA CCTCCAGGTG CCCGTGCCCG TGTCGCTTTG ACTGGTCTTA 500
CCATTGCCGA ATACTTCCGT GATGAAGAAG GACAAGATGT CTTGCTTTTC 550
GTTGACAACA TTTTCAGATT CACCCAAGCC GGTCTCTGAAG TCTCTGCTCT 600
60 TTTGGGTCTG ATTCCATCTG CCGTCGGTTA CCAACCTACC CTTGCTACCG 650

	ATATGGGTGC	CCTCCAAGAA	CGTATTACCA	CCACCCAAAA	GGGTTCGTC	700✓
	ACATCTGTCC	AAGCCGTCTA	TGTCCCAGCA	GACGATTGGA	CTGATCCTGC	750
	CCCAGCCACC	ACTTTCGCTC	ACTTGGACGC	CACCACTGTC	TTGTCTCGTT	800
	CCATTTCCGA	ATTGGGTATC	TACCCAGCTG	TCGATCCTCT	CGATTCCAAG	850
5	TCTCGTCTTT	TGGATCCTGA	AGTTATTGGA	CACGAACACT	ACGAAGTTGC	900
	CACTCAAGTT	CAACAAACCC	TCCAAGCTTA	CAAGTCTCTC	CAAGATATCA	950
	TTGCCATTTT	GGGTATGGAT	GAATTGTCTG	AAGCTGATAA	GCTTACTGTC	1000
	GAACGTGCCC	GTAAGATCCA	AAGATTCCTT	TCCCAACCAT	TCGCTGTTGC	1050
	CGAAGTTTTT	ACTGGTATCG	AAGGTCGTCT	CGTTCCATTG	AAGGAAACCG	1100
10	TCAGATCTTT	CAAGGAAATC	CTTGAAGGTA	AGTACGATCA	C	1141

2) INFORMATION FOR SEQ ID NO: 779

15

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1093 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

25

- (A) ORGANISM: *Cladophialophora carrionii*
 (B) STRAIN: ATCC 22864

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 779

30	GCTGAAGGCC	GAACGTGAGC	GTGGTATCAC	CATCGATATC	GCGCTCTGGA	50
	AGTTCGAGAC	TCCCAAGTAC	TTCGTCACCG	TCATCGATGC	CCCTGGTCAT	100
	CGTGACTTCA	TCAAGAACAT	GATCACTGGT	ACCTCCCAGG	CTGATTGTGC	150
	TATTCTCATC	ATTGCCGCTG	GTACTGGTGA	GTTCGAGGCC	GGTATCTCCA	200
	AGGATGGCCA	GACCCGTGAG	CATGCTCTGC	TCGCCTACAC	CCTGGGCGTG	250
35	AAGCAGCTTA	TCGTCGCCAT	CAACAAGATG	GACACCACCA	AATGGTCTGA	300
	GGATCGTTTC	AACGAAATCA	TCAAGGAGAC	TTCCAACCTC	ATCAAGAAGG	350
	TCGGATACAA	CCCCAAGTCC	GTTCCATTCT	TGCCCCATCT	CGGCTTCAAC	400
	GGTGACAACA	TGATCGACGT	CTCCACCAAT	GCCCCCTGGT	ACAAGGGCTG	450
	GGAAAAGGAG	TCCAAGGCTG	GCAAGGCCAC	CGGCAAGACC	CTCCTTGAGG	500
40	CTATCGACTC	CATCGACCCT	CCTGCTCGTC	CCACCGACAA	GCCTCTCCGT	550
	CTCCCACTCC	AGGATGTCTA	CAAGATTTCT	GGTATCGGCA	CGGTGCCCCGT	600
	CGGTCGTGTT	GAGACTGGTA	CCATCAAGGC	CGGTATGGTC	GTCACCTTTG	650
	CCCCCGCCAA	CGTCACCACT	GAAGTCAAGT	CCGTCGAAAT	GCACCACGAA	700
	CAGCTCGCCG	AGGGCGTTCC	GGGTGACAAC	GTCGGCTTCA	ACGTCAAGAA	750
45	CGTCTCCGTG	AAGGAGGTTC	GTCGTGGAAA	CGTTGCTGGT	GACTCCAAGA	800
	ACGACCCCCC	CAAGGGTGCC	GACTCCTTCA	ACGCCCAGGT	CATCGTCCTC	850
	AACCACCTTG	GTCAGGTCGG	TGCTGGCTAC	GCCCCGGTCT	TGGATTGCCA	900
	CACTGCCCAC	ATTGCCTGCA	AGTTCTCTGA	GCTCCTCGAG	AAGATCGATC	950
	GTCGTACCGG	CAAGTCCATG	GAAAACAACC	CCAAGTTCAT	CAAGTCTGGT	1000
50	GATGCTGCCA	TCGTGAAGAT	GGTTCCCAGC	AAGCCTATGT	GCGTTGAGGC	1050
	TTTCACCGAC	TACCCTCCTC	TTGGTCGTTT	CGCCGTCCGT	GAC	1093

55 2) INFORMATION FOR SEQ ID NO: 780

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 752 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double

60

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

5 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Cunninghamella bertholletiae*

(B) STRAIN: ATCC 42115

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 780

10

TACTTGTA	AAA	TGGTCTCAAG	ATCGTTACAA	CGAAATTGTT	AAGGAAGTTT	50
CTTCCTTCAT	CAAGAAGATT	GGTTACAATC	CTAAATCCGT	TCCTTTCGTY	100	
CCTATCTCTG	GTTGGCACGG	TGATAACATG	TTGGAAGCTT	CTACCAACAT	150	
GCCTTGGTAC	AAGGGATGGA	CCAAGGAAAC	TAAAGCTGGT	TCTTCCACTG	200	
15	GTAAGACTCT	CTTAGAAGCC	ATTGACAGCA	TTGAACCTCC	TACCCGTCCT	250
TCTGACAAGC	CTTTACGTCT	TCCTTTACAA	GATGTTTACA	AGATTGGTGG	300	
TATTGGTACT	GTCCCTGTTG	GTCGTGTTGA	AACTGGTGTC	ATCAAGGCTG	350	
GTATGGTTGT	TACYTTCGCT	CCCGCTAACG	TCACCACTGA	AGTTAAGTCC	400	
GTTGAAATGC	ATCACGAACA	ATTAGAACAA	GGTGTTCCCTG	GTGACAACGT	450	
20	TGGTTTCAAC	GTCAAGAACG	TTTCCGTTAA	GGATATCCGT	CGTGGTAACG	500
TCTGTTCCGA	CTCCAAGAAC	GACCCCGCTA	AGGAATCTGC	TTCCCTTCAAC	550	
GCTCAAGTTA	TCGTCTTGAA	CCACCCTGGT	CAAATTGGTG	CTGGTTATGC	600	
CCCAGTTCTT	GACTGTCACA	CTGCTCACAT	TGCTTGTAAG	TTCGCTGAAT	650	
TATTAGAAAA	GATCGATCGT	CGTTCCGGTA	AGAAACTCGA	AGATGCTCCT	700	
25	AAATTGCTTA	AATCTGGTGA	CTCTGCTATC	GTTAAGATGG	TTCCTTCCAA	750
GC					752	

30 2) INFORMATION FOR SEQ ID NO: 781

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 728 bases

(B) TYPE: Nucleic acid

35 (C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

40 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Curvularia lunata*

(B) STRAIN: ATCC 26425

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 781

45

CAAGTGGTCT	GAGGACCGTT	ACCAGGAAAT	CATCAAGGAG	ACCTCCAAC	50	
TCATCAAGAA	GGTCGGCTAC	AACCCCAAGC	ACGTTCCCTT	CGTCCCCATC	100	
TCCGGTTTCA	ACGGAGACAA	CATGATTGAG	GCCTCCACCA	ACTGCCCTG	150	
GTACAAGGGT	TGGGAGAAGG	AGACCAAGGC	CAAGGCCACT	GGTAAGACCC	200	
50	TCCTTGAGGC	CATCGACGCC	ATCGACCCTC	CTGTCCGTCC	TACCGACAAG	250
CCCCTCCGCC	TTCCCCTCCA	GGATGTTTAC	AAGATTGGTG	GTATTGGCAC	300	
GGTCCCCGTC	GGTCGTGTCG	AGACCGGTAT	CATCAAGCCC	GGTATGGTGC	350	
TCACCTTCGC	CCCCGCTGGT	GTCACCACCG	AAGTCAAGTC	CGTCGAGATG	400	
CACCACGAGC	AGCTTACTGA	GGGTGTCCCC	GGTGACAACG	TCGGCTTCAA	450	
55	CGTCAAGAAC	GTCTCCGTCA	AGGAGATCCG	TCGTGGTAAC	GTTGCCGGTG	500
ACTCCAAGAA	CGACCCCCC	AAGGGTTGCG	AGTCCTTCAA	CGCCCAGGTC	550	
ATCGTCCTCA	ACCACCCTGG	TCAGGTCGGT	GCCGGTTACG	CCCCAGTCCT	600	
TGACTGCCAC	ACTGCCCA	TTGCCTGCAA	GTTCTCCGAG	CTCCTCGAGA	650	
AGATCGACCG	CCGTACCGGA	AAGTCTGTTG	AGAACTCCCC	CAAGTTCATC	700	
60	AAGTCCGGTG	ACGCCGCCAT	CGTCAAGA		728	

2) INFORMATION FOR SEQ ID NO: 782

5

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1145 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

10

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Fonsecaea pedrosoi*
 (B) STRAIN: ATCC 18831

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 782

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20 TGAAGTCCGA GCGTGAGCGT GGTATCACCA TCGATATCGC CCTCTGGAAG      50
   TTCGAGACTC CCAAGTAAGG CTCAACAGAC ACAACAAGCA AATGCATACT      100
   CGCTAACCTA TTCACCCACC ACAGGTACAA CGTCACCGTC ATTGACGCCC      150
   CCGGTCACCG TGATTTTCATC AAGAACATGA TCACTGGTAC CTCCCAGGCT      200
   GACTGCGCCA TTCTCATCAT TGCCGCCGGT ACTGGTGAGT TCGAGGCCGG      250
25 TATCTCCAAG GACGGTCAGA CCCGTGAGCA CGCTCTTCTC GCCTACACCC      300
   TTGGTGTCAA GCAGCTCATC GTTGCCATCA ACAAGATGGA CACCACCAAG      350
   TGGTCTGAGG CCCGTTACCA GGAGATCATC AAGGAGACCT CCGGTTTCAT      400
   CAAGAAGGTC GGCTTCAACC CCAAGCACGT TCCCTTCGTG CCCATCTCCG      450
   GTTTCAACGG TGACAACATG ATCGACGTCT CCACCAACTG CCCCTGGTAC      500
30 AAGGGTTGGG AGAAGGAGAC CAAGGCCAAG GCCACCGGCA AGACCCTCCT      550
   CGAGGCCATT GACGCCATCG ACCCCCCCAC TCGTCCCACC GACAAGCCCC      600
   TCCGTCTTCC CCTYCAGGAT GTCTACAAGA TCGGTGGTAT TGGCACGGTT      650
   CCCGTCGGTC GTGTCGAGAC CGGTACCATC AAGGCCGGCA TGGTCGTCAC      700
   CTTCCGCCCC GCTGGTGTC AACTGAGGT CAAGTCCGTC GAGATGCACC      750
35 ACCAGCAGCT TCCCCGAGGT CTCCCCGGTG ACAACGTCGG CTTCAACGTC      800
   AAGAACGTCT CCGTCAAGGA GATCCGTCGT GGCAACGTCG CCGGTGACTC      850
   CAAGAACGAC CCCCCAAGG GCTGCGACAG CTTCAACGCC CAGGTCATCG      900
   TCCTCAACCA CCCCCGTCAG GTCGGCGCCG GCTACGCGCC CGTCCTCGAC      950
   TGCCACACTG CTCACATTGC TTGCAAGTTC TCTGAGCTCC TCGAGAAGAT     1000
40 CGACCGCCGT ACCGGCAAGT CCATTGAGGC CAGCCCCAAG TTCATCAAGT     1050
   CTGGTGACGC CGCCATCGTC AAGATGGTTC CCTCCAAGCC TATGTGCGTT     1100
   GAGGCCTTCA CCGACTACCC CCCTCTTGA CGTTTCGCCG TCCGT           1145

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45

2) INFORMATION FOR SEQ ID NO: 783

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1151 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: Genomic DNA

55

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Microsporium audouinii*
 (B) STRAIN: ATCC 11347

60

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 783

	GCTCAAGGCT	GAGCGTGAGC	GTGGTATCAC	CATTGACATC	GCCCTCTGGA	50
	AGTTTCGAGAC	CCCCAAGTAC	ATGGTCACCG	TCATCGGTAT	GCTTTATCTG	100
	TTTCCCATT	ATAGTTGCGA	CAAGTAAC	ATAAAAAGTA	GATGCCCCCG	150
5	GACACCGTGA	CTTCATCAAG	AACATGATTA	CTGGTACCTC	CCAGGCCGAC	200
	TGCGCTATTC	TCATCATTGC	TGCCGGTACT	GGTGAGTTCG	AGGCTGGTAT	250
	CTCCAAGGAT	GGCCAGACTC	GTGAGCACGC	CCTGCTCGCT	TTCACCCTCG	300
	GTGTCAAGCA	GCTCATCGTT	GCCATCAACA	AGATGGACAC	CACCAACTGG	350
	TCTGAGTCCC	GTTTCGGTGA	AATCATCAAG	GAAGTCACCA	ACTTCATCAA	400
10	GAAGGTCGGC	TACGACCCCA	AGGGTGTCCC	ATTTCGTCCA	ATCTCTGGCT	450
	TCAACGGTGA	CAACATGATT	GAGCCCTCCA	CCAACTGCCC	ATGGTACAAG	500
	GGATGGAACA	AGGAGACCAA	GGCCGGTGGC	AAATCCTCTG	GTAAGACCCT	550
	CCTTGAGGCC	ATCGATGCCA	TTGACATGCC	CACTCGTCCC	ACCGACAAGC	600
	CTCTCCGTCT	CCCACTCCAG	GATGTCTACA	AGATCTCTGG	TATCGGAACA	650
15	GTACCAGTCG	GTCGTGTTGA	GACTGGTATC	ATCAAGCCTG	GTATGGTTGT	700
	CACTTTTCGCC	CCCGCCAACG	TCACCACTGA	AGTCAAGTCC	GTCGAAATGC	750
	ACCACCAGCA	GCTCGTTCAG	GGTGTTCCTG	GTGACAACGT	TGGCTTCAAC	800
	GTCAAGAACG	TCTCTGTCAA	GGAAGTCCGC	CGTGGTAACG	TTGCCGGTGA	850
	TTCCAAGAAC	GACCCACCAT	CTGGCTGCGC	CTCTTTCAAG	GCCCAGGTCA	900
20	TCGTCTCTCAA	CCACCCCGGC	CAGATCGGTG	CTGGTTACGC	CCCAGTCCTC	950
	GACTGCCACA	CTGCCACAT	TGCTTGCAAG	TTCTCTGAGC	TTCTTGAGAA	1000
	GATTGACCGC	CGTACTGGTA	AATCCGTCGA	AACCAGCCCT	AAGTTCGTCA	1050
	AGTCTGGTGA	TGCCGCTATT	GCCACCATGG	TTCCATCCAA	GCCCATGTGC	1100
	GTTGAGGCTT	TCACTGACTA	CCCACCACTT	GGTCGTTTCG	CCGTCCGTGA	1150
25	C					1151

2) INFORMATION FOR SEQ ID NO: 784

30

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 979 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

40

- (A) ORGANISM: *Mucor circinelloides*
- (B) STRAIN: ATCC 38592

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 784

45	CCAAGTGGTC	TCAAGATCGT	TACAACGAAA	TTGTCAAGGA	AGTTTCCGGT	50
	TTCATCAAGA	AGATCGGTTT	CAACCCCAAG	TCCGTTCCCTT	TCGTTCCCAT	100
	TTCTGGCTGG	CACGGTGATA	ACATGTTGGA	TGAATCCACC	AACATGCCCT	150
	GGTTCAAGGG	ATGGAACAAG	GAGACCAAGG	CCGGTTCCAA	GACTGGTAAG	200
	ACTCTCCTCG	AAGCCATCGA	TGCCATTGAG	CCCCCTGTCC	GTCCTTCTGA	250
50	CAAGCCTCTC	CGTCTTCCTC	TTCAAGATGT	CTACAAGATT	GGTGGTATTG	300
	GTACAGTTCC	CGTCGGTCGT	GTTGAAACTG	GTACTATCAA	GGCTGGTATG	350
	GTTGTCAACT	TCGCTCCCGC	TGCTGTCACC	ACTGAAGTTA	AGTCCGTTGA	400
	AATGCATCAC	GAAACCCCTCT	CTGAAGGTCT	CCCCGGTGAC	AACGTTGGTT	450
	TCAACGTCAA	GAACGTCTCC	GTCAAGGATA	TCCGTCGTGG	TAACGTCTGT	500
55	TCCGACTCCA	AGAACGATCC	CGCTAAGGAA	TCTGCCTCTT	TCACTGCTCA	550
	AGTTATTATC	TTGAACCATC	CCGGTCAAAT	CTCTGCTGGT	TACGCACCAG	600
	TTCTCGATTG	TCACACTGCT	CACATCGCCT	GTAAGTTCTC	TGAATCATT	650
	GAGAAGATTG	ATCGTCGTTC	CGGTAAGTAC	CTGCATCTGT	CAGAATTGAA	700
	GGTCCGCCGT	TATAGCAAAG	GCTGGGTTTA	AATGTTGGGG	TTTGTCTGAT	750
60	CTATAATGAT	GATTGCTCCT	TCAATTTTGG	ACATAATTGG	ATGATCTGAA	800

TTGTGTTGCT	AACGTCGCAT	TTGCTTCTTT	TGCTTCTTTT	GCATGTA ⁵ GGT	850
AAGAAGATGG	AAGATGCTCC	CAAAGTAAGT	ATTACGATTG	ATGGACAATT	900
AAAATAGAAT	ACTAACAATT	ATTGTTTATA	GTTCGTCAAG	TCTGGTGACT	950
CTGCTATCGT	CAAGATGGTT	CCCTCCAAG			979

5

2) INFORMATION FOR SEQ ID NO: 785

10 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1099 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

15

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Phialaphora verrucosa*
 (B) STRAIN: ATCC 38561

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 785

GGACAAGCTG	AAGGCCGAAC	GTGAGCGTGG	TATCACCATC	GATATCGCGC	50
25 TCTGGAAGTT	CGAGACTCCC	AAATACTTCG	TCACCGTCAT	TGATGCCCCCT	100
GGTCATCGTG	ACTTCATCAA	GAACATGATC	ACTGGTACCT	CCCAGGCTGA	150
TTGTGCCATC	CTCATCATTG	CCGCCGGTAC	CGGTGAGTTC	GAAGCCGGTA	200
TCTCCAAGGA	TGGCCAGACC	CGTGAGCACG	CTCTCCTCGC	CTACACCCTA	250
GGTGTGAAGC	AGCTTATCGT	CGCCATCAAC	AAGATGGACA	CCGCCAAATG	300
30 GTCCGAGGAT	CGGTTCAACG	AAATCATCAA	GGAGACTTCC	AACTTCATCA	350
AGAAGGTCGG	ATACAACCCC	AAGTCCGTCC	CGTTCGTGCC	CATCTCCGGT	400
TTCAACGGTG	ACAACATGAT	CGACGTCTCC	TCCAACGCCC	CCTGGTACAA	450
GGGTTGGGAG	AAGGAGACCA	AGGCCGGCAA	GGCCACTGGC	AAGACCCTCC	500
TCGAGGCCAT	CGACGCGATT	GACCCTCCTA	CTCGTCCCAC	CGACAAGCCC	550
35 CTCCGTCTCC	CTCTCCAGGA	TGTCTACAAG	ATCTCTGGTA	TCGGCACGGT	600
GCCCGTTGGT	CGTGTTGAGA	CCGGTACCAT	CAAAGCCGGT	ATGGTCGTCA	650
CCTTCGCTCC	CGCCAACGTC	ACCACTGAAG	TCAAGTCCGT	CGAAATGCAC	700
CACGAACAGC	TCGCCGAAGG	TGTTCCAGGT	GACAATGTCG	GCTTCAACGT	750
CAAGAACGTC	TCCGTCAAGG	AGGTTTCGTCG	TGGAAACGTT	GCCGGTGACT	800
40 CCAAGAATGA	CCCCCCAAG	GGTGCCGACT	CCTTCAACGC	TCAGGTCATC	850
GTCCTCAACC	ACCCTGGTCA	GGTCGGTGCC	GGCTACGCCC	CGGTCTTGGA	900
TTGCCACACT	GCCCACATTG	CTTGCAAGTT	CTCTGAGCTC	CTCGAGAAGA	950
TCGATCGTCG	TACCGGCAAG	TCCATGGAAA	ACAACCCCAA	GTTTATCAAG	1000
TCTGGTGATG	CTGCCATCGT	GAAGATGGTT	CCCAGCAAGC	CTATGTGCGT	1050
45 TGAGGCCTTC	ACCGACTATC	CTCCTCTTGG	TCGTTTCGCC	GTCCGTGAC	1099

2) INFORMATION FOR SEQ ID NO: 786

50

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 750 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

55

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Saksenaea vasiformis*

60

448

(B) STRAIN: ATCC 60625

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 786

5	ACCACCAAGT	GGTCTGAGGC	CCGTTACCAG	GAGATCATCA	AGGAGACCTC	50
	CGGYTTCATC	AAGAAGGTCG	GCTTCAACCC	CAAGCACGTT	CCCTTCGTGC	100
	CCATCTCCGG	TTTCAACGGT	GACAACATGA	TCGACGTCTC	CACCAACTGC	150
	CCCTGGTACA	AGGGTTGGGA	GAAGGAGACC	AAGGCCAAGG	CCACCGGCAA	200
	GACCMTCCTC	GAGGCCATTG	ACGCCATCGA	CCCCCYAGY	CGTCCCACCG	250
10	ACAAGCCCCT	YCGTCTTCCC	CTMCAGGATG	TYTACAAGAT	TGGCGGTATT	300
	GGCACGGTTC	CCGTCGGTTC	TGTYGAGACC	GGTRCCATCA	AGGGTGGCAT	350
	GGTCGTCACC	TTCCCCCCCCG	CTGGTGTCAC	CACTGAGGTC	AAGTCCGTCG	400
	AGATGCACCA	CGAGCAGCTC	GCCGAGGGTS	TCCCCGGTGA	CAACGTCGGC	450
	TTCAACGTCA	AGAACGTCTC	CGTCAAGGAG	ATCCGTCGTG	GCAACGTTGC	500
15	CGGTGACTCC	AAGAACGACC	CCCCCAAGGG	CTGCGACAGC	TTCAACGCCC	550
	AGGTCATCGT	CCTCAACCAC	CCCGGTCAGG	TCGGCGCCGG	CTACGCGCCS	600
	GTCCTSGACT	GCCACACTGC	TCACATTGCC	TGCAAGTTCT	CTGAGCTCCT	650
	CGAGAAGATC	GACCGCCGTT	CCGGCAAGTC	CATCGAGTCC	GGCCCCAAGT	700
	TCATCAAGTC	TGGTGACGCC	GCCATCGTCA	AGATGGTTCC	CTCCAAGCCC	750

2) INFORMATION FOR SEQ ID NO: 787

25 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1084 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

30

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Syncephalastrum racemosum*
 (B) STRAIN: ATCC 32330

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 787

	GCTCAAGGCC	GAGCGTGAGC	GTGGTATCAC	CATCGATATC	GCTCTCTGGA	50
40	AGTTCGAGAC	CCCCAAGTAC	CACGTCACCG	TCATTGATGC	CCCCGGCCAT	100
	CGTGATTTC	TCAAGAACAT	GATCACTGGT	ACCTCGCAGG	CTGACTGCGG	150
	TATCCTCATC	ATTGCCGCCG	GTACTGGTGA	GTTGAGGCT	GGTATCTCCA	200
	AGGATGGCCA	GACCCGTGAG	CACGCTCTGC	TTGCCTTCAC	CCTCGGTGTC	250
	CGTCAGCTGA	TCGTGCCCAT	CAACAAGATG	GACTCGACCA	AGTACTCTGA	300
45	GGCCCGTTAC	AACGAAATCG	TCAAGGAGGT	CTCCACCTTC	ATCAAGAAGA	350
	TCGGTTTCAA	CCCCAAGTCC	GTTCCCTTCG	TCCCCATCTC	TGGCTGGAAC	400
	GGTGACAACA	TGTTGGAGGA	GTCCTCCAAC	ATGCCCTGGT	TCAAGGGCTG	450
	GAAGAAGGAG	ACCAAGGCTG	GCGAGAAGTC	CGGCAAGACC	CTCCTTGAGG	500
	CCATTGACAA	CATTGACCCC	CCGGTCCGTC	CCTCGGACAA	GCCCCCTCCGT	550
50	CTTCCCCTCC	AGGATGTCTA	CAAGATCGGT	GGTATCGGCA	CAGTCCCCGT	600
	CGGTCGTGTC	GAGACTGGTG	TCATCAAGGC	TGGTATGGTC	GTGACCTTCG	650
	CCCCCGCCAA	CGTCACCACT	GAAGTCAAGT	CCGTCGAGAT	GCACCACGAG	700
	CAGCTCGTCG	AGGGTGTCCC	CGGTGACAAC	GTCGGTTTCA	ACGTCAAGAA	750
	CGTTTCCGTC	AAGGATATCC	GCCGTGGTAA	CGTCTGCTCT	GACTCCAAGA	800
55	ACGACCCCGC	CAAGGAGTCT	GCCTCGTTCA	CCGCCCAGGT	CATCGTCCTG	850
	AACCACCCCG	GTCAGATCGG	TGCCGGTTAC	GCCCCGGTTC	TTGACTGCCA	900
	CACCGCTCAC	ATTGCCTGCA	AGTTCGCTGA	GCTCCTCGAG	AAGATCGACC	950
	GTCGTTCCGG	YAAGAAGCTC	GAAGAGTCCC	CCAAGTTCGT	CAAGTCGGGT	1000
	GACTCCGCCA	TCGTCAAGAT	GGTTCCCTCC	AAGCCCATGT	GCGTTGAGGC	1050
60	CTACACTGAG	TACCCCCCTC	TTGGCCGTTT	CGCC		1084

2) INFORMATION FOR SEQ ID NO: 788

5

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1155 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

10

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Trichophyton tonsurans*
(B) STRAIN: ATCC 56185

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 788

20 GCTCAAGGCC GAGCGTGAGC GTGGTATCAC CATCGATATC GCCCTCTGGA 50
AGTTCGAGAC CCCCAGTAC AATGTCACCG TCATTGGTAT GTTTTTCTTT 100
ACCTTTCCCC TCCATCGTCT TGCTGTGCCA TAACTAACGA GAGTAGACGC 150
CCCCGGTCAC CGTGACTTCA TCAAGAACAT GATCACTGGT ACCTCCCAGG 200
CTGACTGTGC TATTCTCATC ATTGCTGCCG GTACTGGTGA GTTCGAGGCT 250
25 GGTATCTCCA AGGATGGCCA GACCCGTGAG CACGCTCTGC TCGCCTTCAC 300
CCTTGGTGTC AAGCAGCTCA TCGTTGCCAT CAACAAGATG GACACCACCA 350
ACTGGTCCGA GGACCGTTTC AAGGAAATCA TCAAGGAAGT CACCAACTTC 400
ATCAAGAAGG TTGGCTACGA CCCCAGGGT GTTCCATTCG TTCCAATCTC 450
TGTTTTCAAC GGTGACAACA TGATTGAGGC CTCCAGCAAC TGCCCATGGT 500
30 ACAAGGGATG GAACAAGGAG ACCAAGGCCG GTGGTGCCAA GACTGGCAAG 550
ACCCTYCTCG AGGCCATCGA TGCCATCGAC ATGCCAACCC GTCCTACCGA 600
CAAGCCCCTY CGTCTCCCAC TCCAGGATGT CTACAAGATC TCTGGTATCG 650
GAACTGTACC AGTCGGTCGT GTTGAGACCG GTATCATCAA GCCTGGTATG 700
GTCGTCACCT TCGCCCCTGC CAACGTCACC ACTGAAGTCA AGTCCGTCGA 750
35 AATGCACCAC CAGCAGCTTC AGCAGGGTGT CCCCAGTGAC AACGTCGGCT 800
TCAACGTCAA GAACGTTTCC GTCAAGGAAG TCCGCCGTGG TAACGTTGCC 850
GGTGACTCCA AGAACGACCC ACCATCCGGC TGTGCCTCCT TCAACGCCCCA 900
GGTCATCGTC CTCAACCACC CCGGCCAGAT CGGTGCTGGT TACGCCCCAG 950
TCCTCGACTG CCACACTGCT CACATTGCTT GCAAGTTCGC TGAGCTCCTC 1000
40 GAGAAGATTG ACCGCCGTAC CGGTAAATCC GTCGAAGCCA ACCCCAAGTT 1050
CGTCAAGTCT GGTGATGCCG CTATCGCCAA GATGGTTCCC TCCAAGCCCCA 1100
TGTGCGTTGA GGCTTTCACT GACTACCCCC CACTTGGTCG TTTCGCCGTC 1150
CGTGA 1155

45

2) INFORMATION FOR SEQ ID NO: 789

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1138 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: Genomic DNA

55

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Trichophyton mentagrophytes*
(B) STRAIN: ATCC 8125

60

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 789

	TCAAGGCCGA	GCGTGAGCGT	GGTATCACCA	TCGATATCGC	CCTCTGGAAG	50
	TTCGAGACCC	CCAAGTACAA	TGTCACCGTC	ATTGGTATGT	TTCTCTTTAC	100
5	CTTTCCCTC	CATCGTCTTG	CTGTGCCATA	ACTAACGAGA	GTAGACGCCC	150
	CCGGTCACCG	TGACTTCATC	AAGAACATGA	TCACTGGTAC	CTCCCAGGCT	200
	GACTGTGCTA	TTCTCATCAT	TGCTGCCGGT	ACTGGTGAGT	TCGAGGCTGG	250
	TATCTCCAAG	GATGGCCAGA	CCCGTGAGCA	CGCTCTGCTC	GCCTTCACCC	300
	TTGGTGTCAA	GCAGCTCATC	GTTGCCATCA	ACAAGATGGA	CACCACCAAC	350
10	TGGTCCGAGG	ACCGTTTCAA	GGAAATCATC	AAGGAAGTCA	CCAAC TTCAT	400
	CAAGAAGGTT	GGCTACGACC	CCAAGGGTGT	TCCATTCGTT	CCAATCTCTG	450
	GTTTCAACGG	TGACAACATG	ATTGAGGCCT	CCAACCACTG	CCCATGGTAC	500
	AAGGGATGGA	ACAAGGAGAC	CAAGGCCGGT	GGTGCCAAGA	CTGGCAAGAC	550
	CCTCCTCGAG	GCCATCGATG	CCATCGACAT	GCCAACCCGT	CCTACCGACA	600
15	AGCCCCCTCCG	TCTCCCCTC	CAGGATGTCT	ACAAGATCTC	TGGTATCGGA	650
	ACTGTACCAG	TCGGTCGTGT	TGAGACCGGT	ATCATCAAGC	CCGGTATGGT	700
	CGTCACCTTC	GCCCCTGCCA	ACGTCACCAC	TGAAGTCAAG	TCCGTCGAAA	750
	TGCACCACCA	GCAGCTTCAG	CAGGGTGTCC	CCGGTGACAA	CGTCGGCTTC	800
	AACGTCAAGA	ACGTTTCCGT	CAAGGAAGTC	CGCCGTGGTA	ACGTTGCCGG	850
20	TGACTCCAAG	AACGACCCAC	CATCCGGCTG	TGCCTCCTTC	AACGCCCAGG	900
	TCATCGTCCT	CAACCACCCC	GGCCAGATCG	GTGCTGGTTA	CGCCCCAGTC	950
	CTCGACTGCC	ACACTGCTCA	CATTGCTTGC	AAGTTCGCTG	AGCTCCTCGA	1000
	GAAGATTGAC	CGCCGTACCG	GTAAATCCGT	CGAAGCCAAC	CCCAAGTTTCG	1050
	TCAAGTCTGG	TGATGCCGCT	ATCGCCAAGA	TGGTTCCATC	CAAGCCTATG	1100
25	TGCGTTGAGG	CTTTCACTGA	CTACCCCCCA	CTTGGTGC		1138

2) INFORMATION FOR SEQ ID NO: 790

30

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 748 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

40

- (A) ORGANISM: *Bipolaris hawaiiensis*
- (B) STRAIN: ATCC 26067

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 790

45	CACCACCAAG	TGGTCTGAGG	AGCGTTACCA	GGAAATCATC	AAGGAGACCT	50
	CCAAC TTCAT	CAAGAAGGTC	GGCTACAACC	CCAAGCACGT	TCCCTTCGTC	100
	CCCATCTCTG	GTTTCAACGG	AGACAACATG	ATTGAGGCTT	CCACCAACTG	150
	CCCCTGGTAC	AAGGGTTGGG	AGAAGGAGAC	CAAGGCCAAG	GCCACTGGTA	200
	AGACCCTTCT	CGAGGCCATC	GACGCCATCG	ACCCCCCTGT	CCGTCCTACC	250
50	GACAAGCCCC	TCCGCCTTCC	CCTCCAGGAT	GTGTACAAGA	TTGGTGGTAT	300
	TGGCACGGTT	CCCGTCGGTC	GTGTGAGAC	CGGTATCATC	AAGCCC GGTA	350
	TGGTCGTAC	CTTCGCCCCC	GCTGGTGTCA	CCACTGAAGT	CAAGTCCGTC	400
	GAGATGCACC	ACGAGCAGCT	TGCCGAGGGT	GTCCCCGGTG	ACAACGTCGG	450
	CTTCAACGTC	AAGAACGTCT	CCGTCAAGGA	GATCCGTCGT	GGTAACGTTG	500
55	CCGGTGACTC	CAAGAACGAC	CCCCCAAGG	GTTGCGAGTC	CTTCAACGCC	550
	CAGGTACATCG	TCCTCAACCA	CCCCGGTCAG	GTCGGTGCCG	GTTACGCACC	600
	AGTCCTTGAC	TGCCACACTG	CCCACATTGC	TTGCAAGTTC	TCCGAGCTCC	650
	TCGAGAAGAT	TGACCGCCGT	ACCGGAAAGT	CTGTTGAGAA	CTCCCCCAAG	700
	TTCATCAAGT	CCGGTGACGC	CGCCATCGTC	AAGATGGTTC	CCTCCAAG	748

60

2) INFORMATION FOR SEQ ID NO: 791

5 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 958 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

10

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Aspergillus fumigatus*
 (B) STRAIN: ATCC 14110

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 791

CGCTATTGTC GTTGTTGCTG CCTCCGACGG TCAGATGTAG GTGGAACATC 50
 20 TTGGGAAATA CGTCGTAAAA CACGGCGCTT ACGTTTTCGC GAATAGGCCC 100
 CAGACTCGTG AGCATTGCT GCTCGCCCGC CAGGTTGGTG TCCAGAAGAT 150
 CGTTGTCTTC GTCAACAAAA TCGATGCTAT TGATGATCCG GAGATGCTGG 200
 AACTGGTCTGA ACTCGAGATG CGTGAGCTGC TGAACAGCTA CGGTTTCGAG 250
 GGTGAAGAGA CTCCGATCAT TTTCGGTTC GCTCTCTGTG CTCTCGAAGG 300
 25 ACGCCGTGAC GACATCGGTA AAGACAGAAT TGAGCAGCTT ATGAACGCTG 350
 TCGACACCTG GATCCCCACT CCTCAGCGTG ACCTCGACAA ACCTTTCTTG 400
 ATGTCGTGTC AGGAAGTGTT CTCTATCGCC GGCCGTGGTA CCGTGGCTTC 450
 TGGTCGTGTC GAGCGTGGTA TCTTGAAGAA GGA CTCTGAG GTTGAGATTG 500
 TTGGAGGCTC CTTCAACCC AAGAAGACCA AAGTCACCGA CATTGAAACC 550
 30 TTCAAGAAGA GCTGTGATGA ATCGCGTGCT GGTGACAACCT CTGGTCTCCT 600
 CCTGCGTGGT ATCCGACGTG AAGACGTCAA GCGTGGTATG GTCATTGCTG 650
 TTCCCGGCAG CACCAAAGCT CACGACAAGT TCCTCGTCTC CATGTACGTC 700
 CTGACCGAGG CGGAGGGTGG TCGTCGTACT GGCTTCGGTG CCAACTACCG 750
 TCCCCAAGTC TTCATCCGTA CTGCAGGTAA GTTCCCGCAC ACCGTGTCCA 800
 35 GATCTTCCGA GAGATTAGCG ATATATGCTA ATGATTCATC AGACGAGGCT 850
 GCTGACCTCA GCTTCCCTGA CGGCGACCAA TCTCGCAGAG TTATGCCTGG 900
 TGACAACGTC GAGATGATCC TGAAGACCCA CCACCCTGTT GCTGCTGAGG 950
 CTGGTCAA 958

40

2) INFORMATION FOR SEQ ID NO: 792

45 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 936 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

50 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Trichophyton mentagrophytes*
 (B) STRAIN: ATCC 8125

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 792

CGTTGTCGCA GCTTCTGACG GTCAAATGTA ATTGAATGCC CGCCCAGACG 50
 GATGAAAGGA TTTGACGTTT CTAACATCAT TCTAGGCCTC AGACCAGAGA 100
 60 ACATTTGCTC CTTGCCCCGCC AGGTCGGTGT CCAGAAGCTG GTCGTTTTCG 150

	TTAACAAGGT	CGATGCCGTT	GAGGACCCAG	AGATGTTGGA	GCTTGTCGAA	200
	CTTGAAATGC	GTGAACTCCT	CAGCCACTAC	GGTTTCGAGG	GTGAGGAGAC	250
	CCCCATCATT	TTTGGCTCTG	CTCTCTGTGC	CCTCGAGTCC	CGTCGACCTG	300
	AGCTTGGTGT	CGAGAAGATT	GACGAGCTAT	TGAACGCCGT	CGACACCTGG	350
5	ATCCCCACCC	CCGAGCGCGC	CACTGATAAG	CCTTTCCTCA	TGTCCATTGA	400
	GGAAGTGTTT	TCTATCTCTG	GTCGTGGTAC	CGTCGTCTCC	GGTCGTGTTG	450
	AGCGTGTTAT	CCTCAAGAAG	GATTCCGACG	TCGAAATTGT	TGGTGGCTCT	500
	ACCACCCCTA	TCAAGACCAA	GGTCACAGAT	ATCGAAACCT	TCAAGAAGTC	550
	CTGCGATGAA	TCTCGAGCTG	GTGACAATC	TGGTCTCCTT	CTCCGAGGTA	600
10	TCAAGCGTGA	GGACTTGAAG	CGTGGAATGG	TTGTTGCTGC	CCCCGGATCC	650
	ACCAAGGCTC	ACACCGACTT	CATGGTCTCC	CTCTACGTCC	TGACTGAGGC	700
	TGAGGGTGGT	CGTTCCAACG	GCTTCACCCA	CAAGTACCGC	CCCCAAATGT	750
	TCATCCGTAC	TGCTGGTATG	TAACCCAAGT	TTCCGCTATT	TACTAAGTAG	800
	ATCATTGCTA	ACTTGTATTT	CCTTCCGTAG	ACGAAGCCGC	ATCTTTCAGC	850
15	TGGCCTGGAG	AAGACCAAGA	CAAGAAGGCT	ATGCCTGGTG	ACAACGTCGA	900
	GATGATTTGC	AAGACCCTCC	ACCCCATTCG	TGCCGA		936

20 2) INFORMATION FOR SEQ ID NO: 793

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
 (B) TYPE: Nucleic acid
 25 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 793

TTATTGTTGC TGCTGGTACT

20

35

2) INFORMATION FOR SEQ ID NO: 794

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
 40 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

45

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Trypanosoma cruzi*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 794

50

GACGACAAGT CGGTGAACTT

20

55 2) INFORMATION FOR SEQ ID NO: 795

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
 60 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single

453

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

5 (vi) ORIGINAL SOURCE:
(A) ORGANISM: *Trypanosoma cruzi*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 795

10 ACTTGACACGC GATGTGGCAG 20

15 2) INFORMATION FOR SEQ ID NO: 796

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
20 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 796

25 GGTCCAATGC CWCAAACWAG A 21

30 2) INFORMATION FOR SEQ ID NO: 797

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 27 bases
(B) TYPE: Nucleic acid
35 (C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 797

CATTAAGAAT GGYTTATCTG TSKCTCT 27

45 2) INFORMATION FOR SEQ ID NO: 798

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 bases
50 (B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

55 (vi) ORIGINAL SOURCE:
(A) ORGANISM: *Cryptosporidium parvum*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 798

60

TGGTTGTCCC AGCCGATCGT TT

22

5 2) INFORMATION FOR SEQ ID NO: 799

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 bases
- (B) TYPE: Nucleic acid
- 10 (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

15 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Cryptosporidium parvum*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 799

20 ACCTGTGAAT ACAAGCAATC T

21

25 2) INFORMATION FOR SEQ ID NO: 800

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: single
- 30 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(vi) ORIGINAL SOURCE:

- 35 (A) ORGANISM: *Cryptosporidium parvum*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 800

GATGAAATCT TCAACGAAGT TGAT

24

40

2) INFORMATION FOR SEQ ID NO: 801

45 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- 50 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(vi) ORIGINAL SOURCE:

- 55 (A) ORGANISM: *Cryptosporidium parvum*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 801

ACAACACCGA GAAGATCCCA

20

60

2) INFORMATION FOR SEQ ID NO: 802

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Cryptosporidium parvum*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 802

TTGCCATTTC TGGTTTCGTT

20

20 2) INFORMATION FOR SEQ ID NO: 803

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Cryptosporidium parvum*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 803

ACTTCAGTGG TAACACCAGC

20

2) INFORMATION FOR SEQ ID NO: 804

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Cryptosporidium parvum*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 804

CCTGGGACGG CCTCTGGCAT

20

2) INFORMATION FOR SEQ ID NO: 805

- (i) SEQUENCE CHARACTERISTICS:

456

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

5

(ii) MOLECULE TYPE: DNA

(vi) ORIGINAL SOURCE:

10

(A) ORGANISM: *Cryptosporidium parvum*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 805

CTCTTGTCCT TCTTAGCAGT

20

15

2) INFORMATION FOR SEQ ID NO: 806

(i) SEQUENCE CHARACTERISTICS:

20

- (A) LENGTH: 21 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

25

(ii) MOLECULE TYPE: DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Cryptosporidium parvum*

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 806

AGCATCACCA GACTTGATAA G

21

35

2) INFORMATION FOR SEQ ID NO: 807

(i) SEQUENCE CHARACTERISTICS:

40

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

45

(ii) MOLECULE TYPE: DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Cryptosporidium parvum*

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 807

AAAGTGGCTT CAAAGGTTGC

20

55

2) INFORMATION FOR SEQ ID NO: 808

(i) SEQUENCE CHARACTERISTICS:

60

- (A) LENGTH: 24 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single

457

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 808

GCITTAIWRG CATTAGAARA YCCA

24

10

2) INFORMATION FOR SEQ ID NO: 809

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 24 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 809

TCTTCCTGTW GCAACTGTTC CTCT

24

25

2) INFORMATION FOR SEQ ID NO: 810

(i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 24 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 810

AGAGMWACAG ATAARSCATT CTTA

24

40

2) INFORMATION FOR SEQ ID NO: 811

(i) SEQUENCE CHARACTERISTICS:

45 (A) LENGTH: 25 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 811

TRAARTAGAA TTGTGGTCTR TATCC

25

55

2) INFORMATION FOR SEQ ID NO: 812

(i) SEQUENCE CHARACTERISTICS:

60 (A) LENGTH: 26 bases

458

- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

5 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 812

GTIACIGGIT CYTYRARRTT ICCICC

26

10

2) INFORMATION FOR SEQ ID NO: 813

15 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 813

25 AATCYGTYGA AATGCAYCAC GA

22

2) INFORMATION FOR SEQ ID NO: 814

30

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 814

40

GCIGGCACGT ACACIGCCTG

20

2) INFORMATION FOR SEQ ID NO: 815

45

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 815

55

TGGTGATYT CKACRGACTT

20

60

2) INFORMATION FOR SEQ ID NO: 816

- 5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

10 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 816

GCTACGACGA GATCAAGGGC

20

15

2) INFORMATION FOR SEQ ID NO: 817

- 20 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

25 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 817

TGGAAGAAGG CCGAGGAGTT

20

30

2) INFORMATION FOR SEQ ID NO: 818

- 35 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

40

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 818

45 AGCCGGGCTG GATCTTCTTC

20

2) INFORMATION FOR SEQ ID NO: 819

- 50 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
55 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 819

60

5 2) INFORMATION FOR SEQ ID NO: 820

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 21 bases
 (B) TYPE: Nucleic acid
10 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

- 15 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Trypanosoma brucei*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 820

20 GAAGGAGGTG TCTGCTTACA C 21

25 2) INFORMATION FOR SEQ ID NO: 821

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 21 bases
 (B) TYPE: Nucleic acid
30 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

- 35 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Trypanosoma brucei*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 821

40 GGCGCAAACG TCACCACATC A 21

2) INFORMATION FOR SEQ ID NO: 822

- 45 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 21 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
50 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Trypanosoma brucei*

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 822

60 CGGCGGATGT CCTTAACAGA A 21

2) INFORMATION FOR SEQ ID NO: 823

- 5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

10 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 823

15 GAGCGGTATG AYGAGATTGT 20

2) INFORMATION FOR SEQ ID NO: 824

- 20 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

25 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 824

30 GGCTTCTGCG GCACCATGCG 20

2) INFORMATION FOR SEQ ID NO: 825

- 35 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
40 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 825

45 ATGAGCARCG SAACCATCGT TCAGTG 26

50 2) INFORMATION FOR SEQ ID NO: 826

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 bases
(B) TYPE: Nucleic acid
55 (C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

60 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 826

TCGATCGTGC CGACCATGTA GAACGC

26

5

2) INFORMATION FOR SEQ ID NO: 827

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 446 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

15

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Clostridium novyi*
 (B) STRAIN: ATCC 19402

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 827

	CACCAACTTG	CTAAATGGGG	AGATGCCCAG	ATTGTTGTAT	ATATAGGCTG	50
	TGGAGAACGT	GGAAATGAAA	TGACAGATGT	TCTTAATGAG	TTTCCAGAAC	100
	TTAAAGATCC	TAAGACTGGC	AAATCAATAA	TGGAAAGAAC	AGTTTTAATA	150
25	GCAAATACTT	CTAATATGCC	AGTTGCAGCC	CGTGAAGCTT	GTATATATAC	200
	AGGAATCACA	ATAGCAGAAT	ATTTTAGAGA	TATGGGATAT	TCAGTAGCAC	250
	TTATGGCGGA	TTCCACTTCA	CGTTGGGCAG	AGGCATTAAG	AGAAATGTCT	300
	GGAAGACTTG	AAGAAATGCC	TGGTGATGAA	GGTTACCCAG	CTTATTTAGG	350
	ATCAAGACTT	GCTGATTTCT	ATGAAAGAGC	TGGAAAAGTT	GTGTGTTTAG	400
30	GAGACGATGA	AAGAGAAGGT	GCCATTACTG	CAATAGGTGC	TGTATC	446

2) INFORMATION FOR SEQ ID NO: 828

35

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 445 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Clostridium difficile*
 (B) STRAIN: 9689

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 828

50	CAGCATCAGC	TTGCTAAATG	GGCAGATGCA	GATATAGTTG	TATATATAGG	50
	CTGTGGCGAG	CGTGGAAATG	AAATGACAGA	TGTTCTTCTT	GAATTTCTCT	100
	AATTAAGAAG	CCCAAGAACA	GGCGAGTCAC	TTATGCAAAG	AACTGTGCTT	150
	ATAGCAAATA	CATCAGATAT	GCCGGTTGCT	GCACGTGAAG	CTTCTATATA	200
	CACTGGTATT	ACAATAGCTG	AATATTTTAG	AGATATGGGA	TATAGTGTTG	250
55	CACTTATGGC	AGACTCTACA	TCAAGATGGG	CTGAGGCTCT	TAGAGAGATG	300
	AGTGGTCGTT	TAGAGGAGAT	GCCTGGTGAA	GAAGGTTATC	CTGCATACTT	350
	AGGTTACAGT	CTTGCTCAAT	TCTATGAGAG	AGCAGGAAAG	GTAAATTGTC	400
	TAGGTATGGA	TGAAAGAGAA	GGAACACTTA	CAGCAATTGG	TGCAG	445

60

2) INFORMATION FOR SEQ ID NO: 829

- (i) SEQUENCE CHARACTERISTICS:
- 5 (A) LENGTH: 445 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

10 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Clostridium septicum*
- 15 (B) STRAIN: ATCC 12464

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 829

	ATGCTATAGC	TAAATGGGGA	GACAGCGAAA	TAGTTGTTTA	CGTTGGATGT	50
	GGAGAACGTG	GTAACGAAAT	GACAGACGTT	CTTAACGAAT	TCCCAGAACT	100
20	TATTGACCCA	AAACTGGGG	AAAGTTTAAT	GAAGAGAACA	GTACTTATAG	150
	CTAATACTTC	AAACATGCCA	GTTGCTGCTA	GAGAAGCTTG	CATATACACA	200
	GGTATTACAA	TAGCTGAATA	CTTCAGAGAT	ATGGGATACT	CAGTATCTAT	250
	AATGGCTGAT	TCAACTTCAA	GATGGGCAGA	AGCATTAAGA	GAAATGTCAG	300
	GTAGACTTGA	AGAAATGCCA	GGTGATGAAG	GATATCCAGC	GTACTTAGGA	350
25	TCAAGACTTG	CTGATTATTA	CGAAAGAGCA	GGTAAGGTTG	TTTGTCTAGG	400
	TAAAGATGGT	AGAGAAGGTG	CTGTAACAGC	AATTGGAGCT	GTATC	445

30 2) INFORMATION FOR SEQ ID NO: 830

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 444 bases
- (B) TYPE: Nucleic acid
- 35 (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

40 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Clostridium botulinum*
- (B) STRAIN: 20:3.1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 830

45	TCAAATTGCT	AAATGGGGAG	ATGCAGAAAT	CGTTGTTTAC	GTTGGATGCG	50
	GAGAACGTGG	TAACGAAATG	ACAGACGTTG	TTAATGAGTT	CCCAGAACTT	100
	ATTGACCCTA	AGACTGGCGA	AAGCTTAATG	AAGAGAACAG	TTCTTATAGC	150
	TAATACTTCA	AACATGCCAG	TTGCAGCGAG	AGAAGCTTCA	ATATATACAG	200
50	GTATCACAAT	AGCTGAATAT	TTCAGAGATA	TGGGATATGC	AGTATCAATA	250
	ATGGCTGACT	CAACTTCAAG	ATGGGCTGAG	GCATTAAGAG	AAATGTCTGG	300
	TAGACTTGAA	GAAATGCCTG	GTGATGAAGG	ATATCCAGCT	TACCTTGGAT	350
	CAAGACTTGC	TGATTACTAT	GAAAGAGCTG	GTAAGGTTGA	ATGTTTAGGT	400
55	AATGATGGAA	GAATTGGTTC	TATAACAGCA	ATCGGTGCGG	TATC	444

2) INFORMATION FOR SEQ ID NO: 831

- (i) SEQUENCE CHARACTERISTICS:
- 60 (A) LENGTH: 456 bases

- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

5 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Clostridium perfringens*
- (B) STRAIN: ATCC 13124

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 831

	TAGTTCAGCA	CCAAGTTGCT	AAATGGGGAG	ATACTGAGAT	AGTTGTTTAC	50
	GTTGGATGTG	GAGAACGTGG	TAACGAGATG	ACAGACGTTC	TTAACGAATT	100
15	CCCAGAACTT	AAAGACCCTA	AAACTGGGGA	AAGCTTAATG	AAGAGAACAG	150
	TTCTTATTGC	TAATACATCT	AACATGCCAG	TTGCTGCCAG	AGAAGCATCA	200
	ATATATACTG	GTATAACAAT	AGCAGAGTAT	TTCAGAGATA	TGGGATACTC	250
	AGTATCAATC	ATGGCTGACT	CAACTTCACG	TTGGGCAGAG	GCTTTAAGAG	300
	AAATGTCAGG	AAGACTTGAA	GAAATGCCAG	GAGACGAAGG	TTACCCAGCA	350
20	TACTTAGGAT	CAAGACTTGC	TGATTACTAT	GAAAGAGCTG	GTAAAGTTGT	400
	AGCTTTAGGT	AAAGATGGAA	GAGAAGGAGC	TGTTACAGCT	ATCGGAGCAG	450
	TATCCC					456

25 2) INFORMATION FOR SEQ ID NO: 832

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 444 bases
- (B) TYPE: Nucleic acid
- 30 (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

35 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Clostridium tetani*
- (B) STRAIN: ATCC 19406

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 832

40	CCAAGTTGCA	AAATGGGCTG	ATGCTCAAAT	AGTTGTGTAC	ATAGGATGTG	50
	GAGAACGTGG	AAATGAAATG	ACAGACGTTT	TAAATGAGTT	CCCAGAATTA	100
	AAGGATCCTA	AAACCGGGGA	ATCTTTAATG	AAAAGAACTG	TGTTAATAGC	150
	AAATACATCT	AATATGCCTG	TTGCAGCTAG	AGAAGCATCT	ATATATACTG	200
45	GTATAACAAT	AGGGGAATAT	TTTAGAGATA	TGGGATATTC	AATAGCACTA	250
	ATGGCAGATT	CGACTTCTAG	ATGGGCAGAG	GCTCTAAGAG	AAATGTCTGG	300
	AAGACTAGAG	GAGATGCCAG	GTGAAGAAGG	TTATCCAGCT	TATTTAGGAT	350
	CTAGATTAGC	AGAGTTCTAT	GAAAGAGCAG	GTAATGTTAT	ATGTTTAGGT	400
50	CAGGATGGAA	GAGAAGGAGC	ATTAACAGCT	ATAGGAGCAG	TTTC	444

2) INFORMATION FOR SEQ ID NO: 833

55 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1786 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- 60 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 5 (A) ORGANISM: *Streptococcus pyogenes*
(C) ACCESSION NUMBER: Genome project

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 833

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10 TGAACCAAGG AAAAATAATA ACCGTTTCGG GACCTCTTGT TGTGGCTTCT 50
   GGGATGCAAG AAGCTAATAT TCAAGATATT TGTCGTGTGG GACATCTTGG 100
   CTTAGTCGGA GAAATTATTG AAATGCGTCG CGATCAAGCG TCTATTCAGG 150
   TTTATGAGGA AACATCAGGG ATCGGTCCAG GAGAACCAGT AGTGACTACT 200
   GGTGTGCTTT TGTCGGTCGA GTTAGGCCCG GGCTGTATTT CAGAAATGTT 250
   TGACGGTATT CAGCGACCGC TTGATCGTTT TCAAAAAGCA ACGGACAGCG 300
15 ACTTTTTTAAT CCGTGGTGTG GCTATCCCAA GTCTTGATCG AAAGGCTAAG 350
   TGGGCATTTA TTCCAAGCT AAGTGTGGT CAAGAAGTAG TTGCAGGTGA 400
   TATTTTAGGA ACTGTGCAAG AAACAGCTGT CATTGAGCAC CGTATCATGG 450
   TTCCTTATAA AGTTTCAGGG ACCTTGGTGG CTATTCATGC AGGGGACTTC 500
   ACAGTAACAG ATACAGTTTA TGAAATTAAG CAGGAAGACG GTTCCATTTA 550
20 CCAAGGTAGC CTCATGCAGA CTTGGCCAGT TCGTCAAAGT CGCCCTGTTG 600
   CTCAAAAGCT TATCCAGTC GAACCTTTGG TTACAGGTCA ACGGGTTATT 650
   GACACCTTTT TCCCTGTTAC AAAAGGTGGT GCCGCTGCCG TTCCTGGACC 700
   ATTTGGGGCA GGAAAAACAG TTGTGCAGCA TCAAATAGCT AAATTTGCCA 750
   ACGTTGATAT TGTTATTTAT GTCGGTTGTG GGAACGCGG CAACGAGATG 800
25 ACCGACGTTT TGAATGAGTT TCCAGAGTTA ATTGACCCAA ATACAGGCCA 850
   GTCCATTATG GAGCGCACGG TGTTAATTGC AAACACCTCT AATATGCCAG 900
   TAGCAGCGCG TGAAGCGTCG ATTTACACAG GTATTACCAT TGCCGAATAT 950
   TTCCGTGATA TGGGCTATTC TGTGGCTATC ATGGCAGACT CGACATCACG 1000
   TTGGGCAGAA GCTCTGCGCG AGATGTCAGG ACGCCTACAA GAAATGCCTG 1050
30 GTGATGAAGG CTACCCGGCT TACTTAGGGA GTCGTATTGC CGAATATTAT 1100
   GAACGGGCTG GTCGTGTTCC GACCTTGGGA AGTCAAGAAC GTGAGGGAAC 1150
   CATTACAGCC ATCGGCGCGG TTTCTCCTCC TGGAGGGGAT ATTCAGAGC 1200
   CTGTCACTCA AAACACCCTT CGGATTGTCA AAGTTTTCTG GGGGCTCGAC 1250
   GCGCCTCTTG CGCAACGGCG TCACTTCCCA GCGATTAACT GGCTGACGTC 1300
35 TTATTCATTG TATCAAGATG ATGTAGGAAG CTATATTGAC CGTAAACAGC 1350
   AATCTAATTG GTCCAACAAG GTAACGCTG CCATGGCTAT TTTGCAGCGT 1400
   GAAGCCAGTC TAGAAGAAAT TGTACGCTTG GTGGGGCTTG ATTCACTGTC 1450
   TGAACAAGAT CGTTTGACCA TGGCTGTTGC CCGGCAAATT CGGGAGGATT 1500
   ATCTCCAGCA AAATGCCTTT GATTCGGTGG ATACCTTTAC TTCCTTTCCG 1550
40 AAACAAGAGG CCATGCTAAC CAATATTTTG ACCTTTAATG AGGAAGCCAG 1600
   CAAAGCCCTT TCTTTGGGAG CTTATTTTAA TGAGATTATG GAAGGCACTG 1650
   CTCAGGTACG CGATCGCATC GCACGCAGCA AATTTATCCC AGAAGAAAAC 1700
   TTAGAGCAGA TTAAAGGGCT TACTCAGAAG GTTACCAAAG AGATTCACCA 1750
   CGTTTTAGCA AAGGGAGGAA TTTAGATGAG CGTTCT 1786
45

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2) INFORMATION FOR SEQ ID NO: 834

50 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 499 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

55

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 60 (A) ORGANISM: *Babesia bovis*
(B) STRAIN: Suarez-3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 834

	TATCTCACGT	AAGTTTTTGC	GCGGCGGTTA	TATATCACTC	CAGGCCCTGG	50
5	CTAAGTACGC	TAATACTGAC	GTTACTGTCT	ATGTGGGATG	TGGAGAGCGT	100
	GGAAACGAGA	TTGCGGAGGT	GCTTAAGGAG	TTCCTTGAGC	TGAAGACCAA	150
	GGTTGATGGC	AAGGAAGTGA	GCATTATGAA	ACGCACTTGC	TTGGTGGCCA	200
	ATACTTCAAA	CATGCCAGTG	GCCGCCAGGG	AGGCTAGTAT	CTACACTGGC	250
	ATTACCCTAT	GTGAATACTT	CAGGGATATG	GGATACAACG	CCTGTGTGAT	300
10	GGCGGATTCC	ACCAGTCGTT	GGGCTGAGGC	TTTGCCTGAG	ATATCAGGTC	350
	GTTTAGCTGA	GATGCCTGCT	GATTCAGGTT	ATCCCGCCTA	CCTTGCTTCT	400
	AGGCTTTTCG	CGTTCTATGA	GCGTGCTGGT	ACAGCTGAGT	GTATTGGAAC	450
	ACCACTTCGT	GAAGGTTTCA	TTACCATTGT	TGGTGCTGTA	TCTCCACCA	499

15

2) INFORMATION FOR SEQ ID NO: 835

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 464 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

25 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Cryptosporidium parvum*

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 835

	TTTCTCAAGC	TTTGAGTAAA	TATAGTAACT	CTGATGTTAT	TATTTACATT	50
	GGTTGTGGAG	AAAGAGGAAA	TGAAATGGCA	GAAGTTCTTA	CAGAATTCCC	100
	TGAGCTTTAT	ACTATGGTTG	ATGGAAAGAA	GGAGTCAATT	ATGCAAAGAA	150
35	CTTGTTTAGT	AGCTAATACA	TCAAATATGC	CTGTCGCTGC	TAGAGAAGCT	200
	TCCATCTACA	CTGGTATTAC	ACTTTCTGAA	TACTTTAGAG	ATATGGGATG	250
	TAATGTTTCT	ATGATGGCAG	ATTCAACTTC	TCGTTGGGCT	GAAGCTCTTA	300
	GAGAAATTTT	TGGTAGATTA	GCTGAAATGC	CTGCAGATTC	GGGTTACCCA	350
	GCAATATTTAG	GCGCCAGACT	TGCTTCATTC	TATGAAAGAT	CAGGAAGAGT	400
40	TAAATGTATG	GGTTCCCCAG	ATAGAGAAGG	TACAGTAACA	ATTGTTGGTG	450
	CAGTTTCTCC	ACCT				464

45 2) INFORMATION FOR SEQ ID NO: 836

3)

(i) SEQUENCE CHARACTERISTICS:

- 50 (A) LENGTH: 446 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

55 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Leishmania infantum*
 (B) STRAIN: MOU

60 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 836

	GCCCTCTCCA	AGTACTCCAA	CTCCGATTGC	GTCATCTATG	TCGGCTGCGG	50
	CGAGCGCGGT	AATGAGATGG	CCGAGGTGCT	CATGGAGTTC	CCGACCCTGA	100
	CGACCGTGAT	CGATGGCCGC	GAGGAGTCGA	TCATGAAGCG	CACCTGCCTC	150
	GTGGCGAACA	CCTCGAACAT	GCCAGTCGCA	GCCCGTGAGG	CCTCTATTTA	200
5	CACCGGCATC	ACCCTGGCCG	AGTACTACCG	TGATATGGGC	AAGCATATCG	250
	CCATGATGGC	TGACTCGACG	TCTCGCTGGG	CCGAGGCGCT	TCGTGAGATT	300
	TCGGGTCGTC	TGGCGGAGAT	GCCGGCGGAT	GGTGGCTACC	CCGCCTACCT	350
	CAGCGCTCGT	CTCGCCTCCT	TCTACGAGCG	CGCCGGCCTC	GTCACCTGCA	400
	TCGGCGGGCC	GAAGCGCCAG	GGCTCCGTCA	CGATCGTCGG	TGCCGT	446
10						

2) INFORMATION FOR SEQ ID NO: 837

- 15 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 456 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Double
 - (D) TOPOLOGY: Linear

- 20 (ii) MOLECULE TYPE: Genomic DNA

- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Leishmania major*
 - 25 (B) STRAIN: ATCC 50122

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 837

	TTAGTCAGGC	CCTCTCCAAG	TACTCCAAC	CCGACTGCGT	CATCTATGTC	50
30	GGCTGCGGCG	AGCGCGGTAA	TGAGATGGCT	GAGGTGCTCA	TGGATTTCCT	100
	AACTCTGACG	ACCGTGATCG	ATGGTCGCGA	GGAGTCCATC	ATGAAGCGCA	150
	CCTGCCTCGT	GGCAAACACT	TCGAACATGC	CAGTCGCAGC	CCGCGAGGCC	200
	TCTATTTACA	CCGGCATCAC	CCTGGCCGAG	TACTACCGTG	ATATGGGCAA	250
	GCATATTGCC	ATGATGGCCG	ACTCGACATC	TCGCTGGGCC	GAGGCGCTTC	300
35	GTGAGATTTC	CGGTCGTCTG	GCGGAGATGC	CAGCCGATGG	TGGCTACCCT	350
	GCCTACCTCA	GCGCTCGTCT	CGCCTCCTTC	TACGAGCGCG	CCGGCCTCGT	400
	CACCTGCATC	GCGGGGCCGA	AGCGCCAGGG	CTCCGTCACG	ATCGTCGGTG	450
	CTGTGT					456

40

2) INFORMATION FOR SEQ ID NO: 838

- 45 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 450 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Double
 - (D) TOPOLOGY: Linear

- 50 (ii) MOLECULE TYPE: Genomic DNA

- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Leishmania tarentolae*
 - 55 (B) STRAIN: MOU-2

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 838

	AGGCCCTCTC	CAAGTACTCC	AACTCCGACT	GCGTCATCTA	CGTCGGCTGC	50
	GGCGAGCGCG	GTAATGAGAT	GGCCGAGGTG	CTCATGGAGT	TCCCGACCCT	100
60	GACGACTGTG	ATTGATGGCC	GTGAGGAGTC	GATCATGAAG	CGGACCTGCC	150

	TCGTGGCCAA	CACCTCCAAC	ATGCCAGTCG	CAGCCCGTGA	AGCCTCTATT	200
	TACACTGGTA	TCACCCTGGC	CGAATACTAC	CGTGATATGG	GCAAGCATAT	250
	CGCCATGATG	GCTGACTCGA	CGTCTCGCTG	GGCGGAGGCG	CTTCGTGAGA	300
	TTTCGGGTCG	CCTGGCGGAG	ATGCCGGCTG	ATGGTGGGTA	CCCCGCCTAC	350
5	CTTAGTGCTC	GTCTTGCTC	CTTCTACGAG	CGTGCCGGCC	TCGTACACCTG	400
	CATCGGTGGG	CCGAAGCGCC	AGGGCTCCGT	CACGATCGTC	GGTGCCGTGT	450

10 2) INFORMATION FOR SEQ ID NO: 839

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 437 bases
 - (B) TYPE: Nucleic acid
 - 15 (C) STRANDEDNESS: Double
 - (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- 20 (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Trypanosoma brucei*
 - (B) STRAIN: EATRO 795
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 839

25	GCACTCTCGA	AGTACTCGAA	CAGTGACGCT	GTTATTTACG	TGGGTTGTGG	50
	TGAGCGTGGC	AATGAGATGG	CGGAGGTGCT	CATGGACTTT	CCCACCCTCA	100
	CCACCATTAT	TGATGGACGT	GAGGAGTCTA	TCATGAAGCG	CACATGCCTG	150
	GTGGCAAATA	CTTCCAATAT	GCCTGTTGCT	GCTCGTGAGG	CATCTATTTA	200
30	CACTGGTATC	ACCTTAGCTG	AGTATTATCG	GGATATGGGA	AAACACATCG	250
	CCATGATGGC	CGATTCAACC	TCCCCTGGG	CTGAGGCTTT	GCGTGAGATT	300
	TCCGGTCGTC	TTGCTGAAAT	GCCTGCAGAT	GGAGGTTATC	CCGCGTACCT	350
	CAGCGCCCGT	TTGGCCTCCT	TCTACGAGCG	TGCTGGCCGT	GTGACATGCA	400
35	TCGGTGGGCC	GAAGCGTGAA	GGGTCTGTAA	CAATTGT		437

2) INFORMATION FOR SEQ ID NO: 840

- 40 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1052 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Double
 - 45 (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Trypanosoma cruzi*
 - 50 (B) STRAIN: MM3
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 840

	TGAAGGCTGA	GCGCGAGCGC	GGCATCACGA	TCGACATCGC	GCTCTGGAAG	50
55	TTCGAGTCGC	CCAAGTCTGT	GTTACGATC	ATCGACGCC	CCGGCCACCG	100
	CGACTTCATC	AAGAACATGA	TCACGGGCAC	GTCTCAGGCG	GACGCCGCCG	150
	TCCTTGTCAT	TGCGTCATCG	CAGGGTGAGT	TTGAGGCGGG	CATCTCGAAG	200
	GACGGCCAGA	CACGCGAGCA	CGCGCTGCTC	GCCTTCACGC	TCGGCGTGAA	250
	GCAGATGGTT	GTGTGCTGCA	ACAAGATGGA	CGACAAGTCG	GTGAACTTCG	300
60	CCCAGGAGCG	CTACGATGAG	ATTGTGAAGG	AGGTGTCGGC	GTACCTGAAG	350

	AAGGTTGGGT	ACAACGTGGA	GAAGGTGCGC	TTCATCCCCA	TCTCCGGCTG	400
	GCAGGGCGAC	AACATGATTG	ACAAGTCGGA	AAATATGCCG	TGGTACAAGG	450
	GCCCCACGCT	GCTGGAGGCA	CTCGACATGC	TGGAGCCCCC	GGTGCGCCCC	500
	AGCGACAAGC	CGCTGCGCCT	GCCGCTGCAG	GACGTGTACA	AGATCGGCGG	550
5	TATCGGCACC	GTGCCGGTCG	GTCGCGTGGA	GACGGGCACG	ATGAAGCCCC	600
	GCGACGTGGT	GACGTTTGCG	CCCGCCAACG	TGACGACGGA	GGTGAAGTCG	650
	ATTGAGATGC	ACCACGAGCA	GCTGGCCGAG	GCCACGCCCC	GCGACAACGT	700
	CGGCTTCAAC	GTGAAGAACG	TGTCCGTGAA	GGACATCCGC	CGTGGCAACG	750
	TGTGCGGCAA	CTCGAAGAAC	GACCCCCCAA	AGGAGGCGGC	CGACTTCACG	800
10	GCGCAGGTGA	TCATCCTGAA	CCACCCCGGC	CAGATCGGCA	ACGGCTATGC	850
	GCCGGTGCTC	GACTGCCACA	CCTGCCACAT	CGCGTGCAAG	TTCGCCGAGA	900
	TCGAGTCCAA	GATCGACCGC	CGCTCCGGCA	AGGAGCTTGA	GAAGAACCCC	950
	AAGTCGATCA	AGTCCGGTGA	CGCCGCCATG	GTGCGCATGG	TGCCGCAGAA	1000
	GCCCATGTGC	GTGGAGGTGT	TCAACGACTA	CGCTCCTCTT	GGCCGCTTTG	1050
15	CC					1052

2) INFORMATION FOR SEQ ID NO: 841

20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1061 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

25

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

30

- (A) ORGANISM: *Trypanosoma cruzi*
- (B) STRAIN: CGL-1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 841

35	TGAAGGCTGA	GCGCGAGCGC	GGCATCACGA	TCGACATCGC	GCTCTGGAAG	50
	TTCGAGTCGC	CCAAGTCTGT	GTTACGATC	ATCGACGCCC	CCGGCCACCG	100
	CGACTTCATC	AAGAACATGA	TCACGGGCAC	GTCTCAGGCG	GATGCCCGCCG	150
	TCCTTGTCAT	TGCGTCATCG	CAGGGTGAGT	TTGAGGCGGG	CATCTCGAAG	200
	GACGGCCAGA	CACGCGAGCA	CGCGCTGCTC	GCCTTCACGC	TCGGCGTGAA	250
40	GCAGATGGTT	GTGTGCTGCA	ACAAGATGGA	CGACAAGTCG	GTGAACTTTG	300
	CCCAGGAGCG	CTACGATGAG	ATTGTGAAGG	AGGTGTCGGC	GTACCTGAAG	350
	AAGGTTGGGT	ACAACGTGGA	GAAGGTGCGC	TTCATCCCCA	TCTCCGGCTG	400
	GCAGGGCGAC	AACATGATTG	ACAAGTCGGA	AAATATGCCG	TGGTACAAGG	450
	GCCCCACGCT	GCTGGAGGCA	CTCGACATGC	TGGAGCCCCC	GGTGCGCCCC	500
45	AGCGACAAGC	CGCTGCGCCT	GCCGCTGCAG	GATGTGTACA	AGATCGGCGG	550
	TATCGGCACC	GTGCCGGTCG	GTCGCGTGGA	GACGGGCACG	ATGAAGCCCC	600
	GCGACGTGGT	GACGTTTGCG	CCCGCCAACG	TGACGACGGA	GGTGAAGTCG	650
	ATTGAGATGC	ACCACGAGCA	GCTGGCCGAG	GCCACGCCCC	GCGACAACGT	700
	CGGCTTCAAC	GTGAAGAACG	TGTCCGTGAA	GGACATCCGC	CGTGGCAACG	750
50	TGTGCGGCAA	CTCGAAGAAC	GATCCCCCAA	AGGAGGCGGC	CGACTTCACG	800
	GCGCAGGTGA	TCATCCTGAA	CCACCCCGGC	CAGATCGGCA	ACGGCTATGC	850
	GCCGGTGCTT	GACTGCCACA	CCTGCCACAT	CGCGTGCAAG	TTCGCCGAGA	900
	TCGAGTCCAA	GATCGACCGC	CGCTCCGGCA	AGGAGCTTGA	GAAGAACCCC	950
	AAGTCGATCA	AGTCCGGTGA	CGCCGCCATG	GTGCGCATGG	TGCCGCAGAA	1000
55	GCCCATGTGC	GTGGAGGTGT	TCAACGACTA	CGCTCCTCTT	GGCCGCTTTG	1050
	CCGTGCGTGA	C				1061

60 2) INFORMATION FOR SEQ ID NO: 842

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1062 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Trypanosoma cruzi*
 (B) STRAIN: PCU-1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 842

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15 GCTGAAGGCT GAGCGCGAGC GCGGCATCAC GATCGACATC GCGCTCTGGA      50
   AGTTCGAGTC GCCCAAGTCT GTGTTACGTA TCATCGACGC CCCCAGCCAC      100
   CGCGACTTCA TCAAGAACAT GATCACGGGC ACGTCTCAGG CGGACGCCGC      150
   CGTCCTTGTC ATTGCGTCAT CGCAGGGTGA GTTTGAGGCG GGCATCTCGA      200
20 AGGACGGCCA GACACGCGAG CACGCGCTGC TCGCCTTCAC GCTCGGCGTG      250
   AAGCAGATGG TTGTGTGCTG CAACAAGATG GACGACAAGT CGGTGAACCT      300
   CGCCCAGGAG CGCTACGATG AGATTGTGAA GGAGGTGTCT GCGTACCTGA      350
   AGAAGGTTGG GTACAACGTG GAGAAGGTGC GCTTCATCCC CATCTCCGGC      400
   TGGCAGGGCG ACAACATGAT TGACAAGTCG GAAAATATGC CGTGGTACAA      450
25 GGGCCCCACG CTGCTGGAGG CACTCGACAT GCTGGAGCCC CCGGTGCGCC      500
   CCAGCGACAA GCCGCTGCGC CTGCCGCTGC AGGACGTGTA CAAGATCGGC      550
   GGTATCGGCA CCGTGCCGGT CGGTGCGGTG GAGACGGGCA CGATGAAGCC      600
   CGGCGACGTG GTGACGTTTG CGCCCGCCAA CGTGACGACG GAGGTGAAGT      650
   CGATTGAGAT GCACCACGAG CAGCTGGCCG AGGCCACGCC CGGCGACAAC      700
30 GTCGGCTTCA ACGTGAAGAA CGTGTCCGTG AAGGACATCC GCCGTGGCAA      750
   CGTGTGCGGC AACTCGAAGA ACGACCCCCC AAAGGAGGCG GCCGACTTCA      800
   CGGCGCAGGT GATCATCCTG AACCACCCCG GCCAGATCGG CAACGGCTAT      850
   GCGCCGGTGC TCGACTGCCA CACCTGCCAC ATCGCGTGCA AGTTCGCCGA      900
   GATCGAGTCC AAGATCGACC GCCGCTCCCG CAAGGAGCTT GAGAAGAACC      950
35 CCAAGTCGAT CAAGTCCGGT GACGCCGCCA TGGTGCGCAT GGTGCCGCAG      1000
   AAGCCCATGT GCGTGGAGGT GTTCAACGAC TACGCTCCTC TTGGCCGCTT      1050
   TGCCGTGCGT GA                                     1062

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40

2) INFORMATION FOR SEQ ID NO: 843

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1057 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

50

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Babesia bovis*
 (B) STRAIN: Suarez-3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 843

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60 TACATTGACA GCTGCATTGA CCAAGGTCTG TTCGATGGGT GGTCATGGCG      50
   AGTACACTCC TTATGAAGCA ATTGACCGTG CTCCTGAGGA GCGTAAACGT      100
   GGTATTACTA TAAATTCGAC ACATGTTGAA TATGAGACTA AGAACCGTCA      150
   TTACGGTCAC GTGGACTGTC CAGGTCACTC TGATTATGTG AAGAACATGA      200

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	TATCTGGCGC	TGCTCAGATG	GATGGTGCCA	TATTGGTTGT	TTCTTGTGTT	250
	GACGGTCCCA	TGCCTCAGAC	TAAGGAGCAC	GTGTTGCTTG	CTAAGCAGAT	300
	TGGTGTACCT	CGTTTAGTTG	TGTTTTTGAA	CAAGCTTGAC	ATGTTAGAGG	350
	ACTCTGAGCT	ATTGGAGTTG	GTGGAGTTAG	AGGTTTCGTGA	GTTATTGAGT	400
5	GAGTTTGGTT	ACGACGGTGA	CAACACGCCT	ATCGTTCGTG	GCAGTGCTAT	450
	AAAGGCATTG	AACAGTAGTT	CCGAGGCTGA	CATTAAGCCA	ATTCAGGATT	500
	TATTGGATGC	GTGTGATGCC	TTTTTACTGA	CTCCAGAACG	TAAGGATGAC	550
	ATGCCGCTCT	TGGTTGCTAT	TGACGATGTT	CTTGCCATTC	CTGGCAAGGG	600
	TACTGTTGTA	ACCGGTAGGA	TAGAGCAGGG	CAAGATTCGT	TGTGGTGACC	650
10	CTATTGAGGT	TTGCGCCGGT	CCGAAGTCCG	GCAAGAAGAC	TGTGTGTGTT	700
	GGTCTTRARA	TGTTCCGCAA	GAGTCTCAGT	RAGGGTATTG	CTGGTGACCA	750
	GATTGGTGTT	TTGCTCAAGG	GTGTGAAGCG	CGACRAGGTA	GAGEGEGGGT	800
	TTGTATTGAT	TCAACCCGGA	AGTTACAAAT	GTCACGGTGA	ATTTGATGCT	850
	GACTTGACG	TGTTGACTAC	GRAGGAAGGT	GGGCGCAAGC	ATCCGTTTGT	900
15	GTCTAACTAC	CGTCCTCAGG	CGTTTATACG	TACTGGAGAC	GTTTGCTGCT	950
	CAGTTCATTT	GGATRAGGGT	GTTGAGATGG	CAGCTCCTGG	TGACAACGTG	1000
	CGTTGCAAGA	TCAAGTTACT	TTATCCCATG	CCTGTCCATG	AAGGTTTACG	1050
	ATTTGCG					1057

20

2) INFORMATION FOR SEQ ID NO: 844

- (i) SEQUENCE CHARACTERISTICS:
- 25 (A) LENGTH: 943 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

- 30 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Leishmania aethiopica*
- (B) STRAIN: ATCC 50119

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 844

	CGGTGGCATC	ATTGTGGTGG	CGGCCACCGA	CGGCGTCATG	CCGCAGACAC	50
	GCGAGCACCT	CCTGATCTGC	TCGCAGATTG	GGCTTCCGGC	GCTCGTAGGG	100
40	TTCATCAACA	AAGTGGATAT	GACGGACGAG	GACACGTGCG	ACCTGGTGGA	150
	CATGGAGGTG	CGCGAGCAGC	TGGAGAAATA	CAAGTTTCCG	GCGGAGGAGA	200
	CACCAATCGT	GCGCGGCTCG	GCCCTCAAGG	CCGTCGAGGG	CGACGCGAAG	250
	TACGAGGAGA	ACATCCTCGA	ACTGGTGCGG	AAGTGCGACG	AGTGGATCCC	300
	CGACCCGCCG	CGCAACACAG	ACAAGCCTTT	CCTTATGGCC	ATCGAGCACG	350
45	TTTACGAGAT	CGGCAAGGAC	AAGAAGAGCG	TCATCGTGAC	CGGCCGCGTC	400
	GATCAGGGCG	TGCTGAAGCT	CAACACAGAC	GCCGAGCTGG	CCGGCTTCAG	450
	CGCCAAGAAG	TCGACGGTGA	GGGTGACGGG	CATCGAGATG	TACCACAAGA	500
	CGCTGAGCGA	GTGCATGCCC	GGTGACTCCG	TCGGCGTCAG	CATTGTGCGC	550
	ACCGGCGACA	CAACCAGTCT	GTCCAAGGAC	AACGTGGAAC	GCGGCATGGT	600
50	AATGGCGGCG	ACGGGTAGCA	CGAACCTGTA	CAACAAGGTG	AAGGCGCAGG	650
	TGTACGTGCT	GACGAAGGAT	GAGGGCGGCC	GCCACACCGG	CTTCAGCCCC	700
	CACTACCGCC	CGCAGCTCTT	CTTCCATTGC	GCTGACGTGA	CAGCGGACAT	750
	GAGCTTCCCG	GAGGCGGAGA	AGCACCGGGA	GGAGCTGAAC	AAGAAATTCT	800
	GCCGCGGCCC	CGAGGAGGAC	AAGAAGAAAG	AGGCGGAGAT	GAAGGAGTTC	850
55	GAGAGCAAGC	TCGTCTGCAT	GCCGGGCGAT	AACCGCGAGC	TGATCCTGAC	900
	GCTCGCGTAC	CCGATGCCCA	TTGAAAAGGG	CCTGAAGTTC	ACC	943

60 2) INFORMATION FOR SEQ ID NO: 845

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 939 bases
 (B) TYPE: Nucleic acid
 5 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

- 10 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Leishmania amazonensis*
 (B) STRAIN: ATCC 50131

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 845

15	CGGTGGCATC	ATTGTGGTGG	CGGCCACCGA	CGGCGTCATG	CCGCAGACAC	50
	GCGAGCATCT	CTTGATCTGC	TCGCAGATTG	GGCTTCCGGC	GCTCGTAGGG	100
	TTCATCAACA	AAGTGGACAT	GACGGACGAG	GACACGTGCG	ACCTGGTGGA	150
	CATGGAGGTG	CGTGAGCAGC	TGGAGAAATA	CAAGTTTCCG	GCGGAAGAGA	200
20	CGCCCATCGT	GCGCGGCTCG	GCCCTCAAAG	CCGTCGAGGG	CGACGCGAAG	250
	TACGAGGAGA	ACATCCTCGA	ACTGGTGCGG	AAGTGCAGAC	AATGGATCCC	300
	CGACCCGCCG	CGCAACACAG	ACAAGCCTTT	CCTTATGGCC	ATTGAGCACG	350
	TTTACGAGAT	CGGCAAGGAC	AAGAAGAGCG	TCATCGTGAC	CGGCCGCGTC	400
	GATCAGGGCG	TGCTGAAGCT	CAACACAGAC	GCCGAGCTGG	CCGGCTTCAG	450
25	CGCCAAGAAG	TCGACGGTGA	GGGTGACGGG	CATCGAGATG	TACCACAAGA	500
	CGCTGAGTGA	GTGCATGCCC	GGTGACTCCG	TCGGCGTCAG	CATTGTCCGC	550
	ACCGGCGACA	CGATCAGTCT	CTCCAAGGAC	AACGTTGAAC	GCGGCATGGT	600
	AATGGCGGCA	ACGGGTAGCA	CGAACCTGTA	CAACAAGGTG	AAGGCGCAGG	650
	TGTACGTGCT	GACGAAGGAT	GAGGGCGGCC	GCCACACTGG	CTTCAGCCCC	700
30	CACTACCGCC	CGCAGCTCTT	CTTCCATTGT	GCTGACGTGA	CGGCGGACAT	750
	GAGCTTCCCG	GAGGCGGAGA	AGCACCGCGA	GGAGCTCAAC	AAGAAATTCT	800
	GCCGCGGCCC	CGAGGAGGAC	AAGCAGAAGG	AGGCGGAGAT	GAAAGAGTTC	850
	GAGAGCAAGC	TCGTCTGCAT	GCCGGGCGAC	AACCGCGAGC	TGATCCTGAC	900
	GCTGGCGTAC	CCGATGCCCA	TTGACAAGGG	TCTGAAGTT		939
35						

2) INFORMATION FOR SEQ ID NO: 846

- 40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 945 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 45 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Leishmania donovani*
 50 (B) STRAIN: ATCC 50212

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 846

55	CATTGTGGTG	GCGGCCACCG	ACGGCGTCAT	GCCGCAGACA	CGCGAGCACC	50
	TCCTGATCTG	CTCGCAGATC	GGGCTTCCGG	CGCTCGTAGG	GTTTCATCAAC	100
	AAGGTGGACA	TGACGGACGA	GGACACGTGC	GACCTGGTGG	ACATGGAGCT	150
	GCGCGAGCAG	CTGGAGAAAT	ACAAGTTTCC	GGCGGAGGAG	ACGCCAATCG	200
	TGCGCGGCTC	AGCCCTCAAA	GCCGTCGAGG	GCGATGCGAA	GTACGAGGAG	250
	AACATTCTCG	AACTGGTGCG	GAAGTGTGAC	GAGTGGATCC	CTGACCCGCC	300
60	GCGCAACACA	GACAAGCCTT	TCCTTATGGC	CATCGAGCAC	GTTTACGAGA	350

	TCGGCAAGGA	CAAGAAGAGC	GTTGTCGTGA	CCGGCCGCGT	CGATCAGGGC	400
	ATTCTGAAGC	TCAACACAGA	CGCCGAGCTG	GCCGGCTTCA	GCTCCAAGAA	450
	GTCGACGGTG	AGGGTGACGG	GCATCGAGAT	GTACCACAAG	ACGCTGAGCG	500
	AGTGCATGCC	TGGTGACTCC	GTCGGCGTCA	GCATTGTCGG	GACCGGCGAC	550
5	ACGACCACTC	TATCCAAGGG	CAACGTGGAA	CGCGGCATGG	TGATGGCGGC	600
	GACGGGTAGC	ACGAACCTGT	ACAACAAGGT	GAAGGCGCAG	GTGTACGTGC	650
	TGACGAAGGA	TGAGGGCGGC	CGCCACACTG	GCTTTAGTCC	TCACTACCGC	700
	CCGCAGCTCT	TCTTCCATTG	TGCTGACGTG	ACGGCGGACA	TGAGCTTCCC	750
	GGAGGCGGAG	AAGCACC GCG	AAGAGCTCAA	CAAGAAATTC	GGCCGCGGCC	800
10	CCGAGGAGGA	CAAGAAGAAA	GAGGCAGCGA	TGAAGGAGTT	CGAGAGCAAG	850
	CTCGTCTGCA	TGCCGGGCGA	TAACCGCGAG	CTGATCCTGA	CGCTGGCGTA	900
	CCCGATGCCC	ATTGAAAAGG	GTCTGAAGTT	CACCATCCGT	GAGGG	945

15

2) INFORMATION FOR SEQ ID NO: 847

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 939 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

25

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Leishmania infantum*
 (B) STRAIN: MOU

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 847

	GGCATCATTG	TGGTGGCGGC	CACCGACGGC	GTCATGCCGC	AGACACGCGA	50
	GCACCTCCTG	ATCTGCTCGC	AGATCGGGCT	TCCGGCGCTC	GTAGGGTTCA	100
	TCAACAAGGT	GGACATGACG	GACGAGGACA	CGTGCGACCT	GGTGGACATG	150
35	GAGCTGCGCG	AGCAGCTGGA	GAAATACAAG	TTTCCGGCGG	AGGAGACGCC	200
	AATCGTGCGC	GGCTCAGCCC	TCAAAGCCGT	CGAGGGCGAT	GCGAAGTACG	250
	AGGAGAACAT	TCTCGAACTG	GTGCGGAAGT	GTGACGAGTG	GATCCCTGAC	300
	CCGCCGCGCG	ACACAGACAA	GCCTTTCCTT	ATGGCCATCG	AGCACGTTTA	350
	CGAGATCGGC	AAGGACAAGA	AGAGCGTTGT	CGTGACCGGC	CGCGTCGATC	400
40	AGGGCGTTCT	GAAGCTCAAC	ACAGACGCCG	AGCTGGCCGG	CTTCAGCTCC	450
	AAGAAGTCGA	CGGTGAGGGT	GACGGGCATC	GAGATGTACC	ACAAGACGCT	500
	GAGCGAGTGC	ATGCCTGGTG	ACTCCGTCGG	CGTCAGCATT	GTCGGCACCG	550
	GCGACACGAC	CAGTCTATCC	AAGGGCAACG	TGGAACGCGG	CATGGTGATG	600
	GCGGCGACGG	GTAGCACGAA	CCTGTACAAC	AAGGTGAAGG	CGCAGGTGTA	650
45	CGTGCTGACG	AAGGATGAGG	GCGGCCGCCA	CACTGGCTTT	AGTCCTCACT	700
	ACCGCCCCGA	GCTCTTCTTC	CATTGTGCTG	ACGTGACGGC	GGACATGAGC	750
	TTCCCGGAGG	CGGAGAAGCA	CCGCGAAGAG	CTCAACAAGA	AATTCGGCCG	800
	CGGCCCCGAG	GAGGACAAGA	AGAAAGAGGC	AGCGATGAAG	GAGTTCGAGA	850
	GCAAGCTCGT	CTGCATGCCG	GGCGATAACC	GCGAGCTGAT	CCTGACGCTG	900
50	GCGTACCCGA	TGCCCATTGA	AAAGGGTCTG	AAGTTCACC		939

2) INFORMATION FOR SEQ ID NO: 848

55

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 933 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

60

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 5 (A) ORGANISM: *Leishmania enriettii*
(B) STRAIN: ATCC 50120

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 848

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10  CACCGACGGC GTCATGCCGC AGACACGGGA GCACCTGCTC ATCTGCTCGC      50
    AGATCGGGCT GCCGGCGCTT GTAGGGTTCA TCAATAAAGT TGACATGACG      100
    GACGAGGATA CGTGCGACCT CGTGGACATG GAGGTGCGGG AACAGETGGA      150
    GAAGTACAAG TTTCCGGCCG AGGAGACGCC CATCGTACGT GGCTCGGCCC      200
    TCAAGGCCCT CGAGGGGGAT GCGCAATACG AGGGGAGTAT TCTCGAGCTG      250
15  GTGCGAAAGT GCGACGAGTG GATCCCCGAC CCGCCGCGCA ACACCGAAAA      300
    GCCTTTCCTC ATGGCTATCG AGCACGTTTA CGAGCTCGGC AAAGACAAGA      350
    AGAGCGTCAT CGTTACCGGC CGCGTCGATC AAGGTGTGCT GAAGCTCAAC      400
    ACAGACGCCG AGCTGGCCGG CTTCAGCGCC AAGAAGGCGA CAGTCAAAGT      450
    GACGGGCATC GAGATGTATC ACAAGACACT CAATGAGTGC ATGCCCCGGC      500
20  ACTCTGTCGG TGTCAGCATC GTCGGTACCG GTGACACGAC CAGCTTATCC      550
    AAGGATAATG TTGAGCGCGG TATGGTAATG GCGGCAACGG GTAGCACGAA      600
    CCTGTACAAC AAGCTGAAGG CGCAGGTTTA CGTGCTGACA AAGGAGGAGG      650
    GTGGCCGCCA CACCGGGTTC AGCCCCCACT ACCGCCCGCA GCTCTTCTTC      700
    CACTGCGCTG ACGTGACCGC AGACATGAGC TTCCCGGAGG CGGAGAAGTA      750
25  CCGCGAGGAG CTCAACAAGA AGTTCGGCCG TGGCCCTGAG GAGGACAAGA      800
    AGAAAGAGGC GGAGATGAAG GAGTTCGAAA GCAAACCTGT CTGCATGCCA      850
    GGCATAAACC GCGAGCTGAT CCTAACTCTG GCGTACCCGA TGCCCATCGA      900
    CAAGGGCCTG AAGTTCACCA TCCGTGAGGG CGG      933

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30

2) INFORMATION FOR SEQ ID NO: 849

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 943 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

40 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Leishmania gerbilli*
(B) STRAIN: ATCC 50121

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 849

```

    CGGTGGCATC ATTGTGGTGG CGGCCACCGA CGGCGTCATG CCGCAGACAC      50
    GCGAGCACCT CCTGATCTGC TCGCAGATTG GGCTTCCGGC GCTCGTAGGG      100
50  TTCATCAACA AAGTGGACAT GACGGACGAG GACACGTGCG ACCTGGTGGA      150
    CATGGAGGTG CGCGAGCAGC TGGAGAAATA CAAGTTTCCG GCGGAGGAGA      200
    CACCAATCGT GCGCGGCTCG GCCCTCAAGG CCGTCGAGGG CGACGCGAAG      250
    TACGAGGAGA ACATCCTCGA ACTGGTGC GG AAGTGC GACG AGTGGATCCC      300
    CGACCCGCCG CGCAACACAG ACAAGCCTTT CTTATGGCC ATCGAGCACG      350
55  TTTACGAGAT CGGCAAGGAC AAGAAGAGCG TCATCGTGAC CGGCCGCGTC      400
    GATCAGGGCG TGCTGAAGCT CAACACGGAC GCCGAGCTGG CCGGCTTCAG      450
    CGCCAAGAAG TCGACGGTGA GGGTGACGGG CATTGAGATG TACCACAAGA      500
    CGCTGAGCGA GTGCATGCCC GGTGACTCCG TCGGCGTCAG CATTGTGCGC      550
    ACCGGCGACA CGACCAGTCT GTCCAAGGAC AACGTGGAAC GCGGCATGGT      600
60  AATGGCGGCG ACGGGTAGCA CGAACCTGTA CAACAAGGTG AAGGCGCAGG      650

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	TGTACGTGCT	GACGAAGGAT	GAGGGCGGGC	GCCACACTGG	CTTCAGCCCC	700
	CACTACCGCC	CGCAGCTCTT	CTTCCATTGC	GCTGACGTGA	CAGCGGACAT	750
	GAGCTTCCCG	GAGGCGGAGA	AGCACCGCGA	GGAGCTCAAC	AAGAAATTCCG	800
	GCCGCGGCCC	CGAGGAGGAC	AAGAAGAAAG	AGGCGGAGAT	GAAGGAGTTC	850
5	GAGAGCAAGC	TCGTCTGCAT	GCCGGGCGAT	AACCGCGAGC	TGATCCTGAC	900
	GCTGGCGTAC	CCGATGCCCA	TTGAAAAGGG	TCTGAAGTTC	ACC	943

10 2) INFORMATION FOR SEQ ID NO: 850

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 918 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

20 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Leishmania major*
(B) STRAIN: ATCC 50122

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 850

25	GGCATCATTG	TGGTGGCGGC	CACCGACGGC	GTCATGCCGC	AGACACGCGA	50
	ACACCTCCTG	ATCTGCTCGC	AAATTGGCCT	TCCGGCGCTC	GTAGGGTTCA	100
	TCAACAAAGT	GGACATGACG	GACGAGGACA	CGTGTGACCT	GGTGGACATG	150
	GAGGTGCGCG	AGCAGCTGGA	GAAATACAAG	TTTCCGGCGG	AGGAGACACC	200
30	AATCGTGCGC	GGCTCGGCCC	TCAAGGCCGT	CGAGGGCGAC	GCGAAGTACG	250
	AGGAGAACAT	CCTCGAACTG	GTGCGGAAGT	GCGACGAGTG	GATCCCCGAC	300
	CCGCCGCGCA	ACACAGACAA	GCCTTTCCTT	ATGGCCATCG	AGCACGTTTA	350
	CGAGATCGGC	AAGGACAAGA	AGAGCGTCAT	CGTGACCGGC	CGCGTCGATC	400
	AGGGCGTGCT	GAAGCTCAAC	ACAGACGCCG	AGCTGGCCGG	CTTCAGCGCC	450
35	AAGAAGTCGA	CGGTGAGGGT	GACGGGCATT	GAAATGTACC	ACAAGACGCT	500
	GAGCGAGTGC	ATGCCCCGGT	ACTCCGTCGG	CGTCAGCATT	GTCGGCACCG	550
	GCGACACGAC	CAGTCTGTCC	AAGGACAACG	TGGAGCGCGG	CATGGTAATG	600
	GCGGCGACGG	GTAGCACGAA	CCTGTACAAC	AAGGTGAAGG	CGCAGGTGTA	650
	CGTGCTGACG	AAGGATGAGG	GCGGCCGCCA	CACTGGCTTC	AGCCCCCACT	700
40	ACCGCCCCGA	GCTCTTCTTC	CATTGCGCTG	ACGTGACAGC	GGACATGAGC	750
	TTCCCGGAGG	CGGAGAAGCA	CCGCGAGGAG	CTCAACAAGA	AATTCGGCCG	800
	CGGCCCCGAG	GAGGACAAGA	AGAAAGAGGC	GGAGATGAAG	GAGTTCGAGA	850
	GCAAGCTCGT	CTGCATGCCG	GGCGATAACC	GCGAGCTGAT	CCTGACGCTG	900
45	GCGTACCCGA	TGCCCCATT				918

2) INFORMATION FOR SEQ ID NO: 851

50 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 939 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
55 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 60 (A) ORGANISM: *Leishmania mexicana*
(B) STRAIN: ATCC 50156

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 851

	CGGTGGCATC	ATTGTGGTGG	CGGCCACCGA	CGGCGTCATG	CCGCAGACAC	50
5	GCGAGCATCT	CCTGATCTGC	TCGCAGATTG	GGCTTCCGGC	GCTCGTAGGG	100
	TTCATCAACA	AAGTGGACAT	GACGGACGAG	GACACGTGCG	ACCTGGTGGA	150
	CATGGAGGTG	CGTGAGCAGC	TGGAGAAATA	CAAGTTTCCG	GCGGAAGAGA	200
	CGCCCATCGT	GCGCGGCTCG	GCCCTCAAGG	CCGTCGAGGG	CGACGCGAAG	250
	TACGAGGAGA	ACATCCTCGA	ACTGGTGCGG	AAGTGCGACG	AATGGATCCC	300
10	CGACCCGCCG	CGCAACACAG	ACAAGCCTTT	CCTTATGGCC	ATTGAGCACG	350
	TTTACGAGAT	CGGCAAGGAC	AAGAAGAGCG	TCATCGTGAC	CGGCCGCGTC	400
	GATCAGGGCG	TGCTGAAGCT	CAACACAGAC	GCEGAGCTGG	CEGGCTTCAG	450
	CGTCAAGAAG	TCGACGGTGA	GGGTGACGGG	CATCGAGATG	TACCACAAGA	500
	CGCTGAGTGA	GTGCATGCCC	GGTGACTCCG	TCGGCGTCAG	CATTGTCGGC	550
15	ACCGGCGACA	CGATCAGTCT	CTCCAAGGAC	AACGTTGAAC	GCGGCATGGT	600
	AATGGCGGCA	ACGGGTAGCA	CGAACCTGTA	CAACAAGGTG	AAGGCGCAGG	650
	TGTACGTGCT	GACGAAGGAT	GAGGGCGGCC	GCCACACTGG	CTTCAGCCCC	700
	CACTACCGCC	CGCAGCTCTT	CTTCCATTGT	GCTGACGTGA	CGGCGGACAT	750
	GAGCTTCCCG	GAGGCGGAGA	AGCACCGCGA	GGAGCTCAAC	AAGAAATTTC	800
20	GCCGCGGCCC	CGAGGAGGAC	AAGCAGAAGG	AGGCGGAGAT	GAAAGAGTTC	850
	GAGAGCAAGC	TCGTCTGCAT	GCCGGGCGAC	AACCGCGAGC	TGATCCTGAC	900
	GCTGGCGTAC	CCGATGCCCA	TTGAGAAGGG	TCTGAAGTT		939

25

2) INFORMATION FOR SEQ ID NO: 852

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 912 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Leishmania tarentolae*
- (B) STRAIN: MOU-2

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 852

	TCATTGTGGT	GGCCGCCACC	GACGGCGTCA	TGCCGCAAAC	ACGGGAGCAC	50
	CTTTTGATCT	GCTCGCAGAT	CGGGCTGCCG	GCGCTCGTAG	GGTTCATCAA	100
	CAAAGTGGAC	ATGACAGACG	AAGACACGTG	CGACCTGGTA	GACCTGGAGG	150
45	TGCGTGAGCA	GCTGGAGAAG	TACAAGTTTC	CGGCAGAGGA	AACACCAATC	200
	GTGCGTGGCT	CGGCCCTCAA	GGCCGTTGAG	GGCGATGCAA	AGTACGAGGA	250
	GAACATCCTC	GAAGTGGTGC	GGAAGTGCGA	CGAGTGGATC	CCAGACCCGC	300
	CACGCAATAC	GGACAAGCCT	TTCCTTATGG	CCATTGAACA	CGTGTACGAG	350
	ATCGGCAAGG	ATAGGAAAAG	CGTCATCGTA	ACCGGCCGCG	TCGATCAAGG	400
50	TGTGCTGAAG	CTGAACACAG	ACGCCGAGCT	GGCCGGCTTC	AGCGCCAAGA	450
	AGTCGACGGT	GAAAGTGACG	GGCATTGAGA	TGTACCACAA	GACACTGACA	500
	GAGTGCATGC	CCGGCGACTC	TGTCGGCGTC	AGCATTGTGG	GCACTGGYGA	550
	CACGACCAGC	CTCTCTAAGG	ACAATGTTGA	GCGTGGCATG	GTAAGTGGCCG	600
	CTACGGGTAG	CACGAACCTG	TACAACAAAG	TAAAGGCGCA	GGTGTATGTA	650
55	CTCACGAAGG	ATGAGGGCGG	CCGCCACACC	GGCTTCAGCC	CCCACTACCG	700
	TCCGCAGCTC	TTCTTCCACT	GCGCTGACGT	AACGGCGGAC	ATGAGCTTCC	750
	CGGAGGCGGA	GAAGCACCGC	GAGGAACTCA	ATAAGAAATT	CGGCCGCGGC	800
	CCCGAGGAGG	ACAAGAAAAA	GGAGGCGGAG	ATGAAGGAGT	TCGAGAGCAA	850
	GCTGGTCTGC	ATGCCAGGCG	ATAACCGCGA	GCTGATCCTG	ACATTGGCGT	900
60	ACCCGATGCC	TA				912

2) INFORMATION FOR SEQ ID NO: 853

5

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 936 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

10

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Trypanosoma cruzi*
 (B) STRAIN: MM3

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 853

20 ATTCTTGTGG TGGCAGCTAA CGACGGATGC ATGCCGCAGA CGCGTGAGCA 50
 CCTGCTTATT TGTTCGCAGA TTGGCCTTCC TGCTCTTGTA TGCTTTATCA 100
 ATAAGTGTGA CATGATGCAA GGGCAGGAGG AAATGATTGA ACTTGTTGAA 150
 ATGGAGGTAC GTGAACTTT GGAGAAGTAC AAGTTCCTG CGGAGGAGAC 200
 GCCATTTGTG CGGGGGTCTG CGGTGAAGGC ATTGGAGGGT GATGCTGAAA 250
 25 ATGAAGGAAA GATTTTGGAG CTTGTAAAAA AATGTGATGA ATGGATTCCC 300
 GACCCACCGC GTGCCATTGA AAAACCGTTC CTTATGGCCA TTGAGCACGT 350
 TTTTGAGGTT GGAAAGGATA AGAAGGCCGT TGTGTGAGC GGGCGTGTGG 400
 ACCAGGGGCA GTTGAAGGTC GGCGCAGATG CAGAACTTTC CGGGTTTAGC 450
 GCAAAGAAGC TGACGGTGAA GGTGTCTAGC ATCGAAATGT ACCATAAAAT 500
 30 TCTGGAGGAT TGCATGCCTG GTGACTCTGT TGGCGCGAAG ATCGTTGGCA 550
 GCGGTGAAAC AGTGAACCTG TCGAAGGAAA ATGTGGAACG CGGCATGGTA 600
 CTCTCCGCAC CAGGTGCAAC GACACTGTTC AACAAGGTCC GCGCGCAGGT 650
 GTACGTGTTG ACAAAGGAAG AAGGCGGTCTG TCACACAGCC TTTAGTCCTC 700
 ACTATCGTCC GCAGCTTTTC TTCCACTGTG CTGATGTCAC GGCAGATATT 750
 35 AACTTCCCGG AAAGCGAGAA GCTTGCAGGG GAGCTGAACA AAAAGTATGG 800
 CCGTGATGCG GCGGAACAGA AGAAGAAGGA GGCAGAACTG AAAGAGTTTG 850
 AAAAGACGCT TGTCTGCATG CCTGGTGATA ACCGCGAACT CCTGCTCACC 900
 CTTGCCTATC CAATGCCAAT GGAAAAGGGA CTCAAG 936

40

2) INFORMATION FOR SEQ ID NO: 854

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 934 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

45

(ii) MOLECULE TYPE: Genomic DNA

50

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Trypanosoma cruzi*
 (B) STRAIN: PCU-1

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 854

CGGCATTCTT GTGGTGGCAG CTAACGACGG ATGCATGCCG CAGACGCGTG 50
 AGCACCTGCT TATTTGTTCT CAGATTGGCC TTCCTGCTCT TGTATGCTTT 100
 60 ATCAATAAGT GTGACATGAT GCAAGGGCAG GAGGAAATGA TTGAGCTTGT 150

	TGAAATGGAG	GTACGTGAAC	TTTTGGAGAA	GTACAAAGTTC	CCTGCGGAGG	200
	AGACGCCATT	TGTGCGGGGG	TCTGCGGTGA	AGGCATTGGA	GGGTGATGCT	250
	GAAAATGAAG	GAAAGATTTT	GGAGCTTGTA	AAAAAATGTG	ATGAATGGAT	300
	TCCCCACCCA	CCGCGTGCCA	TTGAAAAACC	GTTCTTATG	GCCATTGAGC	350
5	ACGTTTTTGA	GGTTGGAAAG	GATAAGAAAG	CCGTTGTTGT	GAGCGGGCGT	400
	GTGGACCAGG	GGCAGTTGAA	GGTCGGCGCA	GATGCAGAAC	TTTCCGGGTT	450
	TAGTGCAAAG	AAGCTGACGG	TGAAGGTGTC	TAGCATCGAA	ATGTACCATA	500
	AAATTCTGGA	GGATTGCATG	CCTGGTGAAT	CTATTGGCGC	GAAGATCGTT	550
	GGCAGCGGTG	AAACAGTGAA	CCTGTGCAAG	GAAAATGTGG	AACGCGGCAT	600
10	GGTACTCTCC	GCACCAGGTG	CAACGACACT	GTTCAACAGG	GTCCGCGCGC	650
	AGGTGTACGT	GTTGACAAAG	GAAGAAGGCG	GTCGTCACAC	AGCCTTTAGT	700
	CCTCACTATC	GTCCGCAGCT	TTTCTTCCAC	TGTGCTGATG	TCACGGCGGA	750
	TATTAACCTC	CCGGAAGCG	AGAAGCTTGC	AGGGGAGCTG	AACAAAAAGT	800
	ATGGCCGTGA	CGCGGCGGAA	CAGAAGAAGA	AGGAGGCAGA	ACTGAAAGAG	850
15	TTTGAAGA	CGCTTGTCTG	CATGCCTGGT	GATAACCGCG	AACTCCTGCT	900
	CACCTTGCC	TATCCAATGC	CAATGGAAAA	GGGA		934

20 2) INFORMATION FOR SEQ ID NO: 855

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 937 bases
 (B) TYPE: Nucleic acid
 25 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

30 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Trypanosoma cruzi*
 (B) STRAIN: CGL-1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 855

35	TGGCGGCATT	CTTGTGGTGG	CAGCTAACGA	CGGATGCATG	CCGCAGACGC	50
	GTGAGCACCT	GCTTATTTGT	TCGCAGATTG	GCCTTCCTGC	TCTTGTATGC	100
	TTTATCAATA	AGTGTGACAT	GATGCAAGGG	CAGGAGGAAA	TGATTGAACT	150
	TGTTGAAATG	GAGGTACGTG	AACTTTTGGG	GAAGTACAAG	TTCCCTGCGG	200
40	AGGAGACGCC	ATTTGTGCGG	GGGTCTGCGG	TGAAGGCATT	GGAGGGTGAT	250
	GCTGAAAATG	AAGGAAAGAT	TTTGGAGCTT	GTAAAAAAT	GTGATGAATG	300
	GATCCCCGAC	CCACCGCGTG	CCATTGAAAA	ACCGTTCCTT	ATGGCCATTG	350
	AGCACGTTTT	TGAGGTTGGA	AAGGATAAGA	AGGCCGTTGT	TGTGAGCGGG	400
	CGTGTGGACC	AGGGGCAGTT	GAAGGTCGGC	GCAGATGCAG	AACTTTCGGG	450
45	GTTTAGCGCA	AAGAAGCTGA	CGGTGAAGGT	TGCTAGCATC	GAAATGTACC	500
	ATAAAATTCT	GGAGGATTGC	ATGCCTGGTG	ACTCTGTTGG	CGCGAAGATC	550
	GTTGGCAGCG	GTGAAACAGT	GAACCTGTGC	AAGGAAAATG	TGGAACGCGG	600
	CATGGTACTC	TCCGCACCAG	GTGCAACGAC	ACTGTTCAAC	AAGGTCCGCG	650
	CGCAGGTGTA	CGTGTTGACA	AAGGAAGAAG	GCGGTGCTCA	CACAGCCTTT	700
50	AGTCCTCACT	ATCGTCCGCA	GCTTTTCTTC	CACTGTGCTG	ATGTCACGGC	750
	AGATATTAAC	TTCCCGGAAA	GCGAGAAGCT	TGCAGGGGAG	CTGAACAAAA	800
	AGTATGGCCG	TGATGCGGCG	GAACAGAAGA	AGAAGGAGGC	AGAACTGAAA	850
	GAGTTTGAAA	AGACGCTTGT	CTGCATGCCT	GGTGATAACC	GCGAACTCCT	900
55	GCTCACCTT	GCCTATCCAA	TGCCAATGGA	AAAGGGA		937

2) INFORMATION FOR SEQ ID NO: 856

60 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 888 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

5

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Babesia bigemina*
 (B) STRAIN: Suarez-2

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 856

	CTTATTATGG	AGCTGATCAA	CAACGTCGCG	AAGAAGCACG	GTGGTTTCTC	50
15	CGTGTTCGCC	GGCGTCGGCG	AGCGCACCAG	GGAGGGCAAC	GAGCTGTACC	100
	ACGAGATGAT	GGAGACCGGC	GTCATCAAGC	GCCGCCAGCT	GGATGACGGC	150
	ACGTTCGACT	TCTCCGGCTC	CAAGGCCGCG	CTGGTGACG	GCCAGATGAA	200
	CGAGCCGCCA	GGTGCCAGGG	CGCGTGTTGC	CCTCACTGGC	CTGACGGTGG	250
	CCGAGTACTT	CCGTGATGAG	GACGGCCAGG	ACGTGCTGCT	CTTCATCGAC	300
20	AACATCTACC	GTTTCACCCA	GGCTGGTTCT	GAGGTGAGTG	CCCTTTTGGG	350
	GCGCATCCCG	TCCGCCGTCG	GTTACCAGCC	GACCCTCGCC	ACCGACCTTG	400
	GCGCGCTGCA	GGAGCGTATC	ACGACGACCA	ACAAGGGCTC	CATCACCTCC	450
	GTGCAGGCCG	TCTACGTGCC	GGCCGACGAT	ATCACCGACC	CGGCGCCTGC	500
	GACCACCTTC	ACCCATCTGG	ACGCGACCAC	TGTGCTCTCC	CGTTCCATCG	550
25	CCGAGCTGGG	TATCTACCCC	GCCGTCGACC	CGCTCGACTC	CACCTCGCGT	600
	ATGCTGTCCG	CGAACATCGT	CGGCGAGGAG	CAGTACAACG	TGGCGCGTGG	650
	CGTGCGAGAA	ATACTGCAGG	ACTACAAATC	GCTGCAGGAT	ATCATCGCCA	700
	TCCTGGGTAT	GGACGAGCTG	TCTGAGCAGG	ACAAGTTCGT	CGTCGCGCGT	750
	GCGCGCAAGG	TTCAGCGTTT	CCTATCCCAG	CCCTTCCAGG	TGGCTGAGGT	800
30	ATTACCCGGC	AAGCCCGGAC	GTTTCGTCGA	GCTGCAGGAC	ACCATCAGCG	850
	GCGTCAAGGA	GATTTTGGAC	GGCGAGTGCG	ACGACATG		888

35 2) INFORMATION FOR SEQ ID NO: 857

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 884 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

40

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Babesia bovis*
 (B) STRAIN: Suarez-3

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 857

50

	TGATTATGGA	ATTGATCAAC	AATGTCGCCA	AGAAACACGG	TGGGTTCTCC	50
	GTGTTTCGCTG	GTGTTGGTGA	ACGTACGAGG	GAAGGTAACG	AACTGTACCA	100
	TGAAATGATG	GAAACGGGTG	TCATCAAGCG	CCGTCAACTG	GAAGACGGAA	150
	CATTTGACTT	CTCGGGCTCT	AAAGCTGCTT	TGGTGACGG	ACAAATGAAC	200
55	GAACCACCAG	GTGCTAGAGC	CCGTGTTGCA	CTCACGGGAT	TGACCGTTGC	250
	CGAGTATTTT	CGTGATGAAG	AGGGGCAGGA	TGTGCTACTC	TTCATCGATA	300
	ACATCTACCG	TTTCACCCAG	GCCGGTTCGG	AAGTGAGTGC	GCTGTTAGGA	350
	AGAATTCCAT	CCGCCGTGGG	TTATCAACCT	ACATTGGCCA	CTGATCTCGG	400
	AGCACTCCAG	GAACGCATTA	CTACAACCAA	CAAGGGTTCG	ATTACATCAG	450
60	TCCAGGCAGT	ATACGTCCCA	GCCGATGATA	TACTGATCC	CGCTCCAGCT	500

	ACCACTTTCT	CGCACTTGGG	TGCCACTACA	GTGCTTTCTC	GTTCAATTGC	550
	GGAGTTGGGT	ATTTACCCTG	CGGTCGACCC	GCTTGACTCA	ACGTCACGTA	600
	TGCTGTCGGC	CAACATTGTA	GGACAGGAAC	AGTACGATGC	CGCACGTGGT	650
	GTACAGAAAA	TTTTACAGGA	CTACAAATCA	CTGCAGGATA	TCATTGCCAT	700
5	TCTGGGTATG	GACGAGCTGT	CTGAGCAGGA	CAAGTTCGTT	GTAGCACGCG	750
	CCCGTAAGGT	ACAGCGTTTC	CTGTCTCAGC	CGTTCCAAGT	GGCTGAGGTG	800
	TTCACCGGCA	AGCCTGGGAG	GTTTCGTTGAA	CTACAGGATA	CCATCAGCGG	850
	TGTCAAGGAA	ATCTGGAAGG	TGAGTGTGAC	GATA		884
10						

2) INFORMATION FOR SEQ ID NO: 858

- (i) SEQUENCE CHARACTERISTICS:
- 15 (A) LENGTH: 871 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear
- 20 (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Babesia microtti*
- (B) STRAIN: Persing-1
- 25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 858

	TGGAAGTATG	TAATAATGTG	GCCAAAAAGC	ATGGCGGTTA	CTCTGTTTTT	50
	GCAGGTGTAG	GTGAAAGGAC	GAGGGAGGGT	AATGAATTGT	ACCATGAAAT	100
30	GATGGAGACA	GGTGTATATA	AGAAAAAGGC	ACTAGGTGGT	GGGAAGTTTG	150
	ATTTCACTGG	ATCTAAAGCA	GCGCTGGTCT	ATGGACAAAT	GAACGAGCCA	200
	CCTGGGGCCC	GTGCTAGAGT	GGCACTAACT	GGATTAACAG	TCGCAGAATA	250
	TTTCCGTGAC	GAACAAGGAC	AAGACGTGTT	GTTGTTTATT	GATAATATTT	300
	ACCGATTTAC	TCAGGCAGGG	TCTGAGGTTT	CAGCCTTGCT	AGGCCGTATA	350
35	CCTTCAGCTG	TGGGATACCA	GCCTACATTG	GCAACAGATC	TTGGCTGTTT	400
	ACAAGAACGA	ATTACTACGA	CCAAATCTGG	TTCAATCACC	AGTGTACAAG	450
	CTGTGTATGT	GCCAGCAGAT	GATATTACTG	ATCCAGCGCC	TGCCACAAC	500
	TTTACTCACT	TGGACGCTAC	TACTGTACTT	AGCAGGCCAA	TTGCTGAACT	550
	CGGTATTTAT	CCAGCGGTAG	ACCCGTTGGA	TTCAACAAGC	CGTATGCTAA	600
40	GCGCGAACAT	TGTGGGAAAT	GAACACTATA	GTGTAGCCCG	TTCCGTGCAG	650
	AAGATACTGC	AAGATTACAA	ATCGCTTCAG	GACATTATTG	CCATTTTGGG	700
	TATGGATGAA	CTGTGCGAAC	AAGACAAAAA	TATAGTAGCC	CGAGCAAGGA	750
	AGATGCAAAG	GTTCTTATCA	CAGCCATTCC	AAGTGGCGGA	AGTTTTTACT	800
	GGTAAACCGG	GAAGATTTGT	GGAATTGGAA	GATACAATTG	CCGGGGCACG	850
45	AGATATAATT	GCGGGTAATT	G			871

2) INFORMATION FOR SEQ ID NO: 859

- 50 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1255 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- 55 (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
- 60 (A) ORGANISM: *Leishmania guyanensis*

(B) STRAIN: ATCC 50126

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 859

5	TGACGGCGCT	GGACGTGACG	GAGGACCTCG	GCCGCGATGA	GCCGCTGACG	50
	CTGGAGATCG	TGCAGCACTT	GGATGCGAAC	ACCGGCCGCT	GCATTGCGAT	100
	GCAGACGACG	GACCTGCTGA	AGCTGAAGTC	GAAGGTTGTG	TCGACCGGCG	150
	GCAACATCTC	CGTGCCCGTG	GGCCGCGAGA	CACTGGGCCG	CATCTTCAAC	200
	GTGCTGGGCG	ACGCGATTGA	CCACCGCGGC	CCCGTGTGCG	AGAAGATGCG	250
10	CATGGCGATC	CACGCCGAGG	CGCCGAAGCT	GGCGGACCAG	GCTGCGGAGG	300
	ACACGATCCT	GACGACCGGC	ATCAAGGTGA	TCGACCTGAT	TCTGCCCTAC	350
	TGCAAGGGCG	GCAAGATCGG	CCTGTTCCGC	GGTGCCGGTG	TGGGCAAGAC	400
	TGTGATCATC	ATGGAGCTGA	TCAACAACGT	CGCGAAGGGG	CACGGCGGCT	450
	TCTCCGTGTT	CGCCGGCGTT	GGCGAGCGCA	CGCGCGAGGG	CACGGACCTG	500
15	TACCTGGAGA	TGATGCAGTC	AAAGGTGATT	GACCTGAAGG	GCGAGTCGAA	550
	GTGCGTGCTT	GTGTACGGGC	AGATGAACGA	GCCCCCGGGT	GCGCGCGCGC	600
	GCGTTGCGCA	GTCTGCGCTG	ACGATGGCCG	AGTACTTCCG	CGACGTGGAG	650
	GGCCAGAACG	TGCTGCTGTT	CATCGACAAC	ATCTTCCGCT	TCACGCAGGC	700
	GAACTCCGAG	GTGTCTGCGC	TGCTGGGCCG	CATCCCGGCC	GCCGTGGGTT	750
20	ACCAGCCGAC	GCTTGCGGAG	GATCTTGCCA	TGCTGCAGGA	GCGCATTACG	800
	TCGACGACGA	AGGGATCGAT	TACGTCTGTG	CAGGCTGTGT	ACGTGCCTGC	850
	GGATGATATC	ACGGACCCCG	CGCCCGCGAC	GACGTTCTCG	CACCTGGACG	900
	CGACGACTGT	GCTGGACCGC	GCGGTGGCGG	AGTCGGGCAT	CTACCCTGCC	950
	GTGAACCCGC	TGGAGTGCGC	GTCGCGCATC	ATGGACCCCG	ATGTGATCGA	1000
25	CGTGGACCAT	TACAACGTTG	CACAGGATAT	CGTCCAGATG	CTGACCAAGT	1050
	ACAAGGAGCT	GCAGGACATC	ATTGCGGTGC	TTGGCATCGA	CGAGCTGAGC	1100
	GAGGAGGACA	AGGTCGTGGT	GGACCGCGCG	CGCAAGGTGA	CGCGGTTCTT	1150
	GTCGCAGCCG	TTCCAGGTTG	CGGAGGTGTT	CACCGGCATG	ACGGGGCCACT	1200
	ACGTGCAGCT	GAGCGACACG	GTGGAGTCGT	TCTCTGGCCT	GCTGATGGGG	1250
30	TCGTA					1255

2) INFORMATION FOR SEQ ID NO: 860

35

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1222 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

40

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

45

- (A) ORGANISM: *Leishmania mexicana*
- (B) STRAIN: ATCC 50156

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 860

50	CTCGGAGGGC	GTCCCGCCCG	TGCTGACGGC	GCTGGATGTG	ACGGAGGACC	50
	TTGGCCGCGA	TGAGCCGCTG	ACGCTGGAGA	TCGTGCAGCA	CCTGGACGCG	100
	AACACCGGCC	GCTGCATTGC	GATGCAGACG	ACGGACCTGC	TGAAGCTGAA	150
	GTCGAAGGTT	GTGTGACCGG	GCGGCAACAT	CTCTGTGCCG	GTGGGCCGTG	200
	AGACGCTGGG	CCGCATCTTC	AACGTGCTGG	GCGACGCGAT	CGACCAGCGC	250
55	GGCCCCGTGG	GTGAGAAGAT	GCGCATGGCG	ATCCACGCCG	AGGCCCCGAA	300
	GCTGGCGGAT	CAGGCCGCGG	AGGACACGAT	CCTGACGACC	GGCATCAAGG	350
	TGATCGACCT	GATTCTGCCC	TACTGCAAGG	GTGGCAAGAT	CGGCCTGTTT	400
	GGCGGCGCCG	GTGTGGGCAA	GACCGTGATC	ATCATGGAGC	TGATTAACAA	450
	CGTCGCAAG	GGCCACGGTG	GTTTCTCGGT	GTTTGCCGGC	GTTGGCGAGC	500
60	GCACGCGCGA	GGGCACGGAC	CTGTACCTGG	AGATGATGCA	GTCGAAGGTG	550

	ATTGACCTGA	AGGGCGAGTC	GAAGTGCGTG	CTTGTGTACG	GGCAGATGAA	600
	CGAGCCCCCG	GGTGCGCGCG	CGCGCGTTGC	GCAGTCTGCG	CTGACGATGG	650
	CGGAGTACTT	CCGAGACGTG	GAGGGCCAGA	ATGTGCTGCT	GTTTCATCGAC	700
	AACATCTTCC	GCTTCACGCA	GGCGAACTCC	GAGGTCTCTG	CGCTGCTGGG	750
5	CCGCATTCCG	GCCGCCGTGG	GCTACCAGCC	GACGCTTGCG	GAGGATCTTG	800
	GTATGCTGCA	GGAGCGCATC	ACGTCGACGA	CGAAGGGGTC	GATCACGTCC	850
	GTGCAGGCCG	TGTACGTGCC	TGCGGATGAT	ATCACGGATC	CGGCGCCCGC	900
	GACGACGTTT	TCGCACCTGG	ACGCGACGAC	TGTGCTGGAC	CGCGCGGTGG	950
	CGGAGTCGGG	GATCTACCCT	GCCGTGAACC	CGCTGGAGTG	CGCGTCGCGT	1000
10	ATCATGGACC	CCGATGTGAT	CGACGTGGAC	CACTACAACG	TTGCGCAGGA	1050
	TATCGTGCAG	ATGCTGACCA	AGTACAAGGA	GCTGCAGGAT	ATCATTGCGG	1100
	TGCTTGGTAT	CGACGAGCTG	AGCGAGGAGG	ACAAGGTCGT	GGTGGACCGC	1150
	GCGCGCAAGG	TGACCCGGTT	CCTGTCGCAG	CCGTTCCAGG	TTGCGGAGGT	1200
	GTTCACGGGC	ATGACGGGCC	AC			1222

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2) INFORMATION FOR SEQ ID NO: 861

20 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1246 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

25

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Leishmania tropica*
- (B) STRAIN: ATCC 50129

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 861

	CCGTGCTGAC	GGCGCTGGAT	GTGACGGAGG	ACCTTGGCCG	CGATGAGCCG	50
35	CTGACGCTGG	AGATCGTGCA	GCACTTGGAC	GCGAACACCG	GCCGCTGCAT	100
	TGCGATGCAG	ACGACGGACC	TGCTGAAGCT	GAAGTCGAAG	GTTGTGTCTGA	150
	CCGGCGGCAA	CATCTCTGTG	CCGGTGGGCC	GTGAGACGCT	GGGCCGCATC	200
	TTCAACGTTC	TGGGCGACGC	GATCGACCAG	CGCGGCCCCG	TGGGCGAGAA	250
	GATGCGCATG	GCGATCCACG	CCGAGGCCCC	GAAGCTGGCG	GATCAGGCCG	300
40	CGGAGGACAC	GATCCTGACG	ACCGGCATCA	AGGTGATCGA	CCTGATTCTG	350
	CCCTACTGCA	AGGGTGGCAA	GATCGGCCTG	TTCGGCGGTG	CCGCTGTGGG	400
	CAAGACTGTG	ATCATCATGG	AGCTGATCAA	CAACGTCGCG	AAGGGCCACG	450
	GTGGTTTCTC	CGTGTTTGCC	GGCGTTGGCG	AGCGCACGCG	CGAGGGCACG	500
	GACCTGTACC	TGGAGATGAT	GCAGTCGAAG	GTGATTGACC	TGAAGGGCGA	550
45	GTCGAAGTGC	GTGCTTGTGT	ACGGGCAGAT	GAACGAGCCC	CCGGGTGCGC	600
	GCGCGCGCGT	TGCGCAGTCT	GCGCTGACGA	TGGCGGAGTA	CTTCCGCGAC	650
	GTGGAGGGCC	AGAACGTGCT	GCTGTTTCATC	GACAACATCT	TCCGCTTCAC	700
	GCAGGCGAAC	TCCGAGGTGT	CTGCGCTGCT	GGGCCGCATT	CCGGCCGCCG	750
	TGGGCTACCA	GCCGACGCTT	GCGGAGGATC	TTGGTATGCT	GCAGGAGCGC	800
50	ATCACGTCGA	CAACGAAGGG	GTCGATCACG	TCCGTGCAGG	CCGTGTACGT	850
	GCCAGCGGAT	GATATCACGG	ATCCCGCGCC	CGCGACGACG	TTCTCGCACC	900
	TGGACGCGAC	GACTGTGCTG	GACCGCGCGG	TGGCGGAGTC	GGGCATCTAC	950
	CCTGCCGTGA	ACCCGCTGGA	GTGCGCGTCG	CGTATCATGG	ACCCCGATGT	1000
	GATCGATGTG	GACCACTACA	ACGTTGCGCA	GGATATCGTG	CAGATGCTGA	1050
55	CCAAGTACAA	GGAGCTGCAG	GATATCATTG	CGGTGCTTGG	CATCGACGAG	1100
	CTGAGCGAGG	AAGACAAGGT	TGTTGTGGAC	CGCGCGCGCA	AGGTGACCCG	1150
	GTTCTGTGTC	CAGCCGTTCC	AGGTTGCGGA	GGTGTTACG	GGCATGACGG	1200
	GCCACTACGT	GCAGCTGGTC	GACACGGTGG	AGTCGTTCTC	TGGCCT	1246

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2) INFORMATION FOR SEQ ID NO: 862

- (i) SEQUENCE CHARACTERISTICS:
- 5 (A) LENGTH: 1265 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

10 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Leishmania tropica*
- 15 (B) STRAIN: ATCC 30815

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 862

	GGCGTGCCGC	CCGTGCTGAC	GGCGCTGGAT	GTGACGGAGG	ACCTTGGCCG	50
	CGATGAGCCG	CTGACGCTGG	AGATCGTGCA	GCACTTGGAC	GCGAACACGG	100
20	GCCGCTGCAT	TGCGATGCAG	ACGACGGACC	TGCTGAAGCT	GAAGTCGAAG	150
	GTCGTGTCGA	CCGGCGGCAA	CATCTCTGTG	CCGGTGGGCC	GTGAGACGCT	200
	GGGCCGCATC	TTCAAYGTTC	TGGGCGACGC	GATCGACCAG	CGCGGCCCCG	250
	TGGGCGAGAA	GATGCGCATG	GCGATCCACG	CCGAGGCCCC	GAAGCTGGCG	300
	GATCAGGCCG	CGGAGGACAC	GATCCTGACG	ACCGGCATCA	AGGTGATCGA	350
25	CCTGATTCTG	CCCTACTGCA	AGGGTGGCAA	GATCGGCCTG	TTCGGCGGTG	400
	CCGGTGTGGG	CAAGACTGTG	ATCATCATGG	AGCTGATCAA	CAACGTCGCG	450
	AAGGGCCACG	GCGGTTTCTC	CGTGTTTGCC	GGCGTTGGCG	AGCGCACGCG	500
	CGAGGGCACG	GACCTGTACC	TGGAGATGAT	GCAGTCGAAG	GTGATTGACC	550
	TGAAGGGCGA	GTCGAAGTGY	GTGCTTGTGT	ATGGGCAGAT	GAACGAGCCC	600
30	CCGGGTGCGC	GCGCGCGCGT	TGCGCAGTCT	GCGCTGACGA	TGGCGGAGTA	650
	CTTCCGCGAC	GTGGAGGGCC	AGAACGTGCT	GCTGTTTCATC	GACAACATCT	700
	TCCGCTTCAC	GCAGGCGAAC	TCCGAGGTGT	CTGCGCTGCT	GGGCCGCATT	750
	CCGGCCGCCG	TGGGCTACCA	GCCGACGCTT	GCGGAGGATC	TTGGTATGCT	800
	GCAGGAGCGC	ATCACGTCGA	CAACGAAGGG	GTCGATCACG	TCCGTGCAGG	850
35	CCGTGTACGT	GCCAGCGGAT	GATATCACGG	ATCCCGCGCC	CGCGACGACG	900
	TTCTCGCACC	TGGACGCGAC	GACTGTGCTG	GACCGCGCGG	TGGCGGAGTC	950
	GGGCATCTAC	CCTGCCGTGA	ACCCGCTGGA	GTGCGCGTCG	CGTATCATGG	1000
	ACCCTGATGT	GATCGATGTG	GACCACTACA	ACGTTGCGCA	GGATATCGTG	1050
	CAGATGCTGA	CCAAGTACAA	GGAGCTGCAG	GATATCATTG	CGGTGCTTGG	1100
40	CATCGACGAG	CTGAGCGAGG	AAGACAAGGT	TGTTGTGGAC	CGCGCGCGCA	1150
	AGGTGACCCG	GTTCTGTGTC	CAGCCGTTCC	AGGTTGCGGA	GGTGTTACAG	1200
	GGCATGACGG	GCCACTACGT	GCAGCTGGTC	GACACGGTGG	AGTCGTTCTC	1250
	TGGCCTGCTG	ATGGG				1265

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2) INFORMATION FOR SEQ ID NO: 863

- (i) SEQUENCE CHARACTERISTICS:
- 50 (A) LENGTH: 1191 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

55 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bordetella pertussis*

60 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 863

	ATGGCAAAAG	GCAAGTTTGA	ACGTACCAAG	CCGCACGTGA	ACGTGGGTAC	50
	GATTGGTCAC	GTTGACCACG	GCAAAACGAC	GTTGACGGCG	GCGATCACGA	100
	CGGTGCTGTC	GAACAAGTTC	GGCGGCGAGG	CTCGCGGCTA	CGACCAGATT	150
5	GACGCGGCGC	CGGAAGAGAA	GGCGCGTGGG	ATCACGATCA	ACACCTCGCA	200
	CGTTGAGTAC	GAGACGGAGA	CGCGTCACTA	CGCGCACGTT	GATTGCCCGG	250
	GTCACGCTGA	CTACGTGAAG	AACATGATCA	CGGGTGCTGC	GCAGATGGAC	300
	GGCGCGATCC	TGGTGGTGTG	GGCCGCAGAC	GGCCCGATGC	CGCAGACGCG	350
	CGAGCACATT	TTGCTGTGCG	GCCAGGTTGG	CGTGCCGTAC	ATCATCGTGT	400
10	TCCTGAACAA	GGCGGACATG	GTTGATGACG	CGGAGCTGCT	CGAGCTGGTG	450
	GAGATGGAAG	TCCGCGAACT	GCTGAGCAAG	TACGATTTCC	CGGGCGATGA	500
	CACGCCGATC	GTGAATGGTG	CGGCCAAGCT	GGCGCTGGAA	AGCGACAAAG	550
	GCGACCTGGG	CGAGCAGGCG	ATTCTGTGCG	TGGCGCAAGC	GCTGGACACG	600
	TACATTCCGA	CGCCGGAGCG	CGCGGTGCGC	GGTGCGTTCC	TGATGCCCGG	650
15	GGAAGACGTG	TTCTCGATCT	CGGGCCGTGG	CACGGTGGTG	ACTGGCCGTA	700
	TCGAGCGCGG	CGTGGTGAAG	GTTGGCGAGG	AAATCGAAAT	CGTGGGCATC	750
	AAGCCGACGG	TGAAGACGAC	CTGCACGGGC	GTGGAGATGT	TCCGCAAGCT	800
	GCTGGACCAG	GGCCAGGCGG	GCGACAACGT	GGGTATCTTG	CTGCGCGGCA	850
	CCAAGCGTGA	AGACGTCGAG	CGTGGCCAGG	TGCTGGCCAA	GCCGGGTTCG	900
20	ATCAACCCGC	ACACGGAATT	CACGGCCGAG	GTGTACATTC	TGTCCAAGGA	950
	AGAGGGTGGC	CGTCACACGC	CGTTCTTCAA	CGGCTATCGT	CCGCAGTTCT	1000
	ACTTCCGCAC	GACGGACGTG	ACCGGCACGA	TCGACCTGCC	GGCGGACAAG	1050
	GAAATGGTGC	TGCCGGGCGA	CAACGTGTCG	ATGACCGTCA	AGCTGCTGGC	1100
	CCCGATCGCC	ATGGAAGAAG	GTCTGCGTTT	CGCCATCCGT	GAAGGCGGTC	1150
25	GTACCGTCCG	TGCCGGGCGT	GTCGCCAAGA	TCATCAAGTA	A	1191

2) INFORMATION FOR SEQ ID NO: 864

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1350 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

40

- (A) ORGANISM: *Trypanosoma brucei*
 (B) STRAIN: LVH/75/USAMRU-K/18
 (C) ACCESSION NUMBER: extracted from U10562

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 864

45

	ATGGGAAAGG	AAAAGGTGCA	CATGAATCTT	GTGGTGGTGG	GCCACGTGCA	50
	TGCCGGTAAA	TCCACTGCAA	CGGGTCACTT	GATCTACAAG	TGCGGTGGTA	100
	TTGACAAACG	TACGATCGAG	AAGTTCGAGA	AAGAAGCTGC	CGACATTGGT	150
	AAGGCCCTCAT	TCAAGTACGC	ATGGGTGCTG	GACAAGCTGA	AGGCTGAGCG	200
50	CGAACGTGGT	ATCACGATCG	ACATTGCACT	GTGGAAATTC	GAGTCACCCA	250
	AGTCTGTCTT	CACTATTATT	GATGCTCCTG	GGCACCGTGA	CTTCATCAAG	300
	AACATGATCA	CCGGCACATC	GCAAGCCGAC	GCAGCCATCC	TCATCATTGC	350
	CTCTGCGCAG	GGTGAGTTCT	AGGCTGGTAT	CTCCAAGGAT	GGACAGACCC	400
	GCGAGCACGC	GTTGCTGGCC	TTCACTTTGG	GTGTGAAGCA	GATGGTTGTG	450
55	TGCTGCAACA	AAATGGACGA	CAAGACTGTG	AACTACGGAC	AGGAGCGGTA	500
	TGACGAGATT	GTGAAGGAGG	TGTCTGCTTA	CATCAAGAAG	GTTGGGTACA	550
	ACGTGGAGAA	GGTGCGCTTC	GTCCCCATCT	CCGGATGGCA	GGGCGACAAC	600
	ATGATTGAGA	AATCCGAGAA	GATGCCATGG	TACAAGGGTC	CAACGCTCCT	650
	GGAGGCACTA	GACATGCTGG	AGCCACCAGT	GCGTCCGAGC	GACAAGCCCC	700
60	TGCGTCTGCC	ACTGCAGACG	TGTACAAAGA	TCGGTGGTAT	TGGCACCGTG	750

	CCCGTTGGTC	GTGTGGAGAC	CGGCGTGATG	AAGCCTGGTG	ATGTGGTGAC	800,
	GTTTGCCCCC	GCCAACGTGA	CGACCGAGGT	GAAATCGATC	GAGATGCACC	850
	ACGAGCAGCT	CGCTGAGGCG	ACCCCCGGTG	ACAACGTCGG	CTTTAACGTG	900
	AAGAACGTTT	CTGTAAAGGA	CATCCGCCGT	GGCAACGTCT	GCGGTAACAC	950
5	CAAGAACGAC	CCCCCAAAGG	AGGCCGCCGA	CTTCACGGCA	CAGGTGATCA	1000
	TCCTGAACCA	CCCCGGACAG	ATTGGAAACG	GTTATGCGCC	CGTGCTGGAC	1050
	TGCCACACAT	CGCACATTGC	CTGCAAGTTC	GCGGAGATCG	AGTCGAAGAT	1100
	CGACCGTCGC	TCTGGCAAGG	AGCTGGAGAA	GGCTCCCAAG	TCGATCAAGT	1150
	CTGGCGACGC	CGCGATCGTG	CGCATGGTGC	CGCAGAAGCC	TATGTGCGTG	1200
10	GAGGTCTTCA	ACGACTACGC	GCCACTCGGC	CGCTTTGCCG	TGCGTGACAT	1250
	GCGCCAGACC	GTCGCTGTCG	GTATCATCAA	GGCCGTGACC	AAGAAGGACG	1300
	GTTCTGGTGG	TAAGGTGACG	AAGGCTGCGG	TGAAGGCTTC	GAAGAAATAA	1350

15

2) INFORMATION FOR SEQ ID NO: 865

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1052 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

25

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Cryptosporidium parvum*

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 865

	AAGCTCAAGG	CTGAGAGAGA	AAGAGGTATT	ACCATCGATA	TTGCTTTATG	50
	GCAATTCGAA	ACCCCAAAT	ACCACTACAC	TGTCATTGAT	GCCCCAGGTC	100
	ACAGAGATTT	CATCAAGAAT	ATGATTACTG	GTACCTCTCA	AGCTGATGTT	150
	GCCTTTATTGG	TTGTCCCAGC	CGATCGTTTC	GAAGGTGCCT	TCTCCAAGGA	200
35	AGGTCAAACC	AGAGAACATG	CTTTATTGGC	CTTCACTTTG	GGTGTGACAG	250
	AAATGATTGT	CGGTATTAAC	AAGATGGATA	CCTGTGAATA	CAAGCAATCT	300
	CGTTTTGATG	AAATCTTCAA	CGAAGTTGAT	GGTTACCTCA	AGAAGGTTGG	350
	TTACAACACC	GAGAAGATCC	CATTCGTTGC	CATTTCTGGT	TTCGTTGGTG	400
	ATAATATGGT	TGAGAGATCT	GACAAGATGC	CATGGTATAA	GGGTAAGACC	450
40	TTAGTCGAAG	CCCTCGACAC	TATGGAACCA	CCAAAGAGAC	CAACTGACAA	500
	GCCACTCCGT	CTCCCATTAC	AAGATGTTTA	CAAGATAGGT	GGTGTAGGTA	550
	CTGTCCCAGT	CGGTCGTGTT	GAGACTGGTA	TCATCAGACC	AGGTATGAAT	600
	GTTACCTTCG	CTCCAGCTGG	TGTTACCACT	GAAGTTAAGT	CAGTAGAAAT	650
	GCACCATGAG	CAGATGCCAG	AGGCCGTCCC	AGGTGACAAC	GTTGGTTTCA	700
45	ATGTTAAGAA	CGTCTCCATC	AAGGATATCA	AGAGAGGTTT	CGTTGCTTCT	750
	GATGCCAAGA	ATGACCCAGC	TAAGGGCTGT	GAAGACTTCA	CTGCTCAAGT	800
	TATCGTCCTC	AACCACCCAG	GTGAAATCAA	GAACGGTTAC	TCTCCAGTCG	850
	TTGACTGTCA	CACCGCTCAC	ATTCCTGCA	AATTCCAGAC	TATCACTGCT	900
	AAGATGGACA	AGAGATCTGG	TAAGGTTTTG	GAAGAAAACC	CAAAGCTTAT	950
50	CAAGTCTGGT	GATGCTGCTT	TGTTGTATTAT	GCAACCTTTG	AAGCCACTTT	1000
	GTGTTGAGGC	CTTCACTGAC	TACCCACCTC	TAGGTCGTTT	CGCTGTCCGT	1050
	GA					1052

55

2) INFORMATION FOR SEQ ID NO: 866

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 837 bases
 (B) TYPE: Nucleic acid

60

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

5

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Staphylococcus saprophyticus*

(B) STRAIN: ATCC 35552

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 866

	CAATGAAGTT	CCAGAAATTA	ACAATGCCTT	AGTEGTAAG	GTTGAAAGAG	50
	ATGAAGGTAC	AGTATCTCTT	ACATTAGAAG	TGGCATTACA	ACTTGGCGAT	100
	GATGTCGTAC	GTACAATTGC	AATGGATTCT	ACTGATGGTG	TTAAACGTGG	150
15	TACAGAAGTT	CGAGATAGCG	GAGATAGCAT	CAGTGTTCCT	GTTGGTGATG	200
	CTACGTTAGG	ACGTGTGTTT	AATGTTCTTG	GTGATACAAT	TGACTTAGAC	250
	GAGAAGCTTG	ATACTTCTGT	CAAACGTGAT	CCAATTCATA	GAGAAGCACC	300
	TGCATTGAT	CAATTATCAA	CAAAAGTTGA	AATCTTAGAA	ACAGGTATTA	350
	AAGTAATTGA	TTTACTTGCA	CCATATATTA	AAGGTGGTAA	AATCGGTTTA	400
20	TTCGGTGGCG	CTGGTGTAGG	TAAAACAGTA	TTAATTCAAG	AATTAATTAA	450
	TAATATAGCT	CAAGAACATG	GTGGTATTTT	AGTATTTGCC	GGCGTAGGTG	500
	AACGTACGCG	TGAAGGTAAT	GACTTATACT	ACGAAATGAG	TGATAGTGGT	550
	GTTATTAAGA	AAACAGCTAT	GGTCTTCGGA	CAAATGAATG	AGCCACCTGG	600
	TGCGCGTATG	CGTGTTGCTT	TATCAGGCTT	AACAATGGCT	GAACACTTCC	650
25	GTGATGTACA	AGGACAAGAT	GTTTTACTAT	TTATTGATAA	CATATTCAGA	700
	TTTACGCAAG	CTGGTTCAGA	AGTATCAGCA	CTATTAGGTC	GTATGCCATC	750
	AGCCGTTGGT	TATCAACCTA	CCCTTGCTAC	TGAAATGGGT	CAATTACAAG	800
	AACGTATTAC	ATCAACAAC	AAAGGATCTG	TAACGTC		837

30

2) INFORMATION FOR SEQ ID NO: 867

(i) SEQUENCE CHARACTERISTICS:

35

(A) LENGTH: 818 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

40 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Zoogloea ramigera*

(B) STRAIN: ATCC 25935

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 867

	AAGGTATTTCG	ATGCCTTGAA	AATGGAAGGC	TCCGAGCTGA	CCCTGGAAGT	50
	ACAACAGCAG	CTGGGCGACG	GCATTGTCCG	TACCATTGCA	CTGGGTACCT	100
50	CCGACGGCCT	GCGTCGCGGC	ATGATGATCC	AGAACACCGG	CAAACCTATC	150
	ATGGTGCCAG	TCGGTAAAGC	AACCCTGGGT	CGCATCATGG	ACGTGCTGGG	200
	TAACCCGATC	GACGAATGCG	GCGCGGTCGC	TCACGACCAG	ATCGCTTCGA	250
	TCCACCGCGC	TCCTCCTGCG	TACGACGAAC	TGTGCGCCATC	GCAAGATCTG	300
	CTGGAACCG	GCATTAAAGT	TATTGACCTG	GTGTGCCCCG	TCGCCAAGGG	350
55	CGGTAAAGTC	GGTCTGTTCG	GCGGTGCAGG	TGTGGGCAAG	ACCGTGAACA	400
	TGATGGAAC	GATCAACAAC	ATCGCCAAAG	CACACTCGGG	TCTGTCCGTG	450
	TTTGCCGGTG	TGGGTGAGCG	TACCCGTGAA	GGTAACGACT	TCTACCACGA	500
	GATGGCTGAC	GCCAAAGTGG	TCGATCTGGA	AAATCCAGAG	AACTCCAAGG	550
	TTGCGATGGT	CTACGGTCAG	ATGAATGAAC	CACCAGGCAA	CCGTCTGCGC	600
60	GTGGCGCTGA	CCGGTCTGAC	CATGGCTGAA	GCATTCCGTG	ACGAAGGCAA	650

AGACGTTCTG	TTCTTCGTGG	ACAACATCTA	C C G C TT C A C C	CTGG C C C G G TA	700
CCGAAGTATC	GGCACTGCTG	GGCCGTATGC	CATCGGCTGT	GGGTTACCAG	750
CCTACGCTGG	CCGAAGAAAT	GGGTCGCCTG	CAAGAGCGCA	TCACTTCGAC	800
CAAGACCGGT	TCGATCAC				818

5

2) INFORMATION FOR SEQ ID NO: 868

10 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 778 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

15

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus saprophyticus*
 (B) STRAIN: ATCC 43867

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 868

CTATCTTAGT	AGTATCTGCT	GCTGATGGCC	CAATGCCACA	AACTCGTGAA	50
CACATTCTTT	TATCACGTAA	CGTTGGTGTT	CCAGCATTAG	TTGTATTCTT	100
AAACAAAGTT	GACATGGTTG	ACGATGAAGA	ATTATTAGAA	TTAGTAGAAA	150
TGGAAGTTCTG	TGACTTATTA	AGCGAATATG	ACTTCCCAGG	TGACGATGTA	200
CCTGTAATCT	CTGGTTCTGC	ATTAAAAGCT	TTAGAAGGCG	ACGCTGACTA	250
TGAGCAAAAA	ATCTTAGACT	TAATGCAAGC	TGTTGATGAC	TTCATTCCAA	300
CACCAGAACG	TGATTCTGAC	AAACCATTC	TGATGCCAGT	TGAGGACGTA	350
TTCTCAATCA	CTGGTCGTGG	TACTGTTGCT	ACAGGCCGTG	TTGAACGTGG	400
TCAAATCAAA	GTCGGTGAAG	AAATCGAAAT	CATCGGTATG	CAAGAAGAAT	450
CAAGCAAAAC	AACTGTTACT	GGTGTAGAAA	TGTTCCGTAA	ATTATTAGAC	500
TACGCTGAAG	CTGGTGACAA	CATTGGTGCA	TTATTACGTG	GTGTTTCACG	550
TGATGACGTA	CAACGTGGTC	AAGTTTTAGC	TGCTCCTGGT	ACTATTACAC	600
CACATACAAA	ATTCAAAGCG	GATGTTTACG	TTTTATCTAA	AGATGAAGGT	650
GGTCGTCATA	CACCATTCTT	CACTAACTAC	CGCCCACAAT	TCTATTTCCG	700
TACTACTGAC	GTAACGTGGT	TTGTTAACTT	ACCAGAAGGT	ACTGAAATGG	750
TTATGCCTTG	CGATAACGTT	GAAATGGA			778

40

2) INFORMATION FOR SEQ ID NO: 869

45 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 640 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus casseliflavus*
 (B) STRAIN: R689

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 869

TGGTCCTATG	CCTCAAACAC	GTGAACACAT	CTTGTTATCA	CGTAACGTTG	50
GTGTACCATA	CATCGTTGTT	TTCTTAAACA	AAATGGATAT	GGTTGATGAC	100

488

	GAAGAATTAC	TAGAATTAGT	TGAAATGGAA	GTTCGTGACT	TATTGTGAGA	150
	ATATGACTTC	CCAGGCGACG	ATGTTCTGT	AATCGCTGGT	TCTGCTTTGA	200
	AAGCTCTTGA	AGGCGATGCT	TCATACGAAG	AAAAAATCAT	GGAATTAATG	250
	GCTGCAGTTG	ACGAATACGT	TCCAACCTCA	GAACGTGACA	CTGACAAACC	300
5	ATTCATGATG	CCAGTCGAAG	ACGTATTCTC	AATCACTGGA	CGTGGTACTG	350
	TTGCTACAGG	CCGTGTTGAA	CGTGGACAAG	TTCGCGTTGG	TGACGAAGTT	400
	GAAATCGTTG	GTATTGCTGA	AGAACTGCT	AAAACAACTG	TAACTGGTGT	450
	TGAAATGTTT	CGTAAATTGT	TAGACTATGC	TGAAGCAGGG	GATAACATTG	500
	GTGCATTGCT	ACGTGGTGTT	GCTCGTGAAG	ACATCCAACG	TGGACAAGTA	550
10	TTGGCTAAAG	CTGGTACAAT	CACACCTCAT	ACAAAATTTA	AAGCTGAAGT	600
	TTACGTTTTA	ACAAAAGAAG	AAGGTGGACG	TCACACTCCA		640

15 2) INFORMATION FOR SEQ ID NO: 870

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 644 bases
 (B) TYPE: Nucleic acid
 20 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

25 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus casseliflavus*
 (B) STRAIN: R754

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 870

30	GTCCTATGCC	TCAAACACGT	GAACACATCT	TGTTATCACG	TAACGTTGGT	50
	GTACCATAACA	TCGTTGTTTT	CTTAAACAAA	ATGGATATGG	TTGATGACGA	100
	AGAATTACTA	GAATTAGTTG	AAATGGAAGT	TCGTGACTTA	TTGTCAGAAT	150
	ATGACTTCCC	AGGCGACGAT	GTTCTGTAA	TCGCTGGTTC	TGCTTTGAAA	200
35	GCTCTTGAAG	GCGATGCTTC	ATACGAAGAA	AAAATCATGG	AATTAATGGC	250
	TGCAGTTGAC	GAATACGTTT	CAACTCCAGA	ACGTGACACT	GACAAACCAT	300
	TCATGATGCC	AGTCGAAGAC	GTATTCTCAA	TCACTGGACG	TGGTACTGTT	350
	GCTACAGGCC	GTGTTGAACG	TGGACAAGTT	CGCGTTGGTG	ACGAAGTTGA	400
	AATCGTTGGT	ATTGCTGAAG	AAACTGCTAA	AACAACTGTA	ACTGGTGTG	450
40	AAATGTTCCG	TAAATTGTTA	GACTATGCTG	AAGCAGGGGA	TAACATTGGT	500
	GCATTGCTAC	GTGGTGTGTC	TCGTGAAGAC	ATCCAACGTG	GACAAGTATT	550
	GGCTAAAGCT	GGTACAATCA	CACCTCATAC	AAAATTTAAA	GCTGAAGTTT	600
	ACGTTTTAAC	AAAAGAAGAA	GGTGGACGTC	ACACACCATT	CTTC	644

45

2) INFORMATION FOR SEQ ID NO: 871

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 637 bases
 (B) TYPE: Nucleic acid
 50 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

55 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus flavescens*
 (B) STRAIN: R758

60

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 871

	TCCTATGCCT	CAAACACGTG	AACACATCTT	GTTATCACGT	AACGTTGGTG	50
	TACCATACAT	CGTTGTTTTC	TTAAACAAAA	TGGATATGGT	TGATGACGAA	100
5	GAATTACTAG	AATTAGTTGA	AATGGAAGTT	CGTGACTTAT	TGTCAGAATA	150
	TGACTTCCCA	GGCGACGATG	TTCCTGTAAT	CGCTGGTTCT	GCTTTGAAAG	200
	CTCTTGAAGG	CGATGCTTCA	TACGAAGAAA	AAATCATGGA	ATTAATGGCT	250
	GCAGTTGACG	AATACGTTCC	AACTCCAGAA	CGTGACACTG	ACAAACCATT	300
	CATGATGCCA	GTCGAAGACG	TATTCTCAAT	CACTGGACGT	GGTACTGTTG	350
10	CTACAGGCCG	TGTTGAACGT	GGACAAGTTC	GCGTTGGTGA	CGAAGTTGAA	400
	ATCGTTGGTA	TTGCTGAAGA	AACTGCTAAA	ACAACTGTAA	CTGGTGTGTA	450
	AATGTTCCGT	AAATTGTTAG	ACTATGCTGA	AGCAGGGGAT	AACATTGGTG	500
	CATTGCTACG	TGGGGTTGCT	CGTGAAGACA	TCCAACGTGG	ACAAGTATTA	550
	GCTAAAGCTG	GTACAATCAC	ACCTCATACA	AAATTTAAAG	CTGAAGTTTA	600
15	CGTTTTAACA	AAAGAAGAAG	GTGGACGTCA	CACTCCA		637

2) INFORMATION FOR SEQ ID NO: 872

20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 643 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

25

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus gallinarum*
 (B) STRAIN: R631

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 872

35	GTCCTATGCC	TCAAACTCGT	GAACACATCT	TGTTATCACG	TAACGTTGGC	50
	GTACCATAACA	TCGTTGTTTT	CTTGAACAAA	ATGGATATGG	TTGATGACGA	100
	AGAATTGCTA	GAATTAGTTG	AAATGGAAGT	TCGTGACCTA	TTGTCTGAAT	150
	ATGACTTCCC	AGGCGACGAT	GTTCTGTAA	TCGCCGGTTC	TGCTTTGAAA	200
	GCTCTTGAAG	GAGATCCTTC	ATACGAAGAA	AAAATCATGG	AATTGATGGC	250
40	TGCAGTTGAC	GAATACGTTT	CAACTCCAGA	ACGTGATACT	GACAAACCAT	300
	TCATGATGCC	AGTCGAAGAC	GTATTCTCAA	TCCTGGACG	TGGTACTGTT	350
	GCTACAGGCC	GTGTTGAACG	TGGACAAGTT	CGCGTTGGTG	ATGAAGTAGA	400
	AATCGTTGGT	ATTGCTGACG	AAACTGCTAA	AACAACTGTA	ACAGGTGTTG	450
	AAATGTTCCG	TAAATTGTTA	GACTATGCTG	AAGCAGGGGA	TAACATTGGT	500
45	GCATTGCTAC	GTGGGGTTGC	TCGTGAAGAC	ATCCAACGTG	GACAAGTATT	550
	GGCTAAAGCT	GGTACAATCA	CACCTCATAC	AAAATTCAAA	GCTGAAGTTT	600
	ATGTTTTGAC	AAAAGAAGAA	GGTGGACGTC	ACACTCCATT	CTT	643

50

2) INFORMATION FOR SEQ ID NO: 873

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 641 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

55

(ii) MOLECULE TYPE: Genomic DNA

60

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Enterococcus gallinarum*

(B) STRAIN: R691

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 873

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GTCCTATGCC TCAAACCTCGT GAACACATCT TGTATCACG TAACGTTGGC      50
GTACCATACA TCGTTGTTTT CTTGAACAAA ATGGATATGG TTGATGACGA      100
AGAATTGCTA GAATTAGTTG AAATGGAAGT TCGTGACCTA TTGTCTGAAT      150
10 ATGACTTCCC AGGCGACGAT GTTCCTGTAA TCGCCGGTTC TGCTTTGAAA      200
GCTCTTGAAG GAGATCCTTC ATACGAAGAA AAAATCATGG AATTGATGGC      250
TGCAGTTGAC GAATACGTTC CAACTCCAGA ACGTGATACT GACAAACCAT      300
TCATGATGCC AGTCGAAGAC GTATTCTCAA TCACTGGACG TGGTACTGTT      350
GCTACAGGCC GTGTTGAACG TGGACAAGTT CGCGTTGGTG ATGAAGTAGA      400
15 AATCGTTGGT ATTGCTGACG AAACTGCTAA AACAACGTGA ACAGGTGTTG      450
AAATGTTCCG TAAATTGTTA GACTATGCTG AAGCAGGGGA TAACATTGGT      500
GCATTGCTAC GTGGGGTTGC TCGTGAAGAC ATCCAACGTG GACAAGTATT      550
GGCTAAAGCT GGTACAATCA CACCTCATAC AAAATTCAA GCTGAAGTTT      600
ATGTTTTGAC AAAAGAAGAA GGTGGACGTC ACACTCCATT C              641
20

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2) INFORMATION FOR SEQ ID NO: 874

25 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 681 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

30

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Staphylococcus haemolyticus*

35 (B) STRAIN: LSPQ 2514

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 874

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ACCAGCATTG TAGTATTCT TAAATAAAGT TGACATGGTT GACGATGAAG      50
40 AATTATTAGA ATTAGTTGAA ATGGAAGTAC GTGACTTATT ATCTGAATAC      100
GACTTCCCAG GTGACGATGT ACCTGTAATC GCTGGTTCAG CATTAAAAGC      150
TTTAGAAGGC GATGCTCAAT ACGAAGAAAA AATCTTAGAA TTAATGCAAG      200
CAGTTGATGA CTACATTCCA ACTCCAGAAC GTGATTCTGA CAAACCATTTC      250
ATGATGCCAG TTGAGGACGT ATTCTCAATC ACTGGTCGTG GTACTGTTGC      300
45 TACAGGCCGT GTTGAACGTG GGCAAATCAA AGTTGGTGAA GAAGTTGAAA      350
TCATTGGTAT CCATGACACT TCTAAAACAA CTGTTACTGG TGTAGAAATG      400
TTCCGTAAAT TATTAGACTA CGCTGAAGCT GGTGACAACA TCGGTGCATT      450
ATTACGTGGT GTTGCTCGTG AAGACGTACA ACGTGGTCAA GTATTAGCTG      500
CTCCAGGTTC AATCACACCT CACACAAAAT TTAAAGCAGA CGTATACGTT      550
50 TTATCTAAAG ACGAAGGTGG ACGTCACACT CCATTCTTCA CAAACTATCG      600
TCCACAATTC TATTTCCGTA CTAATGACGT AACTGGTGTT GTTAACTTAC      650
CAGAAGGTAC TGAAATGGTT ATGCCTGGCG A              681

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55

2) INFORMATION FOR SEQ ID NO: 875

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 675 bases

60 (B) TYPE: Nucleic acid

491

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

5

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Staphylococcus epidermidis*

(B) STRAIN: R591

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 875

	ATTATCACGT	AACGTTGGTG	TACCAGCATT	AGTTGTATTC	TTAAACAAAG	50
	TTGACATGGT	AGACGACGAA	GAATTATTAG	AATTAGTTGA	AATGGAAGTT	100
	CGTGACTIONT	TAAGCGAATA	TGACTTCCCA	GGTGACGATG	TACCTGTAAT	150
15	CGCTGGTTCT	GCATTAAAAG	CATTAGAAGG	CGATGCTGAA	TACGAACAAA	200
	AAATCTTAGA	CTTAATGCAA	GCAGTTGATG	ATTACATTCC	AACTCCAGAA	250
	CGTGATTCTG	ACAAACCATT	CATGATGCCA	GTTGAGGACG	TATTCTCAAT	300
	CACTGGTCGT	GGTACTGTTG	CTACAGGCCG	TGTTGAACGT	GGTCAAATCA	350
	AAGTTGGTGA	AGAAGTTGAA	ATCATCGGTA	TGCACGAAAC	TTCTAAAACA	400
20	ACTGTTACTG	GTGTAGAAAT	GTTCCGTAAA	TTATTAGACT	ACGCTGAAGC	450
	TGGTGACAAC	ATCGGTGCTT	TATTACGTGG	TGTTGCACGT	GAAGACGTAC	500
	AACGTGGTCA	AGTATTAGCT	GCTCCTGGTT	CTATTACACC	ACACACAAAA	550
	TTCAAAGCTG	AAGTATACGT	ATTATCTAAA	GATGAAGGTG	GACGTCACAC	600
	TCCATTCTTC	ACTAACTATC	GCCCACAATT	CTATTTCCGT	ACTACTGACG	650
25	TAACTGGTGT	TGTAAACTTA	CCAGA			675

2) INFORMATION FOR SEQ ID NO: 876

30

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 704 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

35

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

40

(A) ORGANISM: *Staphylococcus epidermidis*

(B) STRAIN: CSG 10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 876

45	TCTTATTATC	ACGTAACGTT	GGTGTACCAG	CATTAGTTGT	ATTCTTAAAC	50
	AAAGTTGACA	TGGTAGACGA	CGAAGAATTA	TTAGAATTAG	TTGAAATGGA	100
	AGTTCGTGAC	TTATTAAGCG	AATATGACTT	CCCAGGTGAC	GATGTACCTG	150
	TAATCGCTGG	TTCTGCATTA	AAAGCATTAG	AAGGCGATGC	TGAATACGAA	200
	CAAAAAATCT	TAGACTTAAT	GCAAGCAGTT	GATGATTACA	TTCCAACCTCC	250
50	AGAACGTGAT	TCTGACAAAC	CATTCATGAT	GCCAGTTGAG	GACGTATTCT	300
	CAATCACTGG	TCGTGGTACT	GTTGCTACAG	GCCGTGTTGA	ACGTGGTCAA	350
	ATCAAAGTTG	GTGAAGAAGT	TGAAATCATC	GGTATGCACG	AAACTTCTAA	400
	AACAACGTGT	ACTGGTGTAG	AAATGTTCCG	TAAATTATTA	GACTACGCTG	450
	AAGCTGGTGA	CAACATCGGT	GCTTTATTAC	GTGGTGTTGC	ACGTGAAGAC	500
55	GTACAACGTG	GTCAAGTATT	AGCTGCTCCT	GGTTCTATTA	CACCACACAC	550
	AAAATTCAAA	GCTGAAGTAT	ACGTATTATC	TAAAGATGAA	GGTGGACGTC	600
	ACACTCCATT	CTTCACTAAC	TATCGCCCAC	AATTCTATTT	CCGTACTACT	650
	GACGTAACCTG	GTGTTGTAAA	CTTACCAGAA	GGTACAGAAA	TGGTTATGCC	700
	TGGC					704

60

2) INFORMATION FOR SEQ ID NO: 877

- 5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 770 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

10 (ii) MOLECULE TYPE: Genomic DNA

- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Staphylococcus epidermidis*
 15 (B) STRAIN: ATCC 35984

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 877

	TCTTAGTTGT	ATCTGCTGCT	GACGGTCCAA	TGCCACAAAC	TCGTGAACAC	50
20	ATCTTATTAT	CACGTAACTG	TGGTGTACCA	GCATTAGTTG	TATTCTTAA	100
	CAAAGTTGAC	ATGGTAGACG	ACGAAGAATT	ATTAGAATTA	GTTGAAATGG	150
	AAGTTCGTGA	CTTATTAAGC	GAATATGACT	TCCCAGGTGA	CGATGTACCT	200
	GTAATCGCTG	GTTCTGCATT	AAAAGCATT	GAAGGCGATG	CTGAATACGA	250
	ACAAAAAATC	TTAGACTTAA	TGCAAGCAGT	TGATGATTAC	ATTCCAACCT	300
25	CAGAACGTGA	TTCTGACAAA	CCATTCATGA	TGCCAGTTGA	GGACGTATTC	350
	TCAATCACTG	GTCGTGGTAC	TGTTGCTACA	GGCCGTGTTG	AACGTGGTCA	400
	AATCAAAGTT	GGTGAAGAAG	TTGAAATCAT	CGGTATGCAC	GAAACTTCTA	450
	AAACAACCTG	TACTGGTGTA	GAAATGTTCC	GTAAATTATT	AGACTACGCT	500
	GAAGCTGGTG	ACAACATCGG	TGCTTTATTA	CGTGGTGTG	CACGTGAAGA	550
30	CGTACAACGT	GGTCAAGTAT	TAGCTGCTCC	TGGTTCTATT	ACACCACACA	600
	CAAAATTCAA	AGCTGAAGTA	TACGTATTAT	CTAAAGATGA	AGGTGGACGT	650
	CACACTCCAT	TCTTCACTAA	CTATCGCCCA	CAATTCTATT	TCCGTACTAC	700
	TGACGTAAC	GGTGTGTAA	ACTTACCAGA	AGGTACAGAA	ATGGTTATGC	750
35	CTGGCGACAA	CGTTGAAATG				770

2) INFORMATION FOR SEQ ID NO: 878

- 40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 716 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

45 (ii) MOLECULE TYPE: Genomic DNA

- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Staphylococcus epidermidis*
 50 (B) STRAIN: ATCC 35983

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 878

	TTGTATTCTT	AAACAAAGTT	GACATGGTAG	ACGACGAAGA	ATTATTAGAA	50
55	TTAGTTGAAA	TGGAAGTTCG	TGACTTATTA	AGCGAATATG	ACTTCCCAGG	100
	TGACGATGTA	CCTGTAATCG	CTGGTTCTGC	ATTAAAAGCA	TTAGAAGGCG	150
	ATGCTGAATA	CGAACAAAAA	ATCTTAGACT	TAATGCAAGC	AGTTGATGAT	200
	TACATTCCAA	CTCCAGAACG	TGATTCTGAC	AAACCATTC	TGATGCCAGT	250
	TGAGGACGTA	TTCTCAATCA	CTGGTCGTGG	TACTGTTGCT	ACAGGCCGTG	300
60	TTGAACGTGG	TCAAATCAAA	GTTGGTGAAG	AAGTTGAAAT	CATCGGTATG	350

	CACGAACTT	CTAAAAAAC	TGTTACTGGT	GTAGAAATGT	TCCGTAAATT	400
	ATTAGACTAC	GCTGAAGCTG	GTGACAACAT	CGGTGCTTTA	TTACGTGGTG	450
	TTGCACGTGA	AGACGTACAA	CGTGGTCAAG	TATTAGCTGC	TCCTGGTTCT	500
	ATTACACCAC	ACACAAAATT	CAAAGCTGAA	GTATACGTAT	TATCTAAAGA	550
5	TGAAGGTGGA	CGTCACACTC	CATTCTTCAC	TAACTATCGC	CCACAATTCT	600
	ATTTCCGTAC	TACTGACGTA	ACTGGTGTG	TAACTTACC	AGAAGGTACA	650
	GAAATGGTTA	TGCCTGGCGA	CAACGTTGAA	ATGACAGTTG	AATTAATCGC	700
	TCCAATCGCT	ATCGAA				716

10

2) INFORMATION FOR SEQ ID NO: 879

- (i) SEQUENCE CHARACTERISTICS:
- 15 (A) LENGTH: 640 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear
- 20 (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Enterococcus gallinarum*
(B) STRAIN: R764

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 879

	CGGTCCTATG	CCTCAAACCTC	GTGAACACAT	CTTGTTATCA	CGTAACGTTG	50
	GCGTACCATA	CATCGTTGTT	TTCTTGAACA	AAATGGATAT	GGTTGATGAC	100
30	GAAGAATTGC	TAGAATTAGT	TGAAATGGAA	GTTCTGTGAC	TATTGTCTGA	150
	ATATGACTTC	CCAGGCGACG	ATGTTCTTGT	AATCGCCGGT	TCTGCTTTGA	200
	AAGCTCTTGA	AGGAGATCCT	TCATACGAAG	AAAAAATCAT	GGAATTGATG	250
	GCTGCAGTTG	ACGAATACGT	TCCAACCTCA	GAACGTGATA	CTGACAAACC	300
	ATTCATGATG	CCAGTCAAG	ACGTATTCTC	AATCACTGGA	CGTGGTACTG	350
35	TTGCTACAGG	CCGTGTTGAA	CGTGGAACAAG	TTCGCGTTGG	TGATGAAGTA	400
	GAAATCGTTG	GTATTGCTGA	CGAAACTGCT	AAAACAACCTG	TAACAGGTGT	450
	TGAAATGTTT	CGTAAATTGT	TAGACTATGC	TGAAGCAGGG	GATAACATTG	500
	GTGCATTGCT	ACGTGGGGTT	GCTCGTGAAG	ACATCCAACG	TGGACAAGTA	550
	TTGGCTAAAG	CTGGTACAAT	CACACCTCAT	ACAAAATTCA	AAGCTGAAGT	600
40	TTATGTTTTG	ACAAAAGAAG	AAGGTGGACG	TCACACTCCA		640

2) INFORMATION FOR SEQ ID NO: 880

45

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 831 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
50 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 55 (A) ORGANISM: *Pseudomonas aeruginosa*
(B) STRAIN: PAO-1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 880

60	CGGCGCGATC	CTGGTTTGCT	CGGCTGCCGA	CGGCCCATG	CCGCAGACCC	50
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	GCGAGCACAT	CCTGCTGTCC	CGCCAGGTAG	GCGTTCCCTA	CATCGTCTGT	100
	TTCCTGAACA	AGGCCGACAT	GGTCGACGAC	GCCGAGCTGC	TGGAAGTGGT	150
	CGAGATGGAA	GTTTCGCGATC	TGCTGAACAC	CTACGACTTC	CCGGGCGACG	200
	AACTCCGAT	CATCATCGGT	TCCGCGCTGA	TGGCGCTGGA	AGGCAAGGAT	250
5	GACAACGGCA	TCGGCGTAAG	CGCCGTGCAG	AAGCTGGTAG	AGACCCTGGA	300
	CTCCTACATT	CCGGAGCCGG	TTCGTGCCAT	CGACCAGCCG	TTCCTGATGC	350
	CGATCGAAGA	CGTGTCTCG	ATCTCCGGCC	GCGGTACCGT	GGTAACCGGT	400
	CGTGTAGAGC	GCGGCATCAT	CAAGGTCCAG	GAAGAAGTGG	AAATCGTCCG	450
	CATCAAGGCG	ACCACCAAGA	CTACCTGCAC	CGGCGTTGAA	ATGTTCCGCA	500
10	AGCTGCTCGA	CGAAGGTCGT	GCTGGTGAGA	ACGTTGGTAT	CCTGCTGCGT	550
	GGCACCAAGC	GTGAAGACGT	AGAGCGTGGC	CAGGTTCTGG	CCAAGCCGGG	600
	CACCATCAAG	CCGCACACCA	AGTTCGAGTG	CGAAGTGTA	GTGCTGTGTA	650
	AGGAAGAAGG	TGGTCGTCAC	ACCCCGTTCT	TCAAGGGCTA	CCGTCCGCAG	700
	TTCTACTTCC	GTACCACCGA	YGTGACCGGT	AACTGCGAAC	TGCCGGAAGG	750
15	CGTAGAGATG	GTAATGCCGG	GCGACAACAT	CAAGATGGTT	GTCACCCTGA	800
	TCGCTCCGAT	CGCCATGGAA	GATGGCCTGC	G		831

20 2) INFORMATION FOR SEQ ID NO: 881

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 642 bases
 (B) TYPE: Nucleic acid
 25 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

30 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus casseliflavus*
 (B) STRAIN: R421

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 881

35	CCTATGCCTC	AAACACGTGA	ACACATCTTG	TTATCACGTA	ACGTTGGTGT	50
	ACCATACATC	GTTGTTTTCT	TAAACAAAAT	GGATATGGTT	GATGACGAAG	100
	AATTACTAGA	ATTAGTTGAA	ATGGAAGTTC	GTGACTTATT	GTCAGAATAT	150
	GACTTCCCAG	GCGACGATGT	TCCTGTAATC	GCTGGTTCTG	CTTTGAAAGC	200
40	TCTTGAAGGC	GATGCTTCAT	ACGAAGAAAA	AATCATGGAA	TTAATGGCTG	250
	CAGTTGACGA	ATACGTTCCA	ACTCCAGAAC	GTGACACTGA	CAAACCATTC	300
	ATGATGCCAG	TCGAAGACGT	ATTCTCAATC	ACTGGACGTG	GTAAGTTGAA	350
	TACAGGCCGT	GTTGAACGTG	GACAAGTTCT	CGTTGGTGAC	GAAGTTGAAA	400
	TCGTTGGTAT	TGCTGAAGAA	ACTGCTAAAA	CAACTGTAAC	TGGTGTGAA	450
45	ATGTTCCGTA	AATTGTTAGA	CTATGCTGAA	GCAGGGGATA	ACATTGGTGC	500
	ATTGCTACGT	GGTGTGCTC	GTGAAGACAT	CCAACGTGGA	CAAGTATTGG	550
	CTAAAGCTGG	TACAATCACA	CCTCATACAA	AATTTAAAGC	TGAAGTTTAC	600
	GTTTTAACAA	AAGAAGAAGG	TGGACGTCAC	ACACCATTC	TC	642

50

2) INFORMATION FOR SEQ ID NO: 882

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 636 bases
 (B) TYPE: Nucleic acid
 55 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

60 (ii) MOLECULE TYPE: Genomic DNA

495

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Enterococcus casseliflavus*

(B) STRAIN: R775

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 882

	CCTATGCCTC	AAACACGTGA	ACACATCTTG	TTATCACGTA	ACGTTGGTGT	50
	ACCATAACATC	GTTGTTTTCT	TAAACAAAAT	GGATATGGTT	GATGACGAAG	100
10	AATTACTAGA	ATTAGTTGAA	ATGGAAGTTC	GTGACTTATT	GTCAGAATAT	150
	GACTTCCCAG	GCGACGATGT	TCCTGTAATC	GCTGGTTCTG	CTTTGAAAGC	200
	TCTTGAAGGC	GATGCTTCAT	ACGAAGAAAA	AATCATGGAA	TTAATGGCTG	250
	CAGTTGACGA	ATACGTTCCA	ACTCCAGAAC	GTGACACTGA	CAAACCATTC	300
	ATGATGCCAG	TCGAAGACGT	ATTCTCAATC	ACTGGACGTG	GTACTGTTGC	350
15	TACAGGCCGT	GTTGAACGTG	GACAAGTTCG	CGTTGGTGAC	GAAGTTGAAA	400
	TCGTTGGTAT	TGCTGAAGAA	ACTGCTAAAA	CAACTGTAAC	TGGTGTGAA	450
	ATGTTCCGTA	AATTGTTAGA	CTATGCTGAA	GCAGGGGATA	ACATTGGTGC	500
	ATTGCTACGT	GGTGTGCTC	GTGAAGACAT	CCAACGTGGA	CAAGTATTGG	550
	CTAAAGCTGG	TACAATCACA	CCTCATACAA	AATTTAAGC	TGAAGTTTAC	600
20	GTTTTAACAA	AAGAAGAAGG	TGGACGTCAT	ACACCA		636

2) INFORMATION FOR SEQ ID NO: 883

25

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 641 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

30

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

35

(A) ORGANISM: *Enterococcus faecalis*

(B) STRAIN: R422

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 883

40	GGTCCTATGC	CTCAAACACG	TGAACATATC	TTATTATCAC	GTAACGTTGG	50
	TGTACCATAC	ATCGTTGTAT	TCTTAAACAA	AATGGATATG	GTTGATGACG	100
	AAGAATTATT	AGAATTAGTA	GAAATGGAAG	TTCGTGACTT	ATTATCAGAA	150
	TACGATTTC	CAGGCGATGA	TGTTCCAGTT	ATCGCAGGTT	CTGCTTTGAA	200
	AGCTTTAGAA	GGCGACGAGT	CTTATGAAGA	AAAAATCTTA	GAATTAATGG	250
45	CTGCAGTTGA	CGAATATATC	CCAACCTCCAG	AACGTGATAC	TGACAAACCA	300
	TTCATGATGC	CAGTCGAAGA	CGTATTCTCA	ATCACTGGAC	GTGGTACTGT	350
	TGCTACAGGC	CGTGTTGAAC	GTGGTGAAGT	TCGCGTTGGT	GACGAAGTTG	400
	AAATCGTTGG	TATTAAAGAC	GAAACATCTA	AAACAACTGT	TACAGGTGTT	450
	GAAATGTTCC	GTAAATTATT	AGACTACGCT	GAAGCAGGCG	ACAACATCGG	500
50	TGCTTTATTA	CGTGGTGTAG	CACGTGAAGA	TATCGAACGT	GGACAAGTAT	550
	TAGCTAAACC	AGCTACAATC	ACTCCACACA	CAAAATTCAA	AGCTGAAGTA	600
	TACGTATTAT	CAAAAGAAGA	AGGCGGACGT	CACACTCCAT	T	641

55

2) INFORMATION FOR SEQ ID NO: 884

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 640 bases

60

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

5

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Enterococcus faecalis*

(B) STRAIN: R575

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 884

	TATGCCTCAA	ACACGTGAAC	ATATCTTATT	ATCACGTAAC	GTTGGTGTAC	50
	CATACATCGT	TGTATTCTTA	AACAAAATGG	ATATGGTTGA	TGACGAAGAA	100
	TTATTAGAAT	TAGTAGAAAT	GGAAGTTCGT	GACTTATTAT	CAGAATACGA	150
15	TTTCCCAGGC	GATGATGTTC	CAGTTATCGC	AGGTTCTGCT	TTGAAAGCTT	200
	TAGAAGGCGA	CGAGTCTTAT	GAAGAAAAAA	TCTTAGAATT	AATGGCTGCA	250
	GTTGACGAAT	ATATCCCAAC	TCCAGAACGT	GATACTGACA	AACCATTTCAT	300
	GATGCCAGTC	GAAGACGTAT	TCTCAATCAC	TGGACGTGGT	ACTGTTGCTA	350
	CAGGCCGTGT	TGAACGTGGT	GAAGTTCGCG	TTGGTGACGA	AGTTGAAATC	400
20	GTTGGTATTA	AAGACGAAAC	ATCTAAAACA	ACTGTTACAG	GTGTTGAAAT	450
	GTTCCGTAAA	TTATTAGACT	ACGCTGAAGC	AGGCGACAAC	ATCGGTGCTT	500
	TATTACGTGG	TGTTGCACGT	GAAGATATCG	AACGTGGACA	AGTATTAGCT	550
	AAACCAGCTA	CAATCACTCC	ACACACAAAA	TTCAAAGCTG	AAGTATACGT	600
	ATTATCAAAA	GAAGAAGGCG	GACGTCACAC	TCCATTCTTC		640

25

2) INFORMATION FOR SEQ ID NO: 885

30 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 632 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Enterococcus faecium*

40 (B) STRAIN: R492

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 885

	TGCCTCAAAC	TCGTGAACAC	ATCCTATTGT	CTCGTCAAGT	TGGTGTTCCT	50
45	TACATCGTTG	TATTCTTGAA	CAAAGTAGAC	ATGGTTGATG	ACGAAGAATT	100
	ACTAGAATTA	GTTGAAATGG	AAGTTCGTGA	CCTATTAACA	GAATACGAAT	150
	TCCCTGGTGA	CGATGTTTCT	GTAGTTGCTG	GATCAGCTTT	GAAAGCTCTA	200
	GAAGGCGACG	CTTCATACGA	AGAAAAAATT	CTTGAATTAA	TGGCTGCAGT	250
	TGACGAATAC	ATCCCAACTC	CAGAACGTGA	CAACGACAAA	CCATTTCATGA	300
50	TGCCAGTTGA	AGACGTGTTC	TCAATTACTG	GACGTGGTAC	TGTTGCTACA	350
	GGTCGTGTTG	AACGTGGACA	AGTTCGCGTT	GGTGACGAAG	TTGAAGTTGT	400
	TGGTATTGCT	GAAGAACTT	CAAAAACAAC	AGTTACTGGT	GTTGAAATGT	450
	TCCGTAAATT	GTTAGACTAC	GCTGAAGCTG	GAGACAACAT	TGGTGCTTTA	500
	CTACGTGGTG	TTGCACGTGA	AGACATCCAA	CGTGGACAAG	TTTTAGCTAA	550
55	ACCAGGTACA	ATCACACCTC	ATACAAAATT	CTCTGCAGAA	GTATACGTGT	600
	TGACAAAAGA	AGAAGGTGGA	CGTCATACTC	CA		632

60 2) INFORMATION FOR SEQ ID NO: 886

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 640 bases
 (B) TYPE: Nucleic acid
 5 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

10 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus faecium*
 (B) STRAIN: R576

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 886

15 CGGCCCAATG CCTCAAACCTC GTGAACACAT CCTATTGTCT CGTCAAGTTG 50
 GTGTTCCCTTA CATCGTTGTA TTCTTGAACA AAGTAGACAT GGTGATGAC 100
 GAAGAATTAC TAGAATTAGT TGAAATGGAA GTTCGTGACC TATTAACAGA 150
 ATACGAATTC CCTGGTGACG ATGTTCTGTG AGTTGCTGGA TCAGCTTTGA 200
 20 AAGCTCTAGA AGGCGACGCT TCATACGAAG AAAAAATTCT TGAATTAATG 250
 GCTGCAGTTG ACGAATACAT CCAACTCCA GAACGTGACA ACGACAAACC 300
 ATTCATGATG CCAGTTGAAG ACGTGTCTC AATTACTGGA CGTGGTACTG 350
 TTGCTACAGG TCGTGTGAA CGTGGACAAG TTCGCGTTGG TGACGAAGTT 400
 GAAGTTGTTG GTATTGCTGA AGAACTTCA AAAACAACAG TTACTGGTGT 450
 25 TGAAATGTTT CGTAAATTGT TAGACTACGC TGAAGCTGGA GACAACATTG 500
 GTGCTTTACT ACGTGGTGTT GCACGTGAAG ACATCCAACG TGGACAAGTT 550
 TTAGCTAAAC CAGGTACAAT CACACCTCAT ACAAATTCT CTGCAGAAGT 600
 ATACGTGTTG ACAAAGAAG AAGGTGGACG TCATACTCCA 640

30

2) INFORMATION FOR SEQ ID NO: 887

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 806 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

40 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Zoogloea ramigera*
 (B) STRAIN: ATCC 25935

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 887

ATCCTGGTTT GCTCCGCAGC TGACGGCCCA ATGCCACAGA CCCGCGAGCA 50
 CATCCTGCTG GCCCGCCAAG TTGGCGTTCC ATACATCATC GTGTTCCCTGA 100
 50 ACAAGTGCGA CCTGGTTGAC GACGCAGAAC TGCTGGAAC TGTGAAATG 150
 GAAGTGCGTG AATTGCTGTC GAAATACGAG TTCCCAGGCG ACGACGTACC 200
 AATCATCAAG GGTTCGGCAC GTATGGCGCT GGAAGGCAA GAAGGCGAGA 250
 TGGGCGTTGA CGCCATCATG CGTCTGGCCG ATGCACTGGA CAGCTACATC 300
 CCTACGCCAG AGCGCGCAGT CGATGGCGCC TTCCTGATGC CAGTGGAAGA 350
 55 CGTGTCTCTG ATCTCGGGTC GCGGTACCGT TGTGACCGGT CGTATCGAGC 400
 GCGGCGTGAT CAAGGTCGGC GAAGAGATCG AAATCGTCGG CATTATCGAC 450
 ACCGTCAAAA CCACTTGAC CCGCGTGGAA ATGTTCCGCA AGCTGCTGGA 500
 CCAGGGTCAA GCCGGCGACA ACGTTGGTCT GCTGCTGCGC GGCACCAAGC 550
 GTGAAGACGT ACAGCGTGGT CAGGTTCTGG CCAAGCCAGC GTCGATCAAG 600
 60 CCGCACAACC ACTTCAACCG CGAGATCTAC GTTCTGTCTGA AAGATGAAGG 650

CGGCCGTCAC	ACCCCGTTCT	TCAACAATA	TCGTCCACAG	TTCTACTTCT	700
GTACGACTGA	CGTGACCGGT	TCGATCGAAC	TGCCAGCAGA	CAAAGAAATG	750
GTCATGCCAG	GCGACAACGT	GTCGATCACC	GTCAAGCTGA	TCAACCCGAT	800
CGCGAT					806

5

2) INFORMATION FOR SEQ ID NO: 888

10 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 634 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

15

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus faecalis*
 (B) STRAIN: R503

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 888

25	TATGCCTCAA	ACACGTGAAC	ATATCTTATT	ATCACGTAAC	GTTGGTGTAC	50
	CATACATCGT	TGTATTCTTA	AACAAAATGG	ATATGGTTGA	TGACGAAGAA	100
	TTATTAGAAT	TAGTAGAAAT	GGAAGTTCGT	GACTTATTAT	CAGAATACGA	150
	TTTCCCAGGC	GATGATGTTC	CAGTTATCGC	AGGTTCTGCT	TTGAAAGCTT	200
	TAGAAGGCGA	CGAGTCTTAT	GAAGAAAAAA	TCTTAGAATT	AATGGCTGCA	250
	GTTGACGAAT	ATATCCCAAC	TCCAGAACGT	GATACTGACA	AACCATTTCAT	300
30	GATGCCAGTC	GAAGACGTAT	TCTCAATCAC	TGGACGTGGT	ACTGTTGCTA	350
	CAGGCCGTGT	TGAACGTGGT	GAAGTTCGCG	TTGGTGACGA	AGTTGAAATC	400
	GTTGGTATTA	AAGACGAAAC	ATCTAAAACA	ACTGTTACAG	GTGTTGAAAT	450
	GTTCCGTAAA	TTATTAGACT	ACGCTGAAGC	AGGCGACAAC	ATCGGTGCTT	500
	TATTACGTGG	TGTAGCACGT	GAAGATATCG	AACGTGGACA	AGTATTAGCT	550
35	AAACCAGCTA	CAATCACTCC	ACACACAAAA	TTCAAAGCTG	AAGTATACGT	600
	ATTATCAAAA	GAAGAAGGCG	GACGTCACAC	TCCA		634

40 2) INFORMATION FOR SEQ ID NO: 889

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 493 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

45

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Aspergillus fumigatus*
 (B) STRAIN: ATCC 14110

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 889

55	TGTCTTCATC	CAGGAATTGA	TTGTGAGTCG	TTCCACATGC	TCACCTAGTT	50
	TTGCTCGAT	CTTTTCACTA	ACGCAAACCA	TGTAGAACAA	CATTGCCAAG	100
	GCCCACGGTG	GTTACTCCGT	CTTCACTGGT	GTTGGTGAGC	GTAATCGTGA	150
	GGGTAACGAT	CTGTACCACG	AAATGCAGGA	GACTGGTGTC	ATTGAGCTCG	200
60	AGGGTGAATC	CAAGGTCGCA	CTGGTGTTTCG	GACAGATGAA	CGAGCCCCCC	250

	GGTGCCCGTG	CCCGTGTCGC	CCTTACCGGT	CTGACCATTG	CCGAGTACTT	300
	CCGTGACGAG	GAGGGTCAGG	ACGTGCTGCT	CTTCATTGAC	AACATTTTCC	350
	GTTTCACCCA	GGCCGGTTCT	GAGGTGTCTG	CCCTTCTCGG	TCGTATCCCC	400
	TCTGCCGTCG	GTTACCAGCC	CACCCTGGCC	GTCGACATGG	GTGGTATGCA	450
5	GGAGCGTATC	ACCACCACCA	AGAAGGGTTC	TATTACCTCC	GTC	493

2) INFORMATION FOR SEQ ID NO: 890

10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 466 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 15 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 20 (A) ORGANISM: *Penicillium marneffe*
 (B) STRAIN: ATCC 64101

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 890

25	TTGATTGTAC	GTCTTTACCT	TTCTGCCTGA	CTGTTTACGA	CAACTAACGA	50
	AAGCGTAGAA	CAACATTGCC	AAGGCTCAGG	GTGGTTACTC	TGCTTCACT	100
	GGTGTCCGTG	AACGTACTCG	TGAGGGTAAC	GATTTGTACC	ACGAAATGCA	150
	GGAAACTGGT	GTCATTCAGC	TCGAGGGTGA	ATCCAAGGTC	GCCCTCGTGT	200
	TCGGTCAGAT	GAACGAGCCC	CCCGGTGCCC	GTGCCCCGTG	CGCTCTTACT	250
30	GGTTTGACCA	TTGCCGAGTA	CTTCCGTGAC	GAGGAAGGTC	AGGACGTGCT	300
	TCTCTTCATT	GACAACATTT	TCCGTTTCAC	TCAGGCCGGT	TCTGAGGTGT	350
	CTGCCCTTCT	GGGTCGTATC	CCCTCTGCCG	TCGGTTACCA	GCCCACCCTT	400
	GCCGTCGACA	TGGGTATCAT	GCAGGAGCGT	ATTACCACCA	CCACCAAGGG	450
	TTCCATCACC	TCCGTC				466

35

2) INFORMATION FOR SEQ ID NO: 891

40 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 478 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 45 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 50 (A) ORGANISM: *Paecilomyces lilacinus*
 (B) STRAIN: ATCC 42570

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 891

	AGGAGCTGAT	CAACAACATC	GCCAAGGCTC	ACGGTGGTTA	CTCCGTCTTC	50
55	ACTGGTGTCTG	GTGAGCGTAC	CCGTGAGGGT	AACGATCTGT	ACCACGAAAT	100
	GCAGGAGACC	TCGGTCATTC	AGCTCGAGGG	CGAGTCTAAG	GTGGCCCTGG	150
	TCTTTGGTCA	GATGAACGAG	CCCCCGGGTG	CTCGTGCCCG	TGTCGCTCTT	200
	ACTGGTCTTA	CCGTCGCCGA	GTA CTTCCTG	GACCAGGAGG	GTCAGGATGG	250
	TTAGTTCTCG	TCCACTCATG	CCGAAACATG	TGCGTGTTCC	GAGGCTAATC	300
60	AACGTGCCAG	TGCTGCTTTT	CATCGACAAC	ATTTTCCGAT	TCACACAGGC	350

500

CGGTTCCGAG	GTGTCTGCCC	TGCTGGGTCG	TATCCCCCTCT	GCCGTCGGTT	400
ACCAGCCCAC	CCTCGCCGTC	GACATGGGTG	GCATGCAGGA	GCGTATCACC	450
ACCACCAAGA	AGGGCTCTAT	CACCTCCG			478

5

2) INFORMATION FOR SEQ ID NO: 892

- (i) SEQUENCE CHARACTERISTICS:
- 10 (A) LENGTH: 481 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear
- 15 (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Penicillium marneffe*
- (B) STRAIN: ATCC 58950

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 892

GTCTTTATCC	AGGAGTTGAT	TGTACGTCTT	TACCTTTCTG	CCTGACTGTT	50
TACGACAACT	AACGAAAGCG	TAGAACAACA	TTGCCAAGGC	TCACGGTGGT	100
25 TACTCTGTCT	TCACTGGTGT	CGGTGAACGT	ACTCGTGAGG	GTAACGATTT	150
GTACCACGAA	ATGCAGGAAA	CTGGTGTCAT	TCAGCTCGAG	GGTGAATCCA	200
AGGTCGCCCT	CGTGTTCCGT	CAGATGAACG	AGCCCCCGG	TGCCCGTGCC	250
CGTGTCGCTC	TTACTGGTTT	GACCATTGCC	GAGTACTTCC	GTGACGAGGA	300
AGGTCAGGAC	GTGCTTCTCT	TCATTGACAA	CATTTTCCGT	TTCACTCAGG	350
30 CCGGTTCTGA	GGTGTCTGCC	CTTCTGGGTC	GTATCCCCTC	TGCCGTCGGT	400
TACCAGCCCA	CCCTTGCCGT	CGACATGGGT	ATCATGCAGG	AGCGTATTAC	450
CACCACCACC	AAGGGTTCCA	TCACCTCCGT	C		481

35

2) INFORMATION FOR SEQ ID NO: 893

- (i) SEQUENCE CHARACTERISTICS:
- 40 (A) LENGTH: 1208 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- 45 (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Sporothrix schenckii*
- (B) STRAIN: ATCC 14285

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 893

CTCGTCCGTG	GTGCTAAGGC	CACTGACACT	GGTTSCCCCA	TTACCATCCS	50
CGTCGGCCCC	GGTACCCTCG	GTCGCATCAT	GAACGTCACC	GGTGACCCGA	100
TCGACGAGCG	CGGTCCCATC	AAGACCGACA	AGTTCCGTCC	CATCCACGCT	150
55 GAGGCTCCCG	AGTTCGTTGA	CCAGTCGACC	ACCGCTGAGG	TTCTCGTGAC	200
TGGTATCAAG	GTCGTCGATC	TGCTTGCTCC	CTACGCCCCG	GGTGGTAAGA	250
TTGGTCTGTT	TGGCGGTGCC	GGTGTGGA	AGACCGTGTT	CATCCAGGAG	300
CTCATCAACA	ACATCGCCAA	GGCCACGGT	GGTTACTCCG	TCTTCACCGG	350
TGTCGGCGAG	CGTACCCGTG	AGGGTAACGA	TCTGTACCAC	GAAATGCAGG	400
60 AGACCTCTGT	CATTGAGCTT	GACGGTGACT	CCAAGGTCGC	CCTGGTGTTC	450

	GGTCAGATGA	ACGAGCCCCC	TGGTGCTCGT	GCCCGTGTCG	CCTTGACCGG	500
	TTTGAAGTGC	GCTGAGTACT	TCCGTGACGA	GGAGGGCCAG	GATGGTATGT	550
	TTTGAATTAT	TTCCTTGTCG	TACAGTTCCA	AATCGAAGAA	TTACTAACTT	600
	GTCAGTGCTT	CTCTTCATCG	ACAACATTTT	CCGCTTCACC	CAGGCCGGTT	650
5	CTGAGGTGTC	TGCCCTTCTG	GGTCGTATTC	CCTCCGCTGT	CGGTTACCAG	700
	CCCACGCTCG	CCGTGGACAT	GGGTCTGATG	CAGGAGCGTA	TTACCACCAC	750
	CCGCAAGGGC	TCAATTACCT	CCGTCCAGGC	CGTCTACGTG	CCCGTGACG	800
	ATCTGACGGA	TCCCGCCCCC	GCCACCACCT	TCGCCCATCT	GGACGCCACC	850
	ACTGTGCTGT	CCCAGGTAT	CTCTGAGCTG	GGTATCTACC	CCGCTGTCGA	900
10	CCCCCTCGAC	TCCAAGTCGC	GTATGCTGGA	CCCCCGTATT	GTCGGTGACG	950
	ACCACTACGA	GACCGCCACT	CGCGTCCAGC	AGATCCTCCA	AGAGTACAAG	1000
	TCGCTGCAGG	ACATCATCGC	CATTCTGGGT	ATGGAGGAGC	TGTCTGAGGC	1050
	CGACAAGCTT	ACAGTCGAGC	GTGCTCGTAA	GATCCAGCGT	TTCTTGAGCC	1100
	AGCCGTTTAC	GGTCGCGCAG	GTCTTCACTG	GTATCGAAGG	CCAGCTGGTC	1150
15	GATCTGAAGG	ACACTATCGC	TTCGTTCAAG	GCTATCCTGA	GCGGTGAGGG	1200
	TGACAGCC					1208

20 2) INFORMATION FOR SEQ ID NO: 894

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 534 bases
 (B) TYPE: Nucleic acid
 25 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

30 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Malbranchea filamentosa*
 (B) STRAIN: ATCC 48174

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 894

35	TTCAGGAACT	TATTGTAAGC	CGCCCTCTTT	ATGCATTGAG	GGTGAATAAG	50
	AAGGCTGACA	GGTAATAGAA	CAACATTGCC	AAGGCTCACG	GTGGTTACTC	100
	CGTGTTCACT	GGTGTCGGTG	AGCGTACCCG	TGAAGGAAAC	GATCTGTACC	150
	ATGAAATGCA	GGAAACCCGC	GTCATCCAGC	TTGATGGCGA	GTCTAAGGTC	200
40	GCCCTTGTTG	TCGGTCAGAT	GAACGAGCCC	CCTGGAGCCC	GTGCCCCTGT	250
	CGTCTTACT	GGTCTTACCG	TTGCCGAATA	CTTCCGTGAC	GAGGAGGGCC	300
	AAGATGGTAC	GCCTTTTAC	TCTTCTTATT	CTTCGGGTGCG	GACTACAGAA	350
	CTAACCTGCT	CCAGTGCTTC	TCTTCATTGA	TAACATTTTC	CGTTTCACAC	400
	AAGCCGGTTC	TGAGGTGTCT	GCCTTGCTTG	GACGTATTCC	CTCTGCCGTC	450
45	GGTTACCAGC	CCACTCTCGC	CGTCGACATG	GGTGGTATGC	AGGAACGTAT	500
	CACAACCACC	AACAAGGGTT	CCATTACTTC	CGTG		534

50 2) INFORMATION FOR SEQ ID NO: 895

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 448 bases
 (B) TYPE: Nucleic acid
 55 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

60 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Paecilomyces lilacinus*

(B) STRAIN: ATCC 60735

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 895

5 CAAGGCTCAC GGTGGTTACT CCGTCTTCAC TGGTGTCGGT GAGCGTACCC 50
 GTGAGGGTAA CGATCTGTAC CACGAAATGC AGGAGACCTC GGTCAATCAG 100
 CTCGAGGGCG AGTCTAAGGT GGCCCTGGTC TTTGGTCAGA TGAACGAGCC 150
 CCCGGGTGCT CGTGCCCGTG TCGCTCTTAC TGGTCTTACC GTCGCCGAGT 200
 10 ACTTCCGTGA CCAGGAGGGT CAGGATGGTT AGTTCTCGTC CACTCATGCC 250
 GAAACATGTG CGTGTTCCGA GGCTAATCAA CGTGCCAGTG CTGCTTTTCA 300
 TCGACAACAT TTTCCGATTC ACCCAGGCCG GTTCCGAGGT GTCTGCCCTG 350
 CTGGGTCGTA TCCCCTCTGC CGTCGGTTAC CAGCCCACCC TCGCCGTCGA 400
 CATGGGTGGC ATGCAGGAGC GTATCACCAC CACCAAGAAG GGCTCTAT 448

2) INFORMATION FOR SEQ ID NO: 896

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 483 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Aspergillus niger*

(B) STRAIN: ATCC 9508

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 896

ATTCAGGAGC TGATTGTAAG TTGCCAATCC ATGAACTGGA GATTGTTGGTGT 50
 35 GACCCATAGA ACTAACAAAT TATTTAGAAC AACATCGCCA AGGCTCACGG 100
 TGGTTACTCC GTCTTCTGTG GTGTCGGTGA GCGTACTCGT GAGGGTAACG 150
 ATCTGTACCA CGAAATGCAG GAGACTGGTG TCATCCAGCT CGAGGGTGAC 200
 TCCAAGGTCG CTCTGGTCTT CGGTCAGATG AACGAGCCCC CGGGTGCCCCG 250
 TGCCCGTGTC GCCCTTACCG GTCTGACCAT TGCCGAGTAC TTCCGTGACG 300
 40 AGGAGGGTCA GGACGTGCTG CTCTTCATTG ACAACATTTT CCGTTTCACC 350
 CAGGCCGGTT CTGAGGTGTC TGCCCTTCTG GGTCGTATCC CCTCTGCCGT 400
 CGGTTACCAG CCCACTCTGG CCGTCGACAT GGGTGGTATG CAGGAGCGTA 450
 TTACCACCAC CACCAAGGGT TCCATTACCT CCG 483

2) INFORMATION FOR SEQ ID NO: 897

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1124 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Aspergillus fumigatus*

(B) STRAIN: ATCC 14110

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 897

	AAGCTCAAGT	CCGAGCGTGA	GCGTGGTATC	ACCATCGACA	TTGCCCTCTG	50
	GAAGTTCCAG	ACTCCCAAGT	ATGAGGTCAC	TGTCATCGGT	AAGCTCGACT	100
5	CGCCCCGATA	TGTTTTGGTG	CTGTAGCTAA	CACGATCTGA	AGATGCCCCC	150
	GGTCACCGTG	ACTTCATCAA	GAACATGATC	ACTGGTACCT	CCCAGGCTGA	200
	CTGCGCTATC	CTCATCATTG	CCTCCGGTAC	TGGTGAGTTC	GAGGCTGGTA	250
	TCTCCAAGGA	TGGCCAGACC	CGTGAGCACG	CTCTGCTGGC	TTTCACCCCTC	300
	GGTGTCAAGC	AGCTCATCGT	CGCCCTCAAC	AAGATGGACA	CCTGCAAGTG	350
10	GTCCGAGGAT	CGTTACAACG	AAATTGTCAA	GGAAACCTCC	AACTTCATCA	400
	AGAAGGTCGG	CTACAACCCC	AAGGCCGTTT	CCTTCGTCCC	CATCTCTGGC	450
	TTCAACGGTG	ACAACATGCT	TGAGCCCTCC	TCCAACCTGCC	CCTGGTACAA	500
	GGGATGGGAG	AAGGAGACCA	AGGCCGGCAA	GGTCACTGGT	AAGACCCTCA	550
	TCGAGGCCAT	CGACGCCATT	GAGCCCCCTG	TCCGTCCCTY	CAACAAGCCC	600
15	CTCCGTCTTC	CCCTCCAGGA	TGTCTACAAG	ATCTCTGGTA	TCGGAACGGT	650
	CCCTGTCTGC	CGTGTCTGAG	CCGGTATCAT	CAAGCCCGGC	ATGGTCGTCA	700
	CCTTCGCCCC	CGCCAACGTC	ACCACTGAAG	TCAAGTCCGT	CGAGATGCAC	750
	CACCAGCAGC	TCCAGGAGGG	TGTCCCCGGT	GACAACGTCG	GTTTCAACGT	800
	CAAGAACGTT	TCCGTCAAGG	AAGTCCGCCG	TGGTAACGTC	TGCGGTGACT	850
20	CCAAGAACGA	TCCCCCTCAG	GGTGCTGCCT	CCTTCAACGC	CCAGGTCATC	900
	GTCCTCAACC	ACCCCGGTCA	GGTCGGCGCT	GGTTACGCCC	CCGTCCTCGA	950
	CTGCCACACT	GCCACATTG	CTTGCAAGTT	CTCTGAGCTG	CTTGAGAAGA	1000
	TTGACCGCCG	TACCGGCAAG	TCTGTTGAGA	ACAACCCCAA	GTTTCATCAAG	1050
	TCCGGTGATG	CGCCATCGT	GAAGATGGTT	CCTTCCAAGC	CCATGTGTGT	1100
25	CGAGTCCTTC	ACTGACTACC	CCCC			1124

2) INFORMATION FOR SEQ ID NO: 898

30

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1363 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

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- (A) ORGANISM: *Penicillium marneffe*
 (D) STRAIN: WSA-214

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 898

45	CTCAAGGCTG	AGCGTGAGCG	TGGTATCACC	ATCGATATTG	CTCTCTGGAA	50
	GTTCCAGACT	GCCAAGTACG	AGGTTACCGT	CATTGACGCC	CCCGGTCACC	100
	GTGATTTTCAT	CAAGAACATG	ATCACTGGTA	CCTCCCAGGC	CGATTGCGCT	150
	ATTCTCATCA	TTGCCTCTGG	TACTGGTGAA	TTGAGGCTG	GTATCTCCAA	200
	GGATGGCCAG	ACTCGTGAGC	ACGCTCTTTT	GGCTTTCACC	CTCGGTGTCC	250
50	GTCAGCTCAT	TGTTGCCCTC	AACAAGATGG	ACACTTGCAA	GTGGTCTCAG	300
	GGTGAGTACT	CGTACCTGCG	TTTGGCCTTG	AATATCTTAC	TAATGCACCA	350
	TAGATCGTTA	CAACGAAATT	GTCAAGGAGA	CTTCCAACCT	CATCAAGAAG	400
	GTCGGATACA	ACCCTAAGAA	CGTTCCTTTT	GTTCTTATCT	CCGGTTTCAA	450
	CGGTGACAAC	ATGCTTGAGC	CCTCCCCCAA	CTGCCCCTGG	TACAAGGGTT	500
55	GGGAGAAGGA	GACCAAGGCC	GGTAAGGTCA	CTGGTAAGAC	CCTCCTCGAG	550
	GCCATCGACG	CCATTGAGCC	CCCTACCCGT	CCCGCCAACA	AGGTTAGTCC	600
	CTCCTCGACT	ACTCAAACCC	TCCTCATAAG	TTCATGATTA	CGACTCGTTC	650
	ACAGCCCCCTC	CGTCTTCCCC	TCCAGGATGT	CTACAAGATC	GGTGGTATTG	700
	GAACGGTTCC	CGTCGGTCGT	GTTGAGACTG	GTACCATCGT	TCCTGGTATG	750
60	GTTGTACACT	TGTAAGTCAC	TCTCCTCGCT	TATCCTACCT	GAAATCATCA	800

	TGTGCTAACT	TGACACTCAG	CGCTCCCGCC	AACGTCACCA	CTGAAGTCAA	850
	GAGTGTGAA	ATGCACCACC	AGCAGCTCAC	TGCCGGTCAG	CCCGGTGACA	900
	ACGTTGGTTT	CAACGTGAAG	AACGTCTCCG	TCAAGGAAAT	CCGTCGTGGT	950
	AACGTTGCTG	GTGACAGCAA	GAACGACCCC	CCTGCCGGTG	CTGCCTCCTT	1000
5	CAACGCCCCAG	GTCATCGTCC	TCAACCACCC	CGGTCAGGTC	GGTGCTGGTT	1050
	ACGCCCCAGT	CCTCGATTGC	CACACTGCCC	ACATTGCTTG	CAAGTTCGCT	1100
	GAGCTCCTCG	AGAAGATTGA	CCGTCGTACC	GGAAAGTCTG	TTGAGGACCA	1150
	CCCCAAGTTC	ATCAAGTCCG	GTGACGCTGC	CATCGTCAAG	ATGATTCTCT	1200
	CCAAGCCCCAT	GTGTGTTGAG	GCTTTCACCG	AGTACCCTCC	TCTCGGTCGT	1250
10	TTCGCCGTTT	GCGAGTAAGT	TTTATCTCCG	TTGTCTATTT	TCCATCCTTC	1300
	CCTTCTCCTC	CGTCTTCCAT	ATATATTTTT	TCAGTTATAT	GTGACTAACC	1350
	ACAAATCACC	GGA				1363

15

2) INFORMATION FOR SEQ ID NO: 899

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1147 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

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(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Piedraia hortai*
 (B) STRAIN: ATCC 24292

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 899

	CAAGCTGAAA	GCCGAGCGTG	AGCGTGGTAT	CACTATCGAC	ATTGCCCTCT	50
	GGAAGTTCGA	GACTCCCAAG	TACTATGTCA	CCGTCATTGG	TACGTCGCAT	100
	TATCTCACTC	CTCACAGAAG	CACGCTCCTA	ACATCACACA	GACGCTCCCG	150
35	GTCACCGTGA	TTTCATCAAG	AACATGATCA	CTGGTACCTC	CCAGGCCGAC	200
	TGCGCTATCC	TCATTATCGC	TGCCGGTACT	GGTGAGTTCT	AGGCTGGTAT	250
	CTCCAAGGAT	GGCCAGACTC	GTGAGCACGC	CCTGCTCGCC	TACACCCTCG	300
	GTGTGCGTCA	GCTCATCGTC	GCCATCAACA	AGATGGACAC	CACCAAGTGG	350
	TCTGAGGCCC	GTTACCAGGA	GATCATCAAG	GAGACCTCCA	ACTTCATCAA	400
40	GAAGGTCGGC	TACAACCCCA	AGACCGTCGC	TTTCGTCCCC	ATCTCTGGCT	450
	TCAACGGCGA	CAACATGCTT	GCCCCCTCCA	CCAAC TGCCC	CTGGTACAAG	500
	GGATGGGAGC	GTGAGGTCAA	GGGCAACAAG	CAGACCGGCA	AGACCCTCCT	550
	CGAGGCCATT	GACGGCATTG	AGCCCCCAA	GCGTCCTTCC	GACAAGCCCC	600
	TCCGTCTTCC	TCTCCAGGAT	GTTTACAAGA	TCCGTGGTAT	CGGAAC TGTT	650
45	CCTGTCGGCC	GTATCGAGAC	TGGTGTCTCT	AAGCCCCGTA	TGGTCGTTAC	700
	CTTCGCTCCC	GCCAACGTCA	CCACTGAAGT	CAAGTCCGTC	GAGATGCACC	750
	ACGAGCAGCT	CACTGAGGGT	CTTCCCGGTG	ACAACGTCGG	TTTCAACGTG	800
	AAGAACGTTT	CCGTCAAGGA	CATCCGCCGT	GGTAACGTTG	CCAGTGACTC	850
	CAAGAACGAC	CCCGCTCTGG	GTGCCGCTTC	TTTCGACGCC	CAGGTCATCG	900
50	TCCTCAACCA	CCCCGGTCAG	GTCGGTGCTG	GTTACGCCCC	GGTCCTCGAT	950
	TGCCCACTG	CCCACATTGC	TTGCAAGTTC	TCCGAGATCA	AGGAGAAGAT	1000
	CGACCGCCGT	ACCGGCAAGT	CTGTTGAGGA	CGCCCCCAAG	TTCATCAAGT	1050
	CTGGTGACTC	TGCCATCGTC	AAGATGGTTC	CCTCCAAGCC	CATGTGCGTT	1100
55	GAGGCTTTCA	CCGACTACCC	TCCTCTGGGC	CGTTTCGCCG	TCCGTGA	1147

2) INFORMATION FOR SEQ ID NO: 900

(i) SEQUENCE CHARACTERISTICS:

505

- (A) LENGTH: 1150 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

5

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Paecilomyces lilacinus*
 (B) STRAIN: ATCC 60735

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 900

	CTCAAGGCCG	AGCGTGAGCG	TGGTATCACC	ATCGACATTG	CCCTCTGGAA	50
15	GTTTCGAGACT	CCCAAGTACT	ATGTCACCGT	CATTGGTACG	TCGACTCGCG	100
	CGAGACTGGT	CGCAATTTCC	ACGTCGCTAA	CGTGCTTGAA	CAGACGCTCC	150
	CGGCCACCGT	GACTTCATCA	AGAACATGAT	CACTGGTACC	TCCCAGGCTG	200
	ACTGCGCTAT	CCTCATTATC	GCTGCCGGA	CTGGTGAGTT	CGAGGCTGGT	250
	ATCTCCAAGG	ATGGCCAGAC	CCGTGAGCAC	GCTCTGCTCG	CCTACACCCT	300
20	CGGTGTTAAG	CAGCTCATCG	TCGCTATCAA	CAAGATGGAC	ACCACCAAGT	350
	GGTCTGAGGC	CCGTTTCCAG	GAGATCATCA	AGGAGACCTC	CAACTTCATC	400
	AAGAAGGTCG	GCTACAACCC	CAAGACCGTC	GCTTTCGTCC	CCATCTCTGG	450
	TTTCCACGGC	GACAACATGC	TTTCCCCCTC	CACCAACTGC	CCCTGGTACA	500
	AGGGCTGGGA	GAAGGAGACC	AAGGCTGGCA	AGTCCACCGG	CAAGACCCTC	550
25	CTTGAGGCCA	TCGACTCCAT	CGAGCCCCC	AAGCGCCCCA	GCGACAAGCC	600
	CCTCCGCCTT	CCCCTTCAGG	ATGTGTACAA	GATCGGCGGT	ATCGGCACAG	650
	TCCCTGTCCG	CCGTATCGAG	ACTGGTGTCA	TCAAGCCCCG	CATGGTCGTG	700
	ACCTTCGCTC	CTTCCAACGT	CACCACCGAA	GTCAAGTCCG	TTGAGATGCA	750
	CCACGAGCAG	CTCTCCGAGG	GTGTCCCCGG	TGACAACGTC	GGCTTCAACG	800
30	TCAAGAACGT	CTCCGTCAAG	GAGATCCGTC	GTGGCAACGT	CGCCGGTGAC	850
	TCCAAGAACG	ACCCCCCTCT	GGGTGCCGCT	TCTTTCGATG	CCCAGGTCAT	900
	CGTCCTCAAC	CACCCCGGCC	AGGTCCGGTG	TGGCTACGCC	CCCGTCCTCG	950
	ACTGCCACAC	CGCCACATT	GCCTGCAAGT	TCGCCGAGAT	CAAGGAGAAG	1000
	ATCGACCGCC	GTACCGGCAA	GTCTGTGCGAG	TCCGCCCCCA	AGTTCATCAA	1050
35	GTCTGGCGAC	TCTGCCATCG	TCAAGATGAT	TCCCTCCAAG	CCCATGTGCG	1100
	TTGAGGCTTT	CACCGACTAC	CCTCCTCTGG	GCCGCTTCGC	CGTCCGTGAC	1150

40 2) INFORMATION FOR SEQ ID NO: 901

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 751 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

45

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Paracoccidioides brasiliensis*
 (B) STRAIN: ATCC 32075

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 901

55

	TACCACTAAG	TGGTCCGAGA	CCCGATTCAA	TGAAATTATC	AAGGAAGTCA	50
	CCAATTTTCAT	TAAGAAGGTC	GGATATAACC	CCAAGACTGT	TCCTTTCGTT	100
	CCCATTTCTG	GTTTCGAGGG	TGACAACATG	ATCGAGCCCT	CTGCCAACTG	150
	CCCATGGTAC	AAGGGCTGGT	CCAAGGAGAC	TGCTCAGGGC	AAGTACTCTG	200
60	GCAAGACCCT	TCTTGAGGCC	ATCGACGCCA	TTGAGCCCCC	CACCCGTCCT	250

	ACCGATAAAC	CTCTCCGTCT	TCCCCTCCAG	GATGTCTACA	AGATCTCCGG	300
	TATTGGCACT	GTTCTGTCTG	GACGTGTTGA	GACTGGAGTC	ATCAAGCCCCG	350
	GTATGGTCGT	GACCTTCGCT	CCCGCCAACG	TCACCACTGA	AGTCAAGTCC	400
	GTCGAAATGC	ACCACCAGCA	GCTTACCGCC	GGTAACCCCG	GTGACAACGT	450
5	CGGCTTCAAC	GTCAAGAATG	TTTCCGTCAA	AGAAAGTCCGC	CGTGGTAACG	500
	TTGCCGGTGA	CTCTAAGAAT	GATCCCCCAA	AGGGCTGCGA	TTCCTTCAAT	550
	GCCCAGGTCA	TCGTCTCTAA	CCACCCTGGT	CAGGTTGGCG	CTGGTTATGC	600
	CCCAGTCCTC	GACTGCCATA	CTGCCCACAT	TGCTTGCAAA	TTCGCTGAGC	650
	TCCTTGAGAA	GATTGATCGA	CGAACC GGAA	AGTCTGTTGA	GAACAACCCC	700
10	AAGTTCATCA	AGTCCGGTGA	TGCTGCTATC	GTCAAGATGA	TTCCTTCCAA	750
	G					751

15 2) INFORMATION FOR SEQ ID NO: 902

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1056 bases
 (B) TYPE: Nucleic acid
 20 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

25 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Sporothrix schenckii*
 (B) STRAIN: ATCC 7968

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 902

30	CGTGAGCGCG	GTATCACCAT	CGATATTGCT	CTGTGGAAGT	TCGAGACCCC	50
	CAAGTACTAC	GTCACCGTCA	TTGACGCCCC	CGGTCATCGC	GATTTCATCA	100
	AGAACATGAT	CACTGGTACC	TCGCAGGCCG	ACTGCGCCAT	TCTCATCATT	150
	GCCGCTGGTA	CTGGTGAGTT	CGAGGCTGGT	ATCTCCAAGG	ATGGCCAGAC	200
35	TCGTGAGCAC	GCTCTGCTCG	CCTACACCCT	GGGTGTGCGG	CAGCTGATCG	250
	TCGCCATCAA	CAAGATGGAC	ACGGCCAAGT	GGGCTGAGGC	TCGTTACCAG	300
	GAGATCATCA	AGGAGACCTC	CAACTTCATC	AAGAAGGTCG	GCTACAACCC	350
	CAAGACTGTT	GCCTTCGTCC	CCATCTCGGG	CTTCCACGGC	GACAACATGC	400
	TTACTCCCTC	GACCAACTGC	CCCTGGTACA	AGGGCTGGGA	GAAGGAGGGC	450
40	AAGAGCGGCA	AGGTTACCGG	TAAGACTCTG	CTGGACGCCA	TTGACGCCGT	500
	CGAGCCCCCC	AAGCGCCCCA	CGGACAAGCC	CCTGCGTCTG	CCCCCTCAGG	550
	ATGTCTACAA	GATCGGCGGT	ATCGGCACTG	TCCCTGTCGG	CCGTATCGAG	600
	ACTGGTGTCC	TGAAGCCCGG	CATGGTCGTC	ACCTTTGCC	CGTCCAACGT	650
	CACCACTGAA	GTCAAGTCCG	TCGAGATGCA	CCACGAGCAG	CTTGTTGAGG	700
45	GTGTTCCCGG	CGACAACGTC	GGCTTCAACG	TCAAGAACGT	CTCCGTCAAG	750
	GAGATCCGTC	GTGGCAACGT	TGCCGGTGAC	TCCAAGAACG	ACCCCCCCTC	800
	GGGCGCCGCC	ACCTTCAACG	CCCAGGTCAT	TGTCCTGAAC	CACCCCGGCC	850
	AGGTCGGCAA	CGGCTACGCC	CCGGTTCTGG	ACTGCCACAC	CGCCACATT	900
	GCCTGCAAGT	TCACCGAGAT	CCTTGAGAAG	ATCGACCGCC	GTACCGGCAA	950
50	GTCGGTTGAG	AACAACCCCA	AGTTCATCAA	GTCGGGTGAC	GCCGCCATTG	1000
	TCAAGCTGAC	GCCCTCGAAG	CCCATGTGCG	TTGAGGCCTT	CACTGACTAC	1050
	CCCCCT					1056

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2) INFORMATION FOR SEQ ID NO: 903

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1366 bases
 60 (B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

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(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Penicillium marneffe*

(B) STRAIN: ATCC 58950

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 903

	CAAGGCTGAG	CGTGAGCGTG	GTATCACCAT	CGATATTGCT	CTCTGGAAGT	50
	TCCAGACTGC	CAAGTACGAG	GTTACCGTCA	TTGACGCCCC	CGGTCACCGT	100
	GATTTCATCA	AGAACATGAT	CACTGGTACC	TCCCAGGCCG	ATTGCGCTAT	150
15	TCTCATCATT	GCCTCTGGTA	CTGGTGAATT	CGAGGCTGGT	ATCTCCAAGG	200
	ATGGCCAGAC	TCGTGAGCAC	GCTCTTTTGG	CTTTCACCCT	CGGTGTCCGT	250
	CAGCTCATTG	TTGCCCTCAA	CAAGATGGAC	ACTTGCAAGT	GGTCTCAGGG	300
	TGAGTACTCG	TACCTGCGTT	TGGCCTTGAA	TATCTTACTA	ATGCACCATA	350
	GATCGTTACA	ACGAAATTGT	CAAGGAGACT	TCCAACCTCA	TCAAGAAGGT	400
20	CGGATACAAC	CCTAAGAACG	TTCTTTTCGT	TCCTATCTCC	GGTTTCAACG	450
	GTGACAACAT	GCTTGAGCCC	TCCCCCAACT	GCCCCTGGTA	CAAGGGTTGG	500
	GAGAAGGAGA	CCAAGGCCGG	TAAGGTCACT	GGTAAGACCC	TCCTCGAGGC	550
	CATCGACGCC	ATTGAGCCCC	CTACCCGTCC	CGCCAACAAG	GTTAGTCCCT	600
	CCTCGACTAC	TCAAACCCTC	CTCATAAGTT	CAGATTACTG	ACTCGTTCAC	650
25	AGCCCCCTCCG	TCTTCCCCTC	CAGGATGTCT	ACAAGATCGG	TGGTATTGGA	700
	ACGGTTCCCG	TCGGTCGTGT	TGAGACTGGT	ACCATCGTTC	CTGGTATGGT	750
	TGTCACCTTG	TAAGTCACTC	TCCTCGCTTA	TCCTACCTGA	AATCATCATG	800
	TGCTAACTTG	ACACTCAGCG	CTCCCGCCAA	CGTCACCACT	GAAGTCAAGA	850
	GTGTTGAAAT	GCACCACCAG	CAGCTCACTG	CCGGTCAGCC	CGGTGACAAC	900
30	GTTGGTTTCA	ACGTGAAGAA	CGTCTCCGTC	AAGGAAATCC	GTCGTGGTAA	950
	CGTTGCTGGT	GACAGCAAGA	ACGACCCCCC	TGCCGGTGCT	GCCTCCTTCA	1000
	ACGCCCAGGT	CATCGTCCTC	AACCACCCCG	GTCAGGTCGG	TGCTGGTTAC	1050
	GCCCCAGTCC	TCGATTGCCA	CACTGCCCAC	ATTGCTTGCA	AGTTCGCTGA	1100
	GCTCCTCGAG	AAGATTGACC	GTCGTACCGG	AAAGTCTGTT	GAGGACCACC	1150
35	CCAAGTTCAT	CAAGTCCGGT	GACGCTGCCA	TCGTCAAGAT	GATTCCTTCC	1200
	AAGCCCATGT	GTGTTGAGGC	TTTCACCGAG	TACCCTCCTC	TCGGTCGTTT	1250
	CGCCGTTTCG	GAGTAAGTTT	TATCTCCGTT	GTCTATTTTC	CATCCTTCCC	1300
	TTCTCCTCCG	TCTTCCATAT	ATATTTTTC	AGTTATATGT	GACTAACCAC	1350
	AAATCACGGG	AATAGC				1366

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2) INFORMATION FOR SEQ ID NO: 904

45 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 841 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

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(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Curvularia lunata*

55 (B) STRAIN: ATCC 26425

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 904

	CTATTATCGT	TGTTGCCGCT	TCCGACGGTC	AAATGCCCCA	GACTCGTGAG	50
60	CATCTGCTGC	TCGCCCCGCCA	GGTCGGTGTC	CAGAAGATCG	TTGTCTTCGT	100

508

	CAACAAGGTC	GATGCTGTTG	AGGACAAGGA	GATGTTGGAG	CTCGTCGAGA	150
	TGGAGATGCG	CGAATTGCTC	AGCAGCTACG	GCTTCGAGGG	CGACGAGACT	200
	CCCATCATCA	TGGGATCTGC	CCTCTGCGCC	ATTGAGGGCC	GCGAACCTGA	250
	GATTGGTGTC	AACCGAATTG	ATGAGCTGCT	CGAGGCCGTT	GATACTTGGA	300
5	TCCCCACCCC	TCAGCGTGAG	ACCGACAAGC	CTTTCCTCAT	GGCCGTCGAG	350
	GATGTCTTCT	CCATTGCTGG	TCGTGGCACT	GTCGTCTCTG	GCCGTGTCGA	400
	GCGAGGTATC	CTGAAGCGCG	ATGCTGAAGT	TGAGCTCGTC	GGCAAGGGCA	450
	CCGCCCCCAT	CAAGACCAAG	GTTACCGATA	TCGAGACCTT	CAAGAAGTCC	500
	TGCGAGGAGT	CTCGCGCTGG	TGACAACTCC	GGTCTCCTTC	TTCGTGGTGT	550
10	CAAGCGTGAT	GAAGTCCGCC	GTGGTATGGT	CGTTTCCGTC	CCTGGACAGG	600
	TCAAGGCGCA	CAAGAAGTTC	CTTGTCTCCA	TGTACGTGTT	GAGCAAGGAG	650
	GAAGGTGGTC	GTCACACTGG	CTTCGGTGAG	AACTACAGGC	CGCAAATGTT	700
	CATCCGCACT	GCCGACGAGT	CGTGTGCCCT	GTAAGGCCCA	GAAGGCACCG	750
	AGGACGCCCA	TGACAAGCTT	GTTATGCCCG	GTGACAACGT	CGAGATGGTT	800
15	TGCGAGCTCC	ATGCACCACA	CGTCTTGAG	CCTGGTCAAC	G	841

2) INFORMATION FOR SEQ ID NO: 905

20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 967 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

25

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

30

- (A) ORGANISM: *Aspergillus niger*
 (B) STRAIN: ATCC 9508

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 905

35	CGGTGCTATC	ATTGTCGTCG	CCGCCTCCGA	CGGTCAGATG	TACGTTAACC	50
	TTAAAGAAT	AACTCTCCTT	CAGTATATAT	GCTTACACTG	GCGATCAACA	100
	GGCCCCAGAC	TCGTGAGCAC	TTGCTGCTTG	CTCGTCAGGT	CGGTGTCCAG	150
	AAGATCGTTG	TCTTCGTCAA	CAAGGTCGAT	GCTATCGATG	ACCCCGAGAT	200
	GCTGGAGCTC	GTTGAGCTGG	AAATGCGCGA	GCTTCTCAGC	ACCTACGGAT	250
40	TCGAGGGTGA	GGAGACCCCC	ATCGTCTTCG	GCTCTGCTCT	CTGCGCCATT	300
	GAGGACCGCC	GCCCCGACAT	CGGTACCGAG	CGTATCGACG	CTCTCCTCGA	350
	GGCCGTTGAC	ACCTGGATCC	CCACTCCCCA	GCGTGACCTT	GACAAGCCTT	400
	TCTTGATGTC	CATTGAGGAA	GTTTTCTCCA	TCCCCGGTCG	TGGTACCGTC	450
	GCCTCCGGCC	GTGTCGAGCG	TGGTCTCCTG	AAGCGTGATA	GCGAGGTTGA	500
45	GATCATCGGT	ACCACCAACG	AGGTCATCAA	GACCAAGGTT	ACCGACATTG	550
	AGACCTTCAA	GAAGTCCTGC	TCCGAGTCCC	GCGCCGGTGA	CAACTCCGGT	600
	CTCCTGCTCC	GTGGTGTCGG	CCGTGAGGAT	CTCCGCCGTG	GTATGGTCAT	650
	TGCGGCTCCT	GGCAGCGCCA	AGGCCAACAG	CAAGTTCATG	GTCTCCATGT	700
	ACGTCCTGAC	CGAGGCTGAR	GGTGGTCGCC	GTACCGGTTT	CGGTGTCCAG	750
50	TACCGTCCCC	AGCTGTTTCAT	CCGCACTGCC	GGTAAGTAAA	ATTGCATTCT	800
	ATTCCGCTAC	TAGGGAACCA	TCTCTAATTC	TATTTGCTAC	AGATGAGGCT	850
	GCTGAGTTCA	GCTTCCCCGA	CGGAGACCAG	TCCCGCCGTA	TCATGCCCGG	900
	TGACAACGTC	GAGATGATCG	TCAAGACCCA	CCGCCCCGTC	GCCGCCGAGG	950
	CCGGTCAGCG	CTTCAAC				967

55

2) INFORMATION FOR SEQ ID NO: 906

60

(i) SEQUENCE CHARACTERISTICS:

509

- (A) LENGTH: 852 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

5

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bipolaris hawaiiensis*
 (B) STRAIN: ATCC 26067

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 906

	TGGTGCTATT	ATTGTTGTTG	CCGCTTCCGA	CGGTCAAATG	CCCCAGACTC	50
15	GTGAGCATCT	GCTGCTCGCC	CGTCAGGTCG	GTGTTTCAGAA	GATCGTTGTC	100
	TTCGTTAACA	AGGTCGACGC	TGTCGAGGAC	AAGGAGATGT	TGGAGCTTGT	150
	CGAGATGGAG	ATGCGCGAAC	TGCTCAGCAG	CTATGGCTTC	GAGGGCGACG	200
	AGACCCCTAT	CATCATGGGT	TCTGCTCTCT	GCGCCATTGA	AGGCCGTCAA	250
	CCCGACATTG	GTGTCGAACG	AATTGACGAG	CTGCTCGAGG	CTGTTGATAC	300
20	TTGGATTCCC	ACCCCTCAGC	GTGAGACCGA	AAAGCCTTTC	CTCATGGCCG	350
	TCGAGGATGT	CTTCTCCATT	GCTGGTCGTG	GTACCGTCGT	CTCTGGCCGT	400
	GTCGAACGAG	GTATCCTGAA	GCGCGATGCT	GAAGTTGAGC	TTGTGGGCAA	450
	GGGCAGCGCA	CCCATCAAGA	CCAAGGTTAC	CGATATCGAG	ACCTTCAAGA	500
	AGTCTTGCGA	GGAGTCCCGC	GCTGGTGACA	ACTCCGGTCT	CCTTCTTCGT	550
25	GGTGTTAAGC	GTGATGAAGT	CCGCCGTGGT	ATGGTCGTTT	CCGTCCCTGG	600
	ACAGGTTAAG	GCGCACAAGA	AGTTCCTTGT	CTCCATGTAT	GTGCTGAGCA	650
	AGGAGGAAGG	TGGCCGACAC	ACTGGCTTCG	GTGAGAACTA	CAGGCCGCAA	700
	ATGTTTCATCC	GCACTGCCGA	CGAGTCGTGT	GCCCTGTACT	GGCCAGAAGG	750
	CACCGAGGAT	GCCCCACGAC	AGCTTGTCAT	GCCCCGGTGAC	AACGTCGAGA	800
30	TGGTTTGCGA	GCTCCATGCA	CCACACGTCT	TGGAGACTGG	TCAGCGCTTC	850
	AA					852

35 2) INFORMATION FOR SEQ ID NO: 907

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 966 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

40

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Aspergillus flavus*
 (B) STRAIN: ATCC 26947

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 907

50

	GGTGCTATTG	TTGTCGTTGC	TGCTTCGGAT	GGTCATGATG	TATGGACAGG	50
	CCCTTTGCTA	CTGAATGGTT	TCAAGATCTC	GCGCTTACAC	GTATTATAAT	100
	AGGCCCCAGA	CCCGGGAGCA	CTTGCTGCTT	GCCCCGTCAGG	TCGGTGTCCA	150
	GAAGATCGTC	GTTTTTGTCA	ACAAGATTGA	TGCCGTTGAG	GACCCTGAGA	200
55	TGTTGGAGCT	TGTCGAGTTG	GAAATGCGCG	AGCTCCTTAG	CAGCTACGGC	250
	TTCGAGGGCG	AAGAGACTCC	CATCATCTTC	GGTTCTGCTC	TGTGTGCTTT	300
	GGAGGACCGT	CGCCCCGACA	TGGTGCCGA	GCGTATCGAC	GAGCTCATGA	350
	AGGCCGTTGA	CACCTGGATC	CCTACCCCTC	AGCGTGATCT	TGACAAGCCT	400
	TTCCTCATGT	CTGTCGAGGA	AGTCTTCTCC	ATCGCCGGTC	GTGGTACCGT	450
60	TGCCTCCGGC	CGTGTCGAAC	GTGGTATCCT	GAAGAAGGAC	AGCGAAGTCG	500

510

	AGATCATCGG	AGGTAGCTTC	GATGCTACCA	AGACCAAGGT	CACCGACATT	550
	GAGACCTTCA	AGAAGTCTTG	TGACGAGTCC	CGCGCTGGTG	ACAACCTCTGG	600
	CTTGCTTCTC	CGTGGTATCC	GTCGTGAAGA	CGTCCGCCGC	GGAATGATCA	650
	TTGCTGCTCC	TGGCAGCACC	AAGGCCACG	ACCAGTTCTT	GGTGTCCATG	700
5	TACGTTCTCA	CTGAGGCTGA	GGGTGGTCGT	CGTACTGGCT	TCGGCTCCAA	750
	CTACCGCCCC	CAGGTGTTTCG	TTCGCACTGC	TGGTAAGTCA	AGCCTTTTGC	800
	TCACTTAACG	GTATTGATTA	AGTTCTAACT	GTTGTATCCT	AGATGAGGCT	850
	GCTGACCTCA	GCTTCCCCGA	CGGTGATGAG	TCCCGGAGGG	TGATGCCTGG	900
	TGACAACGTC	GAGATGGTCC	TCAAGACTCA	CCGCCCCATT	GCTGCTGAGG	950
10	CTGGCCAGCG	CTTCAA				966

2) INFORMATION FOR SEQ ID NO: 908

15

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 845 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

25

- (A) ORGANISM: *Alternaria alternata*
 (B) STRAIN: ATCC 62099

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 908

30	GGTGCTATCA	TCGTCGTTGC	TGCTTCCGAT	GGTCAGATGC	CCCAGACCCG	50
	TGAGCACTTG	CTGCTCGCCC	GTCAGGTCGG	TGTTCAGAAG	ATCGTTGTCT	100
	TCGTCAACAA	GGTCGATGCT	GTCGAAGACC	CGGAGATGTT	GGAACCTCGTC	150
	GAGATGGAGA	TGCGTGAGTT	ACTCACCAGC	TACGGCTTCG	AGGGCGACGA	200
	GACACCCATC	ATCATGGGTT	CCGCTCTATG	CGCCATCGAG	GGCCGCCAGC	250
35	CCGAGATCGG	TGTTACCAAG	GTCGACGAGC	TAATGGACGC	TGTCGACTCA	300
	TGGATCCCCA	CCCCTCAGCG	TGAGACCGAG	AAGCCTTTCC	TCATGGCTGT	350
	TGAGGATGTC	TTCTCGATTG	CTGGACGTGG	TACCGTCGTT	TCGGGCCGTG	400
	TCGAGCGCGG	TATCTTGAAG	CGTGACGCTG	AAGTCGAGCT	TGTCGGCAAG	450
	GGCACCGCGC	CAATCAAGAC	CAAGGTCACT	GATATTGAGA	CCTTCAAGAA	500
40	GTCGTGCGAG	GAGTCGCGCG	CGGGTGATAA	CTCCGGTCTT	CTCCTCCGTG	550
	GTGTCAAGCG	TGATGACGTT	CGCCGCGGTA	TGGTTGTTTC	CGTTCCCGGA	600
	CAAGTCAAGG	CTCACAAGAA	GTTTCCTGTC	TCCATGTACG	TTCTAAGCAA	650
	AGAGGAGGGT	GGTCGTCACA	CCGGCTTCGG	CGAGAACTAC	AGGCCGCAAA	700
	TGTTTCATCCG	AACTGCCGAT	GAATCCTGCG	CACTTCACTT	CCCAGAGGGT	750
45	ACCGAGGATG	CGCACGACAA	GCTAGTTATG	CCCGGTGACA	ACGTCGAGAT	800
	GGTCTGCGAA	CTCCACCAGC	CCCACGTTCT	AGAGACCGGT	CAGCG	845

50 2) INFORMATION FOR SEQ ID NO: 909

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 931 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

55

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

60

(A) ORGANISM: *Penicillium marneffei*

(B) STRAIN: ATCC 64101

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 909

5
 CGCTGTTGTT GTCGTCGCTG CTTCTGATGG TCAAATGTAA CATATCCACG 50
 AGCTGCCAAT TATGGACACT GCTGATAAGA ATAGGCCCCA AACCCGTGAG 100
 CACTTGCTCC TCGCCCGTCA GGTCGGTGTT CAAAAGATCG TCGTCTTCGT 150
 CAACAAGGTT GATGCCGTCG AGGACCCCGA GATGTTGGAA CTTGTCGAAT 200
 10 TGGAAATGCG TGAACCTCTG ACCACCTACG GTTTCGAGGG TGAAGAGACC 250
 CCTATCATTT TCGGATCCGC TCTTTGCGCC TTGGAAGGCC GCAAGCCCGA 300
 GATTGGCGAA CAGAAGATTG ACGAGTCAT GAACGCCGTT GATAECTGGA 350
 TCCCCACCCC CCAGCGTGAC CTTGACAAGC CCTTCTTGAT GTCCGTTGAG 400
 GAAGTTTCT CCATCTCTGG TCGTGGTACC GTTGCATCTG GTCGTGTTGA 450
 15 GCGTGGTATT TTGCGCAAGG ATTCTGAGGT TGAGATTATC GGATACCAGA 500
 AGAACCCCTAT CAAGACCAAG GTTACCGACA TTGAGACCTT CAAGAAGTCT 550
 TGCGATGAAT CTCGTGCTGG TGACAACTCT GGCTTGCTTC TCCGTGGTAT 600
 CAAGCGTGAG GACATTCGTC GTGGTATGGT TATCGCTGCT CCTGGAACCA 650
 CCAAGGCTCA TGACAACTTC TTGGTCTCCA TGTATGTCTT GACTGAGGCT 700
 20 GAAGGTGGTC GTCGTA CTGG ATTTCGGCGCC AACTACCGTC CTCAAGCTTT 750
 CATCCGTACT GCCGGTATGT TCCCTTTCAA AGTCAATTAA TGAGCGATTT 800
 GCTAACGAGT TATAGATGAG GCTGCTACTC TCAGCTTCCC CGGTGACGAT 850
 CAGTCCAAGC AGGTCATGCC CGGTGACAAC GTTGAGATGA TCTTGAAGAC 900
 ACACCGTCCC GTTGCCGCCG AAGCTGGTCA G 931

25

2) INFORMATION FOR SEQ ID NO: 910

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 931 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Penicillium marneffei*
 40 (B) STRAIN: ATCC 58950

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 910

45
 CGCTGTTGTT GTCGTCGCTG CTTCTGATGG TCAAATGTAA CATATCCACG 50
 AGCTGCCAAT TATGGACACT GCTGATAAGA ATAGGCCCCA AACCCGTGAG 100
 CACTTGCTCC TCGCCCGTCA GGTCGGTGTT CAAAAGATCG TCGTCTTCGT 150
 CAACAAGGTT GATGCCGTCG AGGACCCCGA GATGTTGGAA CTTGTCGAAT 200
 TGGAAATGCG TGAACCTCTG ACCACCTACG GTTTCGAGGG TGAAGAGACC 250
 CCTATCATTT TCGGATCCGC TCTTTGCGCC TTGGAAGGCC GCAAGCCCGA 300
 50 GATTGGCGAA CAGAAGATTG ACGAGTCAT GAACGCCGTT GATACTGGA 350
 TCCCCACCCC CCAGCGTGAC CTTGACAAGC CCTTCTTGAT GTCCGTTGAG 400
 GAAGTTTCT CCATCTCTGG TCGTGGTACC GTTGCATCTG GTCGTGTTGA 450
 GCGTGGTATT TTGCGCAAGG ATTCTGAGGT TGAGATTATC GGATACCAGA 500
 AGAACCCCTAT CAAGACCAAG GTTACCGACA TTGAGACCTT CAAGAAGTCT 550
 55 TGCGATGAAT CTCGTGCTGG TGACAACTCT GGCTTGCTTC TCCGTGGTAT 600
 CAAGCGTGAG GACATTCGTC GTGGTATGGT TATCGCTGCT CCTGGAACCA 650
 CCAAGGCTCA TGACAACTTC TTGGTCTCCA TGTATGTCTT GACTGAGGCT 700
 GAAGGTGGTC GTCGTA CTGG ATTTCGGCGCC AACTACCGTC CTCAAGCTTT 750
 CATCCGTACT GCCGGTATGT TCCCTTTCAA AGTCAATTAA TGAGCGATTT 800
 60 GCTAACGAGT TATAGATGAG GCTGCTACTC TCAGCTTCCC CGGTGACGAT 850

CAGTCCAAGC AGGTCATGCC CGGTGACAAC GTTGAGATGA TCTTGAAGAC 900
ACACCGTCCC GTTGCCGCCG AAGCTGGTCA G 931

5

2) INFORMATION FOR SEQ ID NO: 911

- (i) SEQUENCE CHARACTERISTICS:
10 (A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear
-

- 15 (ii) MOLECULE TYPE: DNA

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 911

GACGGMKKCA TGCCGCARAC 20

20

2) INFORMATION FOR SEQ ID NO: 912

- 25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

- 30 (ii) MOLECULE TYPE: DNA

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 912

35 GACGGCGKCA TGCCGCARAC 20

2) INFORMATION FOR SEQ ID NO: 913

- 40 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

- 45 (ii) MOLECULE TYPE: DNA

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 913

50 GACGGYSYCA TGCKCAGAC 20

2) INFORMATION FOR SEQ ID NO: 914

- 55 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
60 (D) TOPOLOGY: Linear

513

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 914

5

GAARAGCTGC GGRCGRTAGT G

21

10 2) INFORMATION FOR SEQ ID NO: 915

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 21 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 915

AAACGCCTGA GGRCGGTAGT T

21

25

2) INFORMATION FOR SEQ ID NO: 916

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 916

GCCGAGCTGG CCGGCTTCAG

20

40

2) INFORMATION FOR SEQ ID NO: 917

(i) SEQUENCE CHARACTERISTICS:

- 45 (A) LENGTH: 22 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 917

TCGTGCTACC CGTYGCCGCC AT

22

55

2) INFORMATION FOR SEQ ID NO: 918

60 (i) SEQUENCE CHARACTERISTICS:

514

- (A) LENGTH: 1391 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

5

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Escherichia coli*
 (E) ACCESSION NUMBER: J01672

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 918

	AGAGAAGCCT	GTCGGCACCG	TCTGGTTTGC	TTTTGCCACT	GCCCGCGGTG	50
15	AAGGCATTAC	CCGGCGGGAT	GCTTCAGCGG	CGACCGTGAT	GCGGTGCGTC	100
	GTCAGGCTAC	TGCGTATGCA	TTGCAGACCT	TGTGGCAACA	ATTTCTACAA	150
	AACACTTGAT	ACTGTATGAG	CATACAGTAT	AATTGCTTCA	ACAGAACATA	200
	TTGACTATCC	GGTATTACCC	GGCATGACAG	GAGTAAAAAT	GGCTATCGAC	250
	GAAAACAAAC	AGAAAGCGTT	GGCGGCAGCA	CTGGGCCAGA	TTGAGAAACA	300
20	ATTTGGTAAA	GGCTCCATCA	TGCGCCTGGG	TGAAGACCGT	TCCATGGATG	350
	TGGAAACCAT	CTCTACCGGT	TCGCTTTCAC	TGGATATCGC	GCTTGGGGCA	400
	GGTGGTCTGC	CGATGGGCCG	TATCGTCGAA	ATCTACGGAC	CGGAATCTTC	450
	CGGTAAACC	ACGCTGACGC	TGCAGGTGAT	CGCCGCAGCG	CAGCGTGAAG	500
	GTAAACCTG	TGCGTTTATC	GATGCTGAAC	ACGCGCTGGA	CCCAATCTAC	550
25	GCACGTAAAC	TGGGCGTCGA	TATCGACAAC	CTGCTGTGCT	CCCAGCCGGA	600
	CACCGGCGAG	CAGGCACTGG	AAATCTGTGA	CGCCCTGGCG	CGTTCTGGCG	650
	CAGTAGACGT	TATCGTCGTT	GACTCCGTGG	CGGCACTGAC	GCCGAAAGCG	700
	GAAATCGAAG	GCGAAATCGG	CGACTCTCAC	ATGGGCCTTG	CGGCACGTAT	750
	GATGAGCCAG	GCGATGCGTA	AGCTGGCGGG	TAACCTGAAG	CAGTCCAACA	800
30	CGCTGCTGAT	CTTCATCAAC	CAGATCCGTA	TGAAAAATTGG	TGTGATGTTT	850
	GGTAACCCGG	AAACCACTAC	CGGTGGTAAC	GCGCTGAAAT	TCTACGCCTC	900
	TGTTCTGCTC	GACATCCGTC	GTATCGGCGC	GGTGAAAGAG	GGCGAAAACG	950
	TGGTGGGTAG	CGAAACCCGC	GTGAAAGTGG	TGAAGAACAA	AATCGCTGCG	1000
	CCGTTTAAAC	AGGCTGAATT	CCAGATCCTC	TACGGCGAAG	GTATCAACTT	1050
35	CTACGGCGAA	CTGGTTGACC	TGGGCGTAAA	AGAGAAGCTG	ATCGAGAAAG	1100
	CAGGCGCGTG	GTACAGCTAC	AAAGGTGAGA	AGATCGGTCA	GGGTAAAGCG	1150
	AATGCGACTG	CCTGGCTGAA	AGATAACCCG	GAAACCGCGA	AAGAGATCGA	1200
	GAAGAAAGTA	CGTGAGTTGC	TGCTGAGCAA	CCCGAACTCA	ACGCCGGATT	1250
	TCTCTGTAGA	TGATAGCGAA	GGCGTAGCAG	AAACTAACGA	AGATTTTTTAA	1300
40	TCGTCTTGTT	TGATACACAA	GGGTCGCATC	TGCGGCCCTT	TTGCTTTTTT	1350
	AAGTTGTAAG	GATATGCCAT	GACAGAATCA	ACATCCCGTC	G	1391

45 2) INFORMATION FOR SEQ ID NO: 919

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: DNA

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 919

GGICCI GART CITMIGGIAA RAC

23

60

2) INFORMATION FOR SEQ ID NO: 920

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 920

TCICCVATIT CICCITCIAI YTC

23

2) INFORMATION FOR SEQ ID NO: 921

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 921

TIYRTIGAYG CIGARCAIGC

20

2) INFORMATION FOR SEQ ID NO: 922

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 922

TARAAATTIA RIGCIYKICC ICC

23

2) INFORMATION FOR SEQ ID NO: 923

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 923

5 2) INFORMATION FOR SEQ ID NO: 924

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 21 bases
 (B) TYPE: Nucleic acid
10 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 924

ACCTCAGTCG TCACGTTGGC G

21

20

2) INFORMATION FOR SEQ ID NO: 925

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 bases
25 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 925

AAGCAGATGG TTGTGTGCTG

20

35

2) INFORMATION FOR SEQ ID NO: 926

- (i) SEQUENCE CHARACTERISTICS:
40 (A) LENGTH: 24 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

45 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 926

CAGCTGCTCG TGGTGCATCT CGAT

24

50

2) INFORMATION FOR SEQ ID NO: 927

- 55 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 19 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
60 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 927

5 ACGCGGAGAA GGTGCGCTT

19

2) INFORMATION FOR SEQ ID NO: 928

10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

15

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 928

20

GGTCGTTCTT CGAGTCACCG CA

22

25 2) INFORMATION FOR SEQ ID NO: 929

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 448 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

30

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacteroides fragilis*
 (B) STRAIN: ATCC 25285

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 929

40

TTCAGCATGC	CATTTCAAAA	CAGGCCGAAG	CCGATATCGT	GATTATCGCT	50
GCTTGTGGGG	AGCGTGCAAA	TGAAGTTGTG	GAAATCTTTA	CCGAATTTCC	100
GGAATTGGTG	GACCCGCACA	CGGGACGTAA	GCTGATGGAG	CGTACCATT	150
TTATCGCAAA	TACATCGAAC	ATGCCGGTAG	CAGCGCGTGA	AGCTTCTGTG	200
TATACGGCCA	TGACGATTGC	CGAATACTAT	CGTGCCATGG	GATTGAAAGT	250
CCTGCTGATG	GCAGACTCCA	CTTCCCGTTG	GGCGCAGGCA	TTGCGTGAGA	300
TGTCGAACCG	TATGGAGGAG	TTGCCCGGAC	CGGATGCATT	CCCGATGGAC	350
CTGTCTCTAA	TCATTTCTAA	CTTCTATGGC	CGTGCAGGCT	ACGTGAAACT	400
GAATAACGGC	GAGAGCGGTT	CTATTACCTT	TATCGGTACA	GTATCACC	448

50

2) INFORMATION FOR SEQ ID NO: 930

55

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 438 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

60

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacteroides distasonis*
 5 (B) STRAIN: ATCC 8503

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 930

	GCTATCTCTA	AACAAGCGGA	AGCGGATATC	GTGATTATCG	CCGCCTGCGG	50
10	TGAGCGTGCG	AATGAGGTCG	TAGAGGTATT	TACGGAGTTC	CCGGAATTGG	100
	TAGACCCGCA	TACGGGACGT	AAATTGATGG	AACGTACGAT	CATTATCGCC	150
	AATACATCCA	ACATGCCGGT	AGCCGCTCGT	GAGGCATCCG	TATATACGGC	200
	GATGACCATC	GCCGAGTATT	ATCGCAGCAT	GGGTTTGAAG	GTTCTGTTGA	250
	TGGCCGACTC	TACTTCCCGC	TGGGCACAGG	CTTTGCGTGA	GATGTCCAAC	300
15	CGTTTGGAGG	AGTTGCCGGG	ACCGGATGCT	TTCCCGATGG	ACTTGTCCGC	350
	TATCGTGGCG	AACTTCTACG	CTCGTGCGGG	ATTCGTTTAT	TTGAATAACA	400
	ACGCTACAGG	CTCCGTCACT	TTCATCGGTA	CGGTATCG		438

20

2) INFORMATION FOR SEQ ID NO: 931

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 453 bases
 25 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

30

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Porphyromonas asaccharolytica*
 (B) STRAIN: ATCC 25260

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 931

	CCTCCAGCAC	GCTATCTCTA	AGCAGGCGGA	GGCTGATATC	GTCATTATGG	50
	CAGCCTGCGG	TGAGCGTGCT	AATGAGGTGG	TGGAGATCTT	TGCCGAGTTC	100
	CCTGAGCTCG	AAGACCCACA	CACGGGACGC	AAGCTGATGG	AGCGTACGAT	150
40	CATCATCGCT	AACACGAGTA	ACATGCCAGT	GGCTGCTCGT	GAGGCTTCGG	200
	TCTACACCGC	TATGACCATC	GCTGAGTACT	ACCGCTCGAT	GGGTCTCAAA	250
	GTACTCCTAA	TGGCTGACTC	GACCTCTCGC	TGGGCACAGG	CACTGCGTGA	300
	GATGTCTAAC	CGTCTAGAGG	AGCTGCCTGG	ACCAGATGCA	TTCCCGATGG	350
	ACTTGTCCGC	TATCGTGGCA	AACTTCTACG	CTCGTGCCGG	CTTCGTCTAT	400
45	CTCAACAACG	GTGAGACAGG	TTCTGTAACC	TTCATCGGTA	CGGTCTCTCC	450
	AGC					453

50 2) INFORMATION FOR SEQ ID NO: 932

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 835 bases
 (B) TYPE: Nucleic acid
 55 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

60 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Listeria monocytogenes*

(B) STRAIN: ATCC 15313

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 932

5
 CGGAGCTATC TTAGTAGTAT CTGCTGCTGA TGGCCCAATG CCACAAACTC 50
 GTGAACATAT CTTACTTTCA CGTCAAGTTG GTGTTCCATA CATCGTTGTA 100
 TTCATGAACA AATGTGACAT GGTGACGAT GAAGAATTAC TAGAATTAGT 150
 TGAAATGGAA ATTTCGTGATC TATTAAGTGA ATATGAATTC CCTGGCGATG 200
 10 ACATTCTGT AATCAAAGGT TCAGCTCTTA AAGCACTTCA AGGTGAAGCT 250
 GACTGGGAAG CTAAAATTGA CGAGTTAATG GAAGCTGTAG ATTCTTACAT 300
 TCCAACCTCCW GAACGTGATA CTGACAAACC ATTCTATGATG CCAGTTGAGG 350
 ATGTATTCTC AATCACTGGT CGTGGAACAG TTGCAACTGG ACGTGTGAA 400
 CGTGGACAAG TTAAAGTTGG TGACGAAGTA GAAGTTATCG GTATCGAAGA 450
 15 AGAAAGCAAA AAAGTAGTAG TAACTGGAGT AGAAATGTTC CGTAAATTAC 500
 TAGACTACGC TGAAGCTGGC GACAACATTG GCGCACTTCT ACGTGGTGT 550
 GCTCGTGAAG ATATCCAACR TGGTCAAGTA TTAGCTAAAC CAGGTTTCGAT 600
 TACTCCACAC ACTAACTTCA AAGCTGAAAC TTATGTTTTA ACTAAAGAAG 650
 AAGGTGGACG TCACACTCCA TTCTTCAACA ACTACCGCCC ACAATTCTAT 700
 20 TTCCGTACTA CTGACGTAAC TGGTATTGTT ACACTTCCAG AAGGTACTGA 750
 AATGGTAAYG CCTGGTGATA ACATTGAGCT TGCAGTTGAA CTAATTGCAC 800
 CAATCGCTAT CGAAGACGGT ACTAAATTCT CTATC 835

25

2) INFORMATION FOR SEQ ID NO: 933

(i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 24 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 933

CATCATCGTI TTCMTGAACA ARTG

24

40

2) INFORMATION FOR SEQ ID NO: 934

(i) SEQUENCE CHARACTERISTICS:

45 (A) LENGTH: 24 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 934

TCACGYTTRR TACCACGCAG IAGA

24

55

2) INFORMATION FOR SEQ ID NO: 935

(i) SEQUENCE CHARACTERISTICS:

60

520

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

5

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 935

10 GGIAARWSIC ARYTITGYCA YAC

23

2) INFORMATION FOR SEQ ID NO: 936

15

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 936

25

TCISIIYTCIG GIARRCAIGG

20

2) INFORMATION FOR SEQ ID NO: 937

30

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 937

40

ATIIACIGARG YITTYGGIGA RTT

23

2) INFORMATION FOR SEQ ID NO: 938

45

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 938

55

CYIGTIGYIS WIGCRTGIGC

20

60

2) INFORMATION FOR SEQ ID NO: 939

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 1203 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

10

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Saccharomyces cerevisiae*
(C) ACCESSION NUMBER: D10023

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 939

ATGTCTCAAG TTCAAGAACA ACATATATCA GAGTCACAGC TTCAGTACGG 50
GAACGGTTCG TTGATGTCCA CTGTACCAGC AGACCTTTCA CAGTCAGTCG 100
TTGATGGAAA CGGCAACGGT AGCAGCGAAG ATATTGAGGC CACCAACGGC 150
20 TCCGGCGATG GTGGCGGATT GCAGGAGCAA GCGGAAGCGC AAGGTGAAAT 200
GGAGGATGAA GCATACGATG AAGCTGCCTT AGGTTCGTTT GTGCCAATAG 250
AAAAACTGCA AGTGAACGGG ATTACTATGG CGGATGTGAA AAAACTAAGG 300
GAGAGTGGGC TTCACACTGC TGAAGCGGTA GCATATGCTC CCAGAAAGGA 350
TTTATTGGAA ATCAAAGGTA TATCGGAAGC TAAGGCAGAT AAGTTGCTAA 400
25 ACGAAGCGGC AAGGCTAGTG CCTATGGGAT TTGTCACGGC TGCTGATTTT 450
CATATGAGAA GATCGGAGCT GATTTGTTTG ACAACGGGTT CTAAGAATTT 500
GGACACTCTT TTGGGTGGTG GTGTGGAAAC TGGTTCATT ACTGAGCTTT 550
TCGGTGAATT CAGGACAGGT AAGTCCCAGC TATGTCACAC TTTGGCCGTG 600
ACATGCCAAA TTCCATTGGA TATTGGTGGC GGTGAAGGTA AGTGTTTGTA 650
30 TATCGATACC GAAGGTACTT TCAGGCCGGT AAGATTGGTA TCCATAGCTC 700
AGCGGTTTCG ATTAGACCCG GATGATGCTT TGAACAACGT TCGGTATGCA 750
AGAGCCTATA ACGCCGATCA TCAGTTAAGA CTTCTGGATG CTGCTGCCCA 800
AATGATGAGC GAGTCTCGGT TTTCTTGAT TGTGGTCGAT TCTGTTATGG 850
CTCTATACCG TACGGATTTT TCTGGTCGTG GTGAAC TAAG CGCAAGGCAA 900
35 ATGCATTTAG CCAAATTTAT GCGTGCTTTG CAAAGGCTGG CCGACCAATT 950
TGGTGTTCGA GTCGTCGTTA CTAACCAAGT GGTCGCCCAA GTTGATGGTG 1000
GTATGGCTTT TAATCCAGAT CCAAAGAAGC CTATCGGTGG TAATATTATG 1050
GCACATTCTT CCACCACGCG ATTAGGTTTC AAAAAGGGTA AGGGATGTCA 1100
AAGATTATGC AAAGTTGTTG ACTCACCTTG CTTACCAGAG GCTGAATGTG 1150
40 TGTTTCGCGAT CTATGAAGAT GGTGTTGGTG ACCCCAGAGA AGAAGACGAG 1200
TAG 1203

45 2) INFORMATION FOR SEQ ID NO: 940

(i) SEQUENCE CHARACTERISTICS:

- 50 (A) LENGTH: 1800 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

55 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Saccharomyces cerevisiae*
(B) STRAIN: GRF88
(C) ACCESSION NUMBER: M87549

60 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 940

522

	CGATCCAATT	GCTGGTCTTA	AGATGCATTT	GATTGATCTA	GGTATTGCCA\	50
	CTGAAGCTGA	AGTCAAAGCT	TACGACAAGT	CCGCTAGAAA	ATACGTTGAC	100
	GAACAAGTTG	AATTAGCTGA	TGCTGCTCCT	CCTCCAGAAG	CCAAATTATC	150
5	CATCTTGTTT	GAAGACGTCT	ACGTGAAAGG	TACAGAAACT	CCAACCCTAA	200
	GAGGTAGGAT	CCCTGAAGAT	ACTTGGGACT	TCAAAAAGCA	AGGTTTTGCC	250
	TCTAGGGATT	AATTAAATCG	TAAGGAAAAA	TAAAATAATA	GTGCTGTGAT	300
	CGCATGATAT	TCTTCCCTGG	AAGCGCCATT	TTATAGCAAG	AAATGTAAGT	350
	CAAGTATATT	TTAAGTGTAT	ATACAACAAT	ATGACTCTTT	TTTATGCCTT	400
10	GTTGTTTTTC	TTCGGGTTTT	CCCACACATT	GTGTGGAGAG	ATAGTTATTA	450
	ACAGACCGAA	AATAGCCGCC	CAAGGATAAA	CTTTTATATA	AAGGGAAGGG	500
	TAGTTGACCC	AAAAATTTGG	ATTCTACTTT	CCAGATTTAC	TTTCACCCTT	550
	TTATATTTGC	TGTAGTCTGT	TATGCCAATC	AGGAAAAGCAT	TTGAACAAAT	600
	ATGTCTGTTA	CAGGAAGTGA	GATCGATAGT	GATACAGCAA	AAAATATTCT	650
15	TAGTGTAGAT	GAATTACAGA	ACTATGGTAT	TAATGCCTCA	GATCTTCAAA	700
	AATTGAAGTC	TGGTGGGATA	TACACAGTCA	ATGTATGTTA	TAATAACATT	750
	TTTAAAACCT	CTGCTGTAGA	GGTTCCTTCC	CCCTTTCTTT	TACTAACTAA	800
	TAATTTGGAA	AGGAACTTTT	ATAGACCGTT	TTGTCAACAA	CAAGAAGACA	850
	TCTATGTAAA	ATTAAAGGGT	TAAGTGAGGT	GAAAGTGGAA	AAAATTAAAG	900
20	AAGCTGCTGG	AAAAATCATA	CAGGTGGGAT	TTATCCCCGC	TACTGTACAA	950
	TTAGATATAA	GACAGCGTGT	GTACTCCTTA	TCAACTGGAT	CTAAGCAACT	1000
	AGATTCAATC	CTAGGTGGTG	GAATAATGAC	AATGAGTATC	ACTGAAGTAT	1050
	TTGGTGAATT	TAGGTGTGGT	AAGACACAGA	TGTCTCATA	TTTGTGTGTT	1100
	ACCACGCAGC	TTCCGAGGGA	AATGGGTGGT	GGTGAAGGGA	AAGTAGCATA	1150
25	TATTGATACA	GAAGGCACTT	TCAGGCCCGA	GAGGATTAAG	CAAATTGCAG	1200
	AAGGTTATGA	ATTGGATCCC	GAGTCATGTT	TGGCAAACGT	TTCATATGCT	1250
	AGAGCCTTGA	ATAGTGAACA	TCAAATGGAA	CTTGTTGAAC	AATTGGGTGA	1300
	AGAACTTAGT	TCTGGAGATT	ATCGCCTTAT	CGTGGTAGAT	TCTATAATGG	1350
	CAAACCTTCA	AGTAGACTAC	TGCGGTAGAG	GTGAACTAAG	CGAAAGACAG	1400
30	CAAAAGCTAA	ATCAACATCT	TTTCAAATTG	AATAGATTGG	CAGAGGAATT	1450
	TAATGTTGCA	GTATTTCTGA	CAAACCAAGT	TCAATCAGAC	CCAGGTGCTT	1500
	CTGCATTATT	TGCCTCGGCA	GATGGTAGGA	AACCAATTGG	AGGGCACGTT	1550
	CTGGCACATG	CGTCAGCAAC	AAGGATTTTG	TTGAGAAAAG	GGCGTGGTGA	1600
	CGAAAGAGTT	GCCAAGTTAC	AAGATTCCCC	AGATATGCCT	GAAAAAGAAT	1650
35	GTGTCTACGT	AATTGGTGAA	AAAGGTATTA	CCGATTCAAG	TGACTAGTTT	1700
	TTGTATACTT	TTTTAATGAA	GATGACATTG	CTCCTTTATT	AAACTTTTCT	1750
	TTTACTTTGT	GTTACTAATA	TTATTAATAT	CTTGTTATGA	TTCTTTGTTT	1800

2) INFORMATION FOR SEQ ID NO: 941

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 430 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

10

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Cryptococcus humicola*
(B) STRAIN: ATCC 38294

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 941

CGTCCTTATC CAGGAGCTCA TTAACAACAT TGCCAAGGCC CACGGTGGTT 50
TCTCCGTCTT CACCGGTGTC GGTGAGCGTA CCCGTGAGGG TAACGACCTG 100
TACCACGAGA TGCCTGAGAC TGGTGTCTATC AACCTCGAGG GCGACTCCAA 150
20 GGTCTGCTCTC GTCTTCGGCC AGATGAACGA GCCCCCGGA GCCCGTGCCC 200
GTGTGCGCCCT TACCGGCCTC ACCATCGCCG AGTACTTCCG TGACGAGGAG 250
GGTCAGGACG TGCTTCTCTT CATCGACAAC ATTTTCCGTT TCACCCAGGC 300
CGGTTCCGAG GTGTCTGCCC TTCTCGGTCG TATCCCCTCG GCCGTCGGTT 350
ACCAGCCCAC CCTCGCTACC GACATGGGTT CCATGCAGGA GCGTATCACC 400
25 ACCACCAAGA AGGGTTCGAT TACCTCCGTC 430

2) INFORMATION FOR SEQ ID NO: 942

30

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 794 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
35 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 40 (A) ORGANISM: *Escherichia coli*
(B) STRAIN: ATCC 43895

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 942

45 CGTGACGAT GCTCTTGAGG TGCAAAATGG TAATGAGCGT CTGGTGCTGG 50
AAGTTCAGCA GCAGCTCGGC GGCAGTATCG TGCGTACCAT CGCAATGGGT 100
TCCTCCGACG GTCTGCGTCG CCGTCTGGAT GTAAAAGACC TCGAACACCC 150
GATCGAAGTC CCGGTAGGTA AAGCGACTCT GGGCCGTATC ATGAACGTAC 200
TGGGTGAACC GGTGACATG AAAGGCGAGA TCGGTGAAGA AGAGCGTTGG 250
50 GCGATTACAC GCGCAGCACC TTCCTACGAA GAGCTGTCAA ACTCTCAGGA 300
ACTGCTGGAA ACCGGTATCA AAGTTATCGA CCTGATGTGT CCGTTCGCTA 350
AGGGCGGTAA AGTTGGTCTG TTCGGTGGTG CGGGTGTAGG TAAAACCGTA 400
AACATGATGG AGCTCATTCG TAACATCGCG ATCGAGCACT CCGGTTACTC 450
TGTGTTTTCG GCGTAGGTG AACGTAATCG TGAGGGGAAC GACTTCTACC 500
55 ACGAAATGAC CGACTCCAAC GTTATCGATA AAGTATCCCT GGTGTATGGC 550
CAGATGAACG AGCCGCCGGG AAACCGTCTG CGCGTAGCTC TGACCGGTCT 600
GACCATGGCT GAGAAATTCC GTGACGAAGG TCGTGACGTT CTGCTGTTCC 650
TTGACAACAT CTATCGTTAC ACCCTGGCCG GTACGGAAGT ATCCGCACTG 700
CTGGGCCGTA TGCCTTCAGC GGTAGGTTAT CAGCCGACCC TGGCGGAAGA 750
60 GATGGGCGTT CTGCAGGAAC GTATCACCTC CACCAAAACC GGT 794

2) INFORMATION FOR SEQ ID NO: 943

5

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 814 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

10

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Escherichia coli*
 (B) STRAIN: ATCC 35401

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 943

20	ATGCCGTACC GCGCGTGTAC GATGCTCTTG AGGTGCAAAA TGGTAATGAG	50
	CGTCTGGTGC TGGAAGTTCA GCAGCAGCTC GCGGGCGGTA TCGTACGTAC	100
	CATCGCAATG GGTTCCTCCG ACGGTCTGCG TCGCGGTCTG GATGTAAAAG	150
	ACCTCGAACA CCCGATTGAA GTCCCGGTAG GTAAAGCGAC TCTGGGCCGT	200
	ATCATGAACG TACTGGGTGA ACCGGTCGAC ATGAAAGGCG AGATCGGTGA	250
25	AGAAGAGCGT TGGGCGATTC ACCGCGCAGC ACCTTCCTAC GAAGAGCTGT	300
	CAAACCTCTCA GGAAGTCTG GAAACCGGTA TCAAAGTTAT CGACCTGATG	350
	TGTCCGTTTCG CTAAGGGCGG TAAAGTTGGT CTGTTCCGGT GTGCGGGTGT	400
	AGGTAAACC GTAAACATGA TGGAGCTCAT TCGTAACATC GCGATCGAGC	450
	ACTCCGGTTA CTCTGTGTTT GCGGGCGTAG GTGAACGTAC TCGTGAGGGT	500
30	AACGACTTCT ACCACGAAAT GACCGACTCC AACGTTATCG ACAAAGTATC	550
	CCTGGTGTAT GGCCAGATGA ACGAGCCGCC GGGAAACCGT CTGCGCGTTG	600
	CTCTGACCGG TCTGACCATG GCTGAGAAAT TCCGTGACGA AGGTCGTGAC	650
	GTTCTGCTGT TCGTTGACAA CATCTATCGT TACACCCTGG CCGGTACGGA	700
	AGTATCCGCA CTGCTGGGCC GTATGCCTTC AGCGGTAGGT TATCAGCCGA	750
35	CCCTGGCGGA AGAGATGGGC GTTCTGCAGG AACGTATCAC CTCCACCAA	800
	ACTGGTTCTA TCAC	814

40 2) INFORMATION FOR SEQ ID NO: 944

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 798 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

45

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Escherichia coli*
 (B) STRAIN: ATCC 11775

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 944

55

55	GTGTACGATG CTCTTGAGGT GCAAAATGGT AATGAGCGTC TGGTGCTGGA	50
	AGTTCAGCAG CAGCTCGGCG GCGGTATCGT GCGTACCATC GCAATGGGTT	100
	CCTCCGACGG TCTGCGTCGC GGTCTGGATG TAAAAGACCT CGAACACCCG	150
	ATCGAAGTCC CGGTAGGTAA AGCGACTCTG GGCCGTATCA TGAACGTACT	200
60	GGGTGAACCG GTCGACATGA AAGGCGAGAT CGGTGAAGAA GAGCGTTGGG	250

	CGATTACCGG	CGCAGCACCT	TCCTACGAAG	AGCTGTCAAA	CTCTCAGGAA	300
	CTGCTGGAAA	CCGGTATCAA	AGTTATCGAC	CTGATGTGTC	CGTTCGCTAA	350
	GGGCGGTAAA	GTTGGTCTGT	TCGGTGGTGC	GGGTGTAGGT	AAAACCGTAA	400
	ACATGATGGA	GCTTATTCGT	AACATCGCGA	TCGAGCACTC	CGGTTACTCT	450
5	GTGTTTTCGG	GCGTAGGTGA	ACGTACTCGT	GAGGGTAACG	ACTTCTACCA	500
	CGAAATGACC	GACTCCAACG	TTATCGACAA	AGTATCCCTG	GTGTATGGCC	550
	AGATGAACGA	GCCGCCGGGA	AACCGTCTGC	GCGTTGCTCT	GACCGGTCTG	600
	ACCATGGCTG	AGAAATTCCG	TGACGAAGGT	CGTGACGTTT	TGCTGTTCGT	650
	TGACAACATC	TATCGTTACA	CCCTGGCCGG	TACGGAAGTA	TCCGCACTGC	700
10	TGGGCCGTAT	GCCTTCAGCG	GTAGGTTATC	AGCCGACCCT	GGCGGAAGAG	750
	ATGGGCGTTC	TGCAGGAACG	TATCACCTCC	ACCAAAACCG	GTTCTATC	798

15 2) INFORMATION FOR SEQ ID NO: 945

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 812 bases
 (B) TYPE: Nucleic acid
 20 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

25 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Escherichia coli*
 (B) STRAIN: ATCC 25922

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 945

30	ATGCCGTACC	GCGCGTGTAC	GATGCTCTTG	AGGTGCAAAA	TGGTAATGAG	50
	CGTCTGGTGC	TGGAAGTTCA	GCAGCAGCTC	GGCGGCGGTA	TCGTGCGTAC	100
	CATCGCAATG	GGTTCCTCCG	ACGGTCTGCG	TCGCGGTCTG	GATGTAAAAG	150
	ACCTCGAACA	CCCGATCGAA	GTCCCGGTAG	GTAAAGCGAC	TCTGGGCCGT	200
35	ATCATGAACG	TACTGGGTGA	ACCGGTCGAC	ATGAAAGGCG	AGATCGGTGA	250
	AGAAGAGCGT	TGGGCGATTG	ACCGCGCAGC	ACCTTCCTAC	GAAGAGCTGT	300
	CAAACCTCTCA	GGAAGTGTCT	GAAACCGGTA	TCAAAGTTAT	CGACCTGATG	350
	TGTCCGTTTC	CTAAGGGCGG	TAAAGTTGGT	CTGTTCGGTG	GTGCGGGTGT	400
	AGGTAAACC	GTAAACATGA	TGGAGCTTAT	TCGTAACATC	GCGATCGAGC	450
40	ACTCCGGTTA	CTCTGTGTTT	GCGGGCGTAG	GTGAACGTAC	TCGTGAGGGT	500
	AACGACTTCT	ACCACGAAAT	GACCGACTCC	AACGTTATCG	ACAAAGTATC	550
	CTTGGTGTAT	GGCCAGATGA	ACGAGCCGCC	GGGAAACCGT	CTGCGCGTTG	600
	CTCTGACCGG	TCTGACCATG	GCTGAGAAAT	TCCGTGACGA	AGGTCGTGAC	650
	GTATTGCTGT	TCGTCGATAA	CATCTATCGT	TACACCCTGG	CCGGTACCGA	700
45	AGTATCCGCA	CTGCTGGGCC	GTATGCCTTC	AGCGGTAGGT	TATCAGCCGA	750
	CCCTGGCGGA	AGAGATGGGC	GTTCTGCAGG	AACGTATCAC	CTCCACCAAA	800
	ACCGGTTCTA	TC				812

50

2) INFORMATION FOR SEQ ID NO: 946

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 832 bases
 55 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

60

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Neisseria polysaccharea*
 (B) STRAIN: ATCC 43768

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 946

```

GCGACGCTAT CCCGCATGTT TACGATGCCC TGAAATTGGA CGAGAACGGT      50
CTGACTCTGG AAGTTCAACA ACTTCTGGGT GACGGCGTTG TCCGTACTAT      100
TGCAATGGGT AGTTCAGACG GCCTGAAACG CGGCATGTCT GTAAGCAATA      150
10 CTGGTGCGCC AATCACTGTG CCGGTAGGTA AAGGTACTTT GGGTCGTATT      200
GTCGACGTAT TGGGTACGCC TGTGTATGAA GCAGGTCCGA TCGATACCGA      250
CAAGAGCCGT GCCATTCACC AAAGTGTCTC GAAATTEGAC GAGTTGTCTG      300
CAACTACCGA ATTGTTGGAA ACCGGTATTA AAGTGATCGA CTTGCTGTGT      350
CCGTTTGCTA AAGGCGGTAA AGTAGGTCTG TTCGGTGGTG CCGGTGTAGG      400
15 CAAAACCGTG AACATGATGG AATTGATCAA CAACATCGCC AAAGCGCACA      450
GCGGTCTGTC CGTGTTCGCA GGTGTGGGCG AGCGTACCCG TGAAGGTAAC      500
GACTTCTACC ACGAGATGAA AGATTCCAAC GTATTGGATA AAGTGGCAAT      550
GGTTTACGGT CAGATGAACG AACCTCCGGG CAACCGTTTG CGCGTCGCAT      600
TGACCGGTTT GACCATGGCG GAATACTTCC GTGACGAAAA AGACGAAAC      650
20 GGTAAAGGTC GCGACGTATT GTTCTTCGTT GACAACATCT ACCGTTACAC      700
TCTGGCCGGT ACCGAAGTAT CTGCACTGTT GGGCCGTATG CCTTCTGCAG      750
TGGGTTACCA ACCGACATTG GCTGAAGAAA TGGGTCGTTT GCAAGAGCGT      800
ATTACCTCTA CCCAAACCGG TTCCATTACT TC                        832

```

25

2) INFORMATION FOR SEQ ID NO: 947

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 840 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

35 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Neisseria sicca*
 (B) STRAIN: ATCC 9913

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 947

```

TCCGCGCGAT GCCATTCCGC ATGTTTACGA CGCCCTGAAA TTGGATGCAA      50
ACGGCCTGAC TTTGGAAGTA CAACAGCTTC TGGGCGACGG CGTGGTTCGT      100
45 ACTATTGCAA TGGGTAGTTC GGACGGTCTG AAACGCGGCA TGAAGTAAG      150
CAATACAGAT GCGCCGATTA CTGTGCCGGT AGGTAAAGGT ACTTTGGGAC      200
GTATTGTCGA TGTGTTGGGT ACACCTGTTG ATGAAGCAGG TCCGATTGAT      250
ACCGACAAAC ACCGTGCTAT CCATCAGACA GCTCCGAAAT TCGATGAGTT      300
GTCTGCTACT ACCGAGCTGC TGGAAACAGG CATTAAAGTG ATTGACTTGC      350
50 TGTGTCCGTT TGCCAAAGGC GGTAAAGTAG GTCTGTTCGG TGGTGCCGGT      400
GTAGGCAAAA CCGTCAACAT GATGGAATTG ATTAACAACA TCGCCAAAGC      450
GCATAGTGGT TTGTCCGTGT TCGCCGGTGT GGGGGAACGT ACCCGTGAAG      500
GTAACGACTT CTACCACGAG ATGAAAGATT CCAACGTATT GGACAAAGTG      550
GCGATGGTTT ACGGTCAGAT GAACGAACCT CCGGGTAACC GTCTGCGTGT      600
55 AGCCTTGACC GGTTTGACGA TGGCCGAATA CTTCCGTGAT GAAAAAGACG      650
AAAGCGGCAA AGGTCGCGAC GTATTGTTCT TCGTGACAA CATTTACCGT      700
TACACTCTGG CCGGTACAGA AGTATCCGCA TTGCTCGGTC GTATGCCTTC      750
AGCAGTAGGT TACCAACCGA CATTGGCTGA AGAAATGGGT CGTCTGCAAG      800
AGCGTATTAC CCTCTACTCA AACAGGCTCC ATTACTTCTA      840

```

60

2) INFORMATION FOR SEQ ID NO: 948

5 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 843 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

10

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus mitis*
 (B) STRAIN: ATCC 903

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 948

```

20 GCAGCTGGCG ACAAGCTACC TGAGATCAAT AATGCACTTG TAGTCTATAA      50
   AAATGACGAA AAAAAATCAA AAATCGTCCT TGAAGTAGCT CTTGAGCTTG      100
   GTGATGGAGT GGTTCGGACC ATCGCTATGG AATCAACGGA TGGGTTGACT      150
   CGTGGCATGG AAGTGCTAGA TACTGGCCGT CCAATTTCTG TGCCAGTCGG      200
   CAAAGAAACA CTTGGTCGCG TCTTTAACGT TTTGGGAGAT ACCATTGACT      250
   TGGATGCTCC TTTTGCGGAT GATGCAGAGC GCCAGCCAAT CCATAAGAAA      300
25 GCTCCAACCT TTGATGAGTT GTCTACTTCT TCAGAGATCT TAGAGACAGG      350
   TATCAAGGTT ATCGACCTGT TAGCCCCTTA TCTGAAAGGT GGTAAAGTTG      400
   GACTCTTCGG TGGTGCCGGA GTTGGTAAGA CCGTCCTGAT TCAAGAATTG      450
   ATCCACAACA TTGCCCAAGA ACACGGTGGT ATTTCTGTAT TTACTGGCGT      500
   TGGGGAACGT ACCCGTGAAG GGAATGACCT TTATTGGGAA ATGAAAGAGT      550
30 CTGGTGTTAT CGAGAAAACA GCCATGGTCT TCGGTCAGAT GAATGAGCCG      600
   CCAGGAGCGC GTATGCGGGT TGCTTTGACT GGTTTGACGA TTGCAGAATA      650
   CTTCCGTGAT GTGGAAGGTC AAGATGTCTT GCTCTTCATT GACAACATCT      700
   TCCGTTTCAC GCAGGCAGGT TCTGAAGTTT CTGCCCTTTT GGGTCGGATG      750
   CCGTCAGCCG TTGGTTACCA ACCAACACTT GCGACAGAAA TGGGGCAATT      800
35 GCAAGAGCGT ATCACATCGA CTAAGAAGGG TTCTGTAACC TCT          843

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2) INFORMATION FOR SEQ ID NO: 949

40

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 841 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

45

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus mitis*
 (B) STRAIN: ATCC 49456

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 949

```

55 GCAGCAGGGG AAAAATTCC TGAGATTAAC AATGCACTTG TCGTCTACAA      50
   AAATGACGAA AGAAAAACAA AAATCGTCCT TGAAGTAGCC TTGGAGTTGG      100
   GAGATGGTAT GGTCCGTACT ATCGCCATGG AATCAACAGA TGGTTTGACT      150
   CGTGGAAATGG AAGTATTGGA CACAGGTCGT CCAATCTCTG TACCAGTAGG      200
   TAAAGAAACT TTGGGACGTG TCTTCAATGT TTTGGGAGAT ACCATTGACT      250
60 TGGAAGCTCC TTTTACAGAA GATGCAGAGC GTCAGCCAAT TCATAAAAAA      300

```

	GCTCCAACCTT	TTGATGAATT	GTCTACCTCT	TCTGAAATCC	TTGAAACAGG	350
	GATTAAGGTT	ATCGACCTTC	TTGCCCCTTA	CCTTAAAGGT	GGTAAGGTTG	400
	GACTTTTCGG	TGGTGCCGGA	GTTGGTAAAA	CCGTCTTAAT	CCAAGAATTG	450
	ATTCACAACA	TTGCCCAAGA	ACACGGTGGT	ATTTCAAGTAT	TTACCGGTGT	500
5	TGGGGAACGT	ACTCGTGAGG	GTAATGACCT	TTACTGGGAA	ATGAAAGAAT	550
	CAGGTGTTAT	CGAGAAAACA	GCCATGGTAT	TTGGTCAGAT	GAATGAGCCG	600
	CCAGGAGCAC	GTATGCGTGT	TGCCCTAACT	GGTTTGACAA	TCGCCGAATA	650
	CTTCCGTGAT	GTGGAAGGCC	AAGACGTGCT	TCTCTTTATC	GATAATATCT	700
	TCCGTTTCAC	TCAGGCTGGT	TCAGAAAGTAT	CTGCCCTTTT	GGGTCGTATG	750
10	CCATCAGCCG	TTGGTTACCA	ACCAACACTT	GCTACGGAAA	TGGGTCAATT	800
	GCAAGAGCGT	ATTACATCAA	CTAAAAAGGG	TTCTGTAACC	T	841

15 2) INFORMATION FOR SEQ ID NO: 950

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 827 bases
 (B) TYPE: Nucleic acid
 20 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

25 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus mitis*
 (B) STRAIN: LSPQ 2583

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 950

30	GCTACCTGAG	ATCAATAATG	CACTTGTAGT	CTATAAAAAT	GACGAAAATA	50
	AATCAAAAAT	CGTCCTTGAA	GTAGCTCTTG	AGCTTGGTGA	TGGAGTGGTT	100
	CGGACCATCG	CTATGGAATC	AACGGATGGG	TTGACTCGTG	GCATGGAAGT	150
	GCTAGATACT	GGTCGTCCAA	TTTCTGTGCC	AGTCGGCAAA	GAAACACTTG	200
35	GTCGCGTCTT	TAACGTTTTG	GGAGATACCA	TTGACTTGGA	TGCTCCTTTT	250
	GCGGATGATG	CAGAGCGCCA	GCCAATCCAT	AAGAAAGCTC	CAACCTTTGA	300
	TGAGTTGTCT	ACTTCATCAG	AGATCTTAGA	GACAGGTATC	AAGGTTATCG	350
	ACCTGTTAGC	ACCTTATCTG	AAAGGTGGTA	AAGTCGGACT	CTTCGGTGGT	400
	GCCGGAGTTG	GTAAGACCGT	CCTGATTCAG	GAATTGATCC	ACAACATTGC	450
40	CCAAGAGCAT	GGTGGTATTT	CCGTGTTTAC	CGGTGTTGGG	GAACGTACCC	500
	GTGAAGGGAA	TGACCTTTAC	TGGGAAATGA	AGGAGTCTGG	CGTTATCGAG	550
	AAAACAGCCA	TGGTCTTCGG	TCAGATGAAT	GAGCCACCAG	GAGCGCGTAT	600
	GCGGGTTGCT	TGACTGGTTT	TGACGATTGC	AGAGTACTTC	CGTGATGTAG	650
	AAGGTCAAGA	TGTCTTGCTC	TTCATTGACA	ACATCTTCCG	TTTCACGCAG	700
45	GCAGGTTCTG	AAGTCTCTGC	CCTTTTGGGT	CGGATGCCAT	CAGCCGTTGG	750
	TTACCAACCA	ACACTTGCGA	CTGAAATGGG	ACAACTCCAA	GAGCGTATTA	800
	CATCGACTAA	GAAAGGTTCT	GTAACCT			827

50

2) INFORMATION FOR SEQ ID NO: 951

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 844 bases
 55 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

60

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus oralis*
 (B) STRAIN: ATCC 35037

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 951

```

GCAGCAGGGG AAACACTTCC TGAGATTAAT AATGCACTTG TCGTCTACAA      50
AAATGACGAA AGAAAAACAA AAATCGTCCT TGAAGTAGCC TTGGAGTTGG      100
GTGATGGTAT GGTCCGTACG ATCGCCATGG AATCAACAGA TGGTTTGA CT      150
10 CGTGGAATGG AAGTTTTGGA CACAGGCCGT CCAATCTCTG TACCAGTAGG      200
TAAAGAAACT TTGGGACGTG TCTTCAACGT TTTGGGAGAT ACTATTGA CT      250
TGGATGCTCC TTTGCTGAA GACGCTGAGC GTCAGCCAAT TCATAAGAAA      300
GCTCCAAC TTGATGAATT GTCTACCTCA TCTGAAATCT TGGAAACAGG      350
GATTAAGGTT ATCGACCTTC TTGCCCCTTA CCTTAAAGGT GGGAAAGTTG      400
15 GACTCTTCGG TGGTGCCGGA GTTGGTAAAA CTGTCTTGAT CCAAGAGTTG      450
ATTACAACA TTGCCCAAGA ACATGGTGGT ATTTCAAGTAT TTACCGGTGT      500
TGGAGAACGT ACCCGTGAGG GGAACGACCT TTAAGGGGAA ATGAAAGAAT      550
CAGGCGTTAT CGAGAAAACA GCCATGGTAT TTGGTCAGAT GAATGAGCCA      600
CCTGGAGCAC GTATGCGTGT TGCTCTTACT GGTTTGACAA TCGCCGAATA      650
20 CTTCCGTGAT GTAGAAGGCC AAGATGTGCT TCTCTTTATC GACAATATCT      700
TCCGTTTCAC TCAAGCTGGT TCAGAAGTAT CTGCCCTTTT GGGTCGGATG      750
CCTTCAGCCG TTGGTTACCA ACCAACACTT GCTACGGAAA TGGGTCAATT      800
GCAAGAACGT ATCACATCAA CTAAGAAGGG TTCTGTAACC TCTA          844

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25

2) INFORMATION FOR SEQ ID NO: 952

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 830 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

35 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
 (B) STRAIN: StrR-06

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 952

```

GCAGCAGGGG AAAA ACTTCC TGAGATTAAC AATGCACTTG TCGTCTACAA      50
AAATGACGAA AGAAAAACAA AAATCGTCCT TGAAGTAGCC TTGGAGTTAG      100
45 GAGATGGTAT GGTTTCGTACT ATCGCCATGG AATCAACAGA TGGGTTGA CT      150
CGTGGAATGG AAGTATTGGA CACAGGTCGT CCAATCTCTG TACCAGTAGG      200
TAAAGAAACT TTGGGACGTG TCTTCAACGT TTTGGGAGAT ACCATTGA TT      250
TGGAAGCTCC TTTTACAGAA GACGCAGAGC GTCAGCCAAT TCATAAAAAA      300
GCTCCAAC TTGATGAGTT GTCTACCTCT TCTGAAATCC TTGAAACAGG      350
50 GATCAAGGTT ATTGACCTTC TTGCCCCTTA CCTTAAAGGT GGTAAAGTTG      400
GACTTTTCGG TGGTGCCGGA GTTGGTAAAA CCGTCTTAAT CCAAGAATTG      450
ATTACAACA TTGCCCAAGA GCACGGTGGT ATTTCAAGTAT TTAAGGTTG      500
TGGGGAACGT ACTCGTGAGG GGAATGACCT TTAAGGGGAA ATGAAAGAAT      550
CAGGCGTTAT CGAGAAAACA GCCATGGTCT TTGGTCAGAT GAATGAGCCA      600
55 CCAGGAGCAC GTATGCGTGT TGCCCTTACT GGTTTGACAA TCGCTGAATA      650
CTTCCGTGAT GTGGAAGGCC AAGACGTGCT TCTCTTTATC GATAATATCT      700
TCCGTTTCAC TCAGGCTGGT TCAGAAGTAT CTGCCCTTTT GGGTCGTATG      750
CCATCAGCCG TTGGTTACCA ACCAACACTT GCTACGGAAA TGGGTCAATT      800
GCAAGAACGT ATCACATCAA CCAAGAAGGG          830

```

60

2) INFORMATION FOR SEQ ID NO: 953

5 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 823 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

10

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
 (B) STRAIN: StrR-11

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 953

20	AAAAACTTCC	TGAGATTAAC	AATGCACTTG	TCGTCTACAA	AAATGACGAA	50
	AGAAAAACAA	AAATCGTCCT	TGAAGTAGCC	TTGGAGTTAG	GAGATGGTAT	100
	GGTTCGTACT	ATCGCCATGG	AATCAACAGA	TGGGTTGACT	CGTGGAATGG	150
	AAGTATTGGA	CACAGGTCGT	CCAATCTCTG	TACCAGTAGG	TAAAGAACT	200
	TTGGGACGTG	TCTTCAACGT	TTTGGGAGAT	ACCATTGATT	TGGAAGCTCC	250
	TTTTACAGAA	GACGCAGAGC	GTCAGCCAAT	TCATAAAAAA	GCTCCAACCT	300
25	TTGATGAGTT	GTCTACCTCT	TCTGAAATCC	TTGAAACAGG	GATCAAGGTT	350
	ATTGACCTTC	TTGCCCTTA	CCTTAAAGGT	GGTAAAGTTG	GACTTTTCGG	400
	TGGTGCCGGA	GTTGGTAAAA	CCGTCTTAAT	CCAAGAATTG	ATTCACAACA	450
	TTGCCCAAGA	GCACGGTGGT	ATTTCAGTAT	TTACTGGTGT	TGGGGAACGT	500
	ACTCGTGAGG	GGAATGACCT	TTACTGGGAA	ATGAAAGAAT	CAGGCGTTAT	550
30	CGAGAAAACA	GCCATGGTCT	TTGGTCAGAT	GAATGAGCCA	CCAGGAGCAC	600
	GTATGCGTGT	TGCCCTTACT	GGTTTGACAA	TCGCTGAATA	CTTCCGTGAT	650
	GTGGAAGGCC	AAGACGTGCT	TCTCTTTATC	GATAATATCT	TCCGTTTCAC	700
	TCAGGCTGGT	TCAGAAGTAT	TGCCCTTTT	GGGTCGTATG	CCATCAGCCG	750
	TTGGTTACCA	ACCAACACTT	GCTACGGAAA	TGGGTCAATT	GCAAGAACGT	800
35	ATCACATCAA	CTAAGAAGGG	TTC			823

2) INFORMATION FOR SEQ ID NO: 954

40

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 844 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

45

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
 (B) STRAIN: StrR-55

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 954

55	GCAGCAGGGG	AAAAACTTCC	TGAGATTAAC	AATGCACTTG	TCGTCTACAA	50
	AAATGACGAA	AGAAAAACAA	AAATCGTCCT	TGAAGTAGCC	TTGGAGTTAG	100
	GAGATGGTAT	GGTTCGTACT	ATCGCCATGG	AATCAACAGA	TGGGTTGACT	150
	CGTGGAATGG	AAGTATTGGA	CACAGGTCGT	CCAATCTCTG	TACCAGTAGG	200
	TAAAGAACT	TTGGGACGTG	TCTTCAACGT	TTTGGGAGAT	ACCATTGACT	250
60	TGGAAGCTCC	TTTTACAGAA	GACGCAGAGC	GTCAGCCAAT	TCATAAAAAA	300

	GCTCCAACCTT	TTGATGAGTT	GTCTACCTCT	TCTGAAATCC	TTGAAACAGG	350
	GATCAAGGTT	ATTGACCTTC	TTGCCCCTTA	CCTTAAAGGT	GGTAAAGTTG	400
	GACTTTTCGG	TGGTGCCGGA	GTTGGTAAAA	CTGTCTTAAT	CCAAGAATTG	450
	ATTCACAACA	TTGCCCCAAGA	GCACGGTGGT	ATTTTCAGTAT	TTGCTGGTGT	500
5	TGGGGAACGT	ACTCGTGAGG	GGAATGACCT	TTACTGGGAA	ATGAAAGAAT	550
	CAGGCGTTAT	CGAGAAAACA	GCCATGGTCT	TTGGTCAGAT	GAATGAGCCA	600
	CCAGGAGCAC	GTATGCGTGT	TGCCCTTACT	GGTTTGACAA	TCGCTGAATA	650
	CTTCCGTGAT	GTGGAAGGCC	AAGACGTGCT	TCTCTTTATC	GATAATATCT	700
	TCCGTTTCAC	TCAGGCTGGT	TCAGAAGTAT	CTGCCCTTTT	GGGTCGTATG	750
10	CCATCAGCCG	TTGGTTACCA	ACCAACACTT	GCTACGGAAA	TGGGTCAATT	800
	GCAAGAACGT	ATCACATCAA	CCAAGAAGGG	TTCTGTAACC	TCTA	844

15 2) INFORMATION FOR SEQ ID NO: 955.

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 834 bases
 (B) TYPE: Nucleic acid
 20 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

25 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
 (B) STRAIN: StrR-05

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 955

30	AAAAACTTCC	TGAGATTAAC	AATGCACTTG	TCGTCTACAA	AAATGACGAA	50
	AGAAAAACAA	AAATCGTCCT	TGAAGTAGCC	TTGGAGTTAG	GAGATGGTAT	100
	GGTTCGTACT	ATCGCCATGG	AATCAACAGA	TGGGTTGACT	CGTGGAAATGG	150
	AAGTATTGGA	CACAGGTCGT	CCAATCTCTG	TACCAGTAGG	TAAAGAAACT	200
35	TTGGGACGTG	TCTTCAACGT	TTTGGGAGAT	ACCATTGATT	TGGAAGCTCC	250
	TTTTACAGAA	GACGCAGAGC	GTCAGCCAAT	TCATAAAAAA	GCTCCAACCTT	300
	TTGATGAGTT	GTCTACCTCT	TCTGAAATCC	TTGAAACAGG	GATCAAGGTT	350
	ATTGACCTTC	TTGCCCCTTA	CCTTAAAGGT	GGTAAAGTTG	GACTTTTCGG	400
	TGGTGCCGGA	GTTGGTAAAA	CCGTCTTAAT	CCAAGAATTG	ATTCACAACA	450
40	TTGCCCCAAGA	GCACGGTGGT	ATTTTCAGTAT	TTACTGGTGT	TGGGGAACGT	500
	ACTCGTGAGG	GGAATGACCT	TTACTGGGAA	ATGAAAGAAT	CAGGCGTTAT	550
	CGAGAAAACA	GCCATGGTCT	TTGGTCAGAT	GAATGAGCCA	CCAGGAGCAC	600
	GTATGCGTGT	TGCCCTTACT	GGTTTGACAA	TCGCTGAATA	CTTCCGTGAT	650
	GTGGAAGGCC	AAGACGTGCT	TCTCTTTATC	GATAATATCT	TCCGTTTCAC	700
45	TCAGGCTGGT	TCAGAAGTAT	CTGCCCTTTT	GGGTCGTATG	CCATCAGCCG	750
	TTGGTTACCA	ACCAACACTT	GCTACGGAAA	TGGGTCAATT	GCAAGAACGT	800
	ATCACATCAA	CCAAGAAGGG	TTCTGTAACC	TCTA		834

50

2) INFORMATION FOR SEQ ID NO: 956

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 495 bases
 55 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

60

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Babesia microti*
 (B) STRAIN: Persing-1

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 956

	TTGTATATCA	CAGGCACTCA	GCAAATATTC	CGATACTGAC	GTAATTATAT	50
	ACGTGGGTTG	TGGTGAACGT	GGGAATGAAA	TGGCTGAGAT	TCTATGCGAA	100
	TTCCCTGAAC	TATCTACTGT	AGTTAATGAT	GAAAAGGTGG	CCATTATGGA	150
10	ACGTACATGC	TTAGTTGCCA	ATACTTCTAA	TATGCCAGTG	GCCGCTAGAG	200
	AAGCTAGTAT	ATACACTGGT	ATTACAATTG	CTGAATATTT	CCGTGATATG	250
	GGTTACAAC	GCACCTCTTAT	GGCCGATTCC	ACTAGCCGAT	GGGCAGAGGC	300
	TCTAAGGGAA	ATTTCTGGTA	GATTGGCTGA	AATGCCTGCA	GATTCTGGCT	350
	ATCCGGCCTA	TTTATCGTCA	AGGTTGTCAG	CTTTTATGA	ACGTGCAGGT	400
15	GGGATAACTG	TCTAATTAAT	TTAGGCTTGA	TTAAGTGCTT	AGGTTACCA	450
	ACACGAACCG	GATCTATTAC	GGTTGTAGGA	GCAGTTTCTC	CACCA	495

20 2) INFORMATION FOR SEQ ID NO: 957

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 469 bases
 (B) TYPE: Nucleic acid
 25 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

30 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Entamoeba histolytica*
 (B) STRAIN: HM1-1MSS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 957

35	AGTTATTTCA	CAAGCATTAA	GTAAATATAG	TAATTCAGAT	GTTATTATTT	50
	ATGTAGGATG	TGGTGAACGA	GGAAATGAAA	TGGCAGAAGT	TCTTCGAGAT	100
	TTTCCAGCTC	TTTCTATTAA	AGTAGGAGAT	AAAGAAGAAT	CTATTATGAC	150
	AAGAACAGCA	CTTGTTGCTA	ATACATCTAA	TATGCCTGTT	GCAGCACGTG	200
40	AAGCATCAAT	TTTACTGGA	ATTACATTAT	CAGAATATTA	TAGAGATATG	250
	GGATATAATG	TTGCTATGAT	GGCAGATTCA	ACATCAAGAT	GGGCTGAAGC	300
	ACTTAGAGAA	ATTTCAGGAC	GTCTTGCA	AATGCCAGCT	GATTCTGGAT	350
	ATCCAGCATA	TCTTGACGCA	CGTTTAGCAT	CATTTTATGA	ACGTGCAGGT	400
	ATGGTTGAAT	GTTTAGGATC	ACCAAAAAGA	ATAGGGTCAG	TTTCTATTGT	450
45	AGGAGCTGTT	TCACCACCT				469

50 2) INFORMATION FOR SEQ ID NO: 958

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 452 bases
 (B) TYPE: Nucleic acid
 55 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 60 (A) ORGANISM: *Fusobacterium nucleatum* subsp. *polymorphum*

(B) STRAIN: ATCC 10953

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 958

5	TACAACACCA	ACTTGCTAAA	TGGGCAGATG	CAGAAGTAGT	TGTTTATGTT	50
	GGTTGTGGGG	AACGTGGAAA	TGAAATGACC	GATGTACTTA	TGGAATTCCC	100
	AGAAATTATT	GACCCTAAGA	CAGGACAATC	TTTAATGAAG	AGAACAGTTC	150
	TTATAGCTAA	TACTTCTAAT	ATGCCAGTTG	CTGCTCGTGA	GGCTTCAATC	200
	TATACTGGTA	TAACTATTGC	AGAATATTTT	AGAGATATGG	GATATTTCAGT	250
10	GGCACTTATG	GCAGATTCAA	CAAGTCGTTG	GGCAGAAGCA	CTTCGTGAAA	300
	TGTCAGGACG	TTTGGAAGAA	ATGCCAGGTG	ATGAAGGATA	TCCAGCATAT	350
	CTATCAAGTA	GAATAGCAGA	GTTTTATGAA	AGAGCAGGGC	TTGTTGAATG	400
	TCTAGGTAAT	GGAGAAGAAG	GAGCATTAAC	TGTAATTGGA	GCAGTATCTC	450
	CA					452

15

2) INFORMATION FOR SEQ ID NO: 959

20 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 469 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

25

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Leishmania aethiopica*
- (B) STRAIN: ATCC 50119

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 959

	TGTAATTAGT	CAGGCCCTCT	CCAAGTACTC	CAACTCCGAC	TGCGTCATCT	50
35	ATGTCGGCTG	CGGCGAGCGC	GGTAATGAGA	TGGCCGAGGT	GCTCATGGAG	100
	TTCCCGACCC	TGACGACCGT	GATCAATGGT	CGCGAGGAGT	CGATCATGAA	150
	GCGCACCTGC	CTCGTGCGGA	ACACTTCGAA	CATGCCAGTC	GCAGCCCGTG	200
	AGGCCTCTAT	TTACACCGGC	ATCACCCCTGG	CCGAGTACTA	CCGTGATATG	250
	GGCAAGCATA	TCGCCATGAT	GGCCGACTCG	ACGTCTCGCT	GGGCCGAGGC	300
40	GCTTCGTGAG	ATTTCTGGGTC	GTCTGGCGGA	GATGCCGGCC	GATGGTGGCT	350
	ACCCTGCCTA	TCTCAGCGCT	CGTCTCGCCT	CCTTCTACGA	GCGCGCCGGC	400
	CTCGTCACCT	GCATCGGCGG	GCCGAAGCGC	CAGGGCTCCG	TCACGATTGT	450
	CGGTGCCGTG	TCTCCGCCG				469

45

2) INFORMATION FOR SEQ ID NO: 960

50 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 469 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

55 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Leishmania tropica*
- (B) STRAIN: ATCC 30815

60

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 960

	TGTAATTAGT	CAGGCCCTCT	CCAAGTACTC	CAACTCCGAC	TGCGTCATCT	50
	ATGTCGGCTG	CGGCGAGCGC	GGTAATGAGA	TGGCCGAGGT	GCTCATGGAG	100
5	TTCCCGACCC	TGACGACCGT	GATCGATGGT	CGCGAGGAGT	CGATCATGAA	150
	GCGCACCTGC	CTCGTGGCGA	ACACTTCGAA	CATGCCAGTC	GCAGCCCGTG	200
	AGGCCTCTAT	TTACACCGGC	ATCACCCCTGG	CCGAGTACTA	CCGTGATATG	250
	GGCAAGCATA	TCGCCATGAT	GGCCGACTCG	ACGTCTCGCT	GGGCCGAGGC	300
	GCTTCGTGAG	ATTTTCGGGTC	GTTTGGCGGA	GATGCCGGCC	GATGGTGGCT	350
10	ACCCTGCCTA	TCTCAGCGCT	CGTCTCGCCT	CCTTCTACGA	GCGCGCCGGC	400
	CTCGTCACCT	GCATCGGCGG	GCCGAAGCGC	CAGGGCTCCG	TCACGATTGT	450
	CGGTGCCGTG	TCTCCGCCG				469

15

2) INFORMATION FOR SEQ ID NO: 961

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 469 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

25

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Leishmania guyanensis*
 (B) STRAIN: ATCC 50126

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 961

	TGTCATCAGT	CAGGCCCTCT	CCAAGTACTC	CAACTCCGAC	TGTGTCATCT	50
	ATGTCGGCTG	CGGTGAACGC	GGTAACGAGA	TGGCCGAGGT	GCTCATGGAG	100
	TTCCCGACCC	TGACGACTGT	GATCGATGGT	CGCGAAGAGT	CCATCATGAA	150
35	GCGCACCTGC	CTCGTGGCGA	ACACCTCGAA	CATGCCCGTC	GCAGCCCGTG	200
	AGGCCTCTAT	TTATACCGGC	ATCACCCCTTG	CTGAGTACTA	CCGTGATATG	250
	GGCAAGCACA	TTGCCATGAT	GGCCGACTCG	ACGTCTCGCT	GGGCCGAGGC	300
	GCTGCGTGAG	ATTTTCGGGTC	GATTGGCGGA	GATGCCGGCT	GATGGTGGCT	350
	ACCCTGCCTA	CCTCAGCGCC	CGCCTCGCCT	CCTTCTACGA	GCGCGCCGGT	400
40	CTCGTCACCT	GCATCGGCGG	GCCGAAGCGC	CAGGGCTCCG	TCACGATCGT	450
	CGGTGCAGTG	TCTCCACCG				469

45 2) INFORMATION FOR SEQ ID NO: 962

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 469 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

55 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Leishmania donovani*
 (B) STRAIN: ATCC 50212

60

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 962

	TGTCATTAGT	CAGGCCCTCT	CCAAGTACTC	CAACTCCGAT	TGCGTCATCT	50
	ATGTCGGCTG	CGGCGAGCGC	GGTAATGAGA	TGGCCGAGGT	GCTCATGGAG	100
	TCCCCGACCC	TGACGACCGT	GATCGATGGC	CGCGAGGAGT	CGATCATGAA	150
	GCGCACCTGC	CTCGTGCGCA	ACACCTCGAA	CATGCCAGTC	GCAGCCCGTG	200
5	AGGCCTCTAT	TTACACCGGC	ATCACCTGG	CCGAGTACTA	CCGTGATATG	250
	GGCAAGCATA	TCGCCATGAT	GGCTGACTCG	ACGTCTCGCT	GGGCCGAGGC	300
	GCTTCGTGAG	ATTTCCGGTC	GTCTGGCGGA	GATGCCGGCC	GATGGTGGCT	350
	ACCCCGCCTA	CCTCAGCGCT	CGTCTCGCCT	CCTTCTACGA	GCGCGCCGGC	400
	CTCGTCACCT	GCATCGGCGG	GCCGAAGCGC	CAGGGCTCCG	TCACGATCGT	450
10	CGGTGCCGTG	TCTCCACCG				469

2) INFORMATION FOR SEQ ID NO: 963

15

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 469 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

25

- (A) ORGANISM: *Leishmania hertigi*
 (B) STRAIN: ATCC 50125

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 963

30	TGTGATCAGT	CAGGCCCTTT	CCAAGTACTC	CAACTCGGAC	TGCGTCATCT	50
	ACGTCGGCTG	TGGTGAGCGC	GGGAACGAGA	TGGCCGAGGT	GCTCATGGAT	100
	TCCCCGACTT	TGACGACTGT	GATCGATGGT	CGCGAGGAGT	CCATCATGAA	150
	GCGCACCTGC	CTCGTGCGCA	ACACCTCCAA	CATGCCAGTT	GCAGCCCGTG	200
	AGGCTTCTAT	CTATACCGGC	ATCACACTGG	CTGAGTACTA	TCGTGATATG	250
35	GGCAAGCACA	TTGCCATGAT	GGCCGACTCG	ACGTCTCGCT	GGGCCGAGGC	300
	GTTGCGTGAG	ATTTCCGGTC	GGCTGGCGGA	GATGCCGGCC	GATGGTGGTT	350
	ACCCCGCCTA	CCTCAGTGCC	CGTCTCGCCT	CCTTCTACGA	GCGCGCTGGC	400
	CTCGTGACCT	GTATCGGCGG	GCCGAAGCGC	CAGGGCTCCG	TCACAATTGT	450
40	TGGTGCGGTG	TCTCCACCG				469

2) INFORMATION FOR SEQ ID NO: 964

45

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 469 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

55

- (A) ORGANISM: *Leishmania mexicana*
 (B) STRAIN: ATCC 50156

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 964

60	GGTCATTAGT	CAGGCCCTTT	CCAAGTACTC	CAACTCTGAC	TGCGTCATCT	50
	ACGTCGGCTG	CGGCGAGCGC	GGTAATGAGA	TGGCCGAGGT	GCTCATGGAG	100

	TTCCCGACCC	TGACGACCAT	GATCGATGGT	CGGGAGGAGT	CGATCATGAA	150
	GCGCACCTGC	CTCGTGCGGA	ACACCTCGAA	CATGCCCGTC	GCAGCCCGTG	200
	AGGCCTCTAT	CTACACCGGC	ATCACCCCTCG	CCGAGTACTA	CCGTGATATG	250
	GGCAAGCATA	TCGCCATGAT	GGCCGACTCG	ACGTCTCGCT	GGGCTGAGGC	300
5	GCTTCGTGAG	ATTTTCGGGTC	GTCTGGCGGA	GATGCCGGCC	GATGGTGGCT	350
	ACCCCGCCTA	CCTCAGCGCT	CGTCTCGCCT	CCTTCTACGA	GCGCGCCGGC	400
	CTCGTCACCT	GCATCGGCGG	GCCGAAGCGC	CAGGGCTCCG	TCACGATCGT	450
	CGGTGCCGTG	TCTCCGCCG				469

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2) INFORMATION FOR SEQ ID NO: 965

- (i) SEQUENCE CHARACTERISTICS:
- 15 (A) LENGTH: 469 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear
- 20 (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Leishmania tropica*
- (B) STRAIN: ATCC 50129
- 25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 965

	TGTAATTAGT	CAGGCCCTCT	CCAAGTACTC	CAACTCCGAC	TGCGTCATCT	50
	ATGTCGGCTG	CGGCGAGCGC	GGTAATGAGA	TGGCCGAGGT	GCTCATGGAG	100
30	TTCCCGACCC	TGACGACCGT	GATCGATGGT	CGCGAGGAGT	CGATCATGAA	150
	GCGCACCTGC	CTCGTGCGGA	ACACTTCGAA	CATGCCAGTC	GCAGCCCGTG	200
	AGGCCTCTAT	TTACACCGGC	ATCACCCCTGG	CCGAGTACTA	CCGTGATATG	250
	GGCAAGCATA	TCGCCATGAT	GGCCGACTCG	ACGTCTCGCT	GGGCCGAGGC	300
	GCTTCGTGAG	ATTTTCGGGTC	GTTTGGCGGA	GATGCCGGCC	GATGGTGGCT	350
35	ACCTGCCTA	TCTCAGCGCT	CGTCTCGCCT	CCTTCTACGA	GCGCGCCGGC	400
	CTCGTCACCT	GCATCGGCGG	GCCGAAGCGC	CAGGGCTCCG	TCACGATTGT	450
	CGGTGCCGTG	TCTCCGCCG				469

40

2) INFORMATION FOR SEQ ID NO: 966

- (i) SEQUENCE CHARACTERISTICS:
- 45 (A) LENGTH: 449 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- 50 (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Peptostreptococcus anaerobius*
- (B) STRAIN: ATCC 27337
- 55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 966

	CACCAGTTCG	CCAAGTGGGC	AGATGCTCAG	ATAGTTGTAT	ACGTTGGTTG	50
	TGGAGAACGT	GGTAACGAGA	TGACAGACGT	TCTAAATGAA	TTCCAGAAC	100
	TGATTGACCC	TCATACAGGC	GAATCTCTAA	TGAAGAGAAC	AGTTCTTATA	150
60	GCTAATACGT	CAAATATGCC	AGTTGCAGCC	AGAGAGGCAA	GTATATATAC	200

	AGGTATTACA	ATAGCTGAAT	ATTTTAGAGA	CATGGGATAT	TCAGTAGCGG	250
	TAATGGCCGA	CTCTACATCA	AGATGGGCAG	AGGCCCTAAG	AGAGATGTCA	300
	GGTCGTCTAG	AAGAAATGCC	TGGTGATGAA	GGTTATCCAG	CCTATCTAGG	350
	TTCTAGAGCT	GCAGAGTTCT	ATGAAAGAGC	AGGTAAGGTA	ATATGTAAGG	400
5	GTAGCGATAA	TAGAGAGGGA	GCCCTTACAA	TAATAGGTGC	CGTGTCCACC	449

2) INFORMATION FOR SEQ ID NO: 967

10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 826 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 15 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 20 (A) ORGANISM: *Bordetella pertussis*
 (B) STRAIN: ATCC 9797

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 967

25	CTGGTGGTGT	CGGCCGCAGA	CGGCCCCGATG	CCGCAGACGC	GCGAGCACAT	50
	TTTGCTGTCTG	CGCCAGGTTG	GCGTGCCGTA	CATCATCGTG	TTCCTGAACA	100
	AGGCGGACAT	GGTTGATGAC	GCGGAGCTGC	TCGAGCTGGT	GAAGATGGAA	150
	GTCCGCGAAC	TGCTGAGCAA	GTACGATTTC	CCGGGCGATG	ACACGCCGAT	200
	CGTGAAGGGT	TCGGCCAAGC	TGGCGCTGGA	AGGCGACAAG	GGCGAACTGG	250
30	GCGAGCAGGC	GATTCTGTCTG	CTGGCGCAAG	CGCTGGACAC	GTACATTCCG	300
	ACGCCGGAGC	GCGCGGTCGA	CGGTGCGTTC	CTGATGCCCG	TGGAAGACGT	350
	GTTCTCGATC	TCGGGCCGTG	GCACGGTGGT	GACTGGCCGT	ATCGAGCGCG	400
	GCGTGGTGAA	GGTTGGCGAG	GAAATCGAAA	TCGTGGGCAT	CAAGCCGACG	450
	GTGAAGACGA	CCTGCACGGG	TGGTGAGATG	TTCCGCAAGC	TGCTGGACCA	500
35	GGGCCAGGCG	GGCGACAACG	TGGGTATCTT	GCTGCGCGGC	ACCAAGCGTG	550
	AAGACGTCTGA	GCGTGGCCAG	GTGCTGGCCA	AGCCGGGTTC	GATCAACCCG	600
	CACACGGACT	TCACGGCCGA	GGTGTACATT	CTGTCCAAGG	AAGAGGGTGG	650
	CCGTACACCG	CCGTTCTTCA	ACGGCTATCG	TCCGCAGTTC	TACTTCCGCA	700
	CGACGGACGT	GACCGGCACG	ATCGACCTGC	CGGCGGACAA	GGAAATGGTG	750
40	CTGCCGGGCG	ACAACGTGTC	GATGACCGTC	AAGCTGCTGG	CCCCGATCGC	800
	CATGGAAGAA	GGTCTGCGTT	TCGCCA			826

45 2) INFORMATION FOR SEQ ID NO: 968

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 817 bases
 (B) TYPE: Nucleic acid
 50 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 55 (A) ORGANISM: *Bordetella pertussis*
 (B) STRAIN: BD180

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 968

60

	CGATCCTGGT	GGTGTGGGCC	GCAGACGGCC	CGATGCCGCA	GACGCGCGAG	50
	CACATTTTGC	TGTCGCGCCA	GGTTGGCGTG	CCGTACATCA	TCGTGTTTCCT	100
	GAACAAGGCG	GACATGGTTG	ATGACGCGGA	GCTGCTCGAG	CTGGTGGAGA	150
	TGGAAGTCCG	CGAACTGCTG	AGCAAGTACG	ATTTCCCGGG	CGATGACACG	200
5	CCGATCGTGA	AGGGTTCGGC	CAAGCTGGCG	CTGGAAGGCG	ACAAGGGCGA	250
	ACTGGGCGAG	CAGGCGATTG	TGTCGCTGGC	GCAAGCGCTG	GACACGTACA	300
	TTCCGACGCC	GGAGCGCGCG	GTCGACGGTG	CGTTCCTGAT	GCCGCTGGAA	350
	GACGTGTTCT	CGATCTCGGG	CCGTGGCAGG	GTGGTGAAGT	GCCGTATCGA	400
	GCGCGGCGTG	GTGAAGGTTG	GCGAGGAAAT	CGAAATCGTG	GGCATCAAGC	450
10	CGACGGTGAA	GACGACCTGC	ACGGGCGTGG	AGATGTTCCG	CAAGCTGCTG	500
	GACCAGGGCC	AGGCGGGCGA	CAACGTGGGT	ATCTTGCTGC	GCGGCACCAA	550
	GCGTGAAGAC	GTCGAGCGTG	GCCAGGTGCT	GGCCAAGCCG	GGTTCGATCA	600
	ACCCGCACAC	GGACTTCACG	GCCGAGGTGT	ACATTCTGTC	CAAGGAAGAG	650
	GGTGGCCGTC	ACACGCCGTT	CTTCAACGGC	TATCGTCCGC	AGTTCTACTT	700
15	CCGCACGACG	GACGTGACCG	GCACGATCGA	CCTGCCGGCG	GACAAGGAAA	750
	TGGTGCTGCC	GGGCGACAAC	GTGTCGATGA	CCGTCAAGCT	GCTGGCCCCG	800
	ATCGCCATGG	AAGAAGG				817

20

2) INFORMATION FOR SEQ ID NO: 969

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 637 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

25

(ii) MOLECULE TYPE: Genomic DNA

30

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus columbae*
 (B) STRAIN: ATCC 51263

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 969

	CCTATGCCAC	AAACTCGTGA	ACACATTCTT	TTATCACGTA	ACGTTGGTGT	50
	GCCATACATC	GTTGTTTTCT	TAAACAAAGT	TGATATGGTT	GACGACGAAG	100
	AATTATTAGA	ATTAGTTGAA	ATGGAAGTTC	GTGACTTATT	AACTGAATAT	150
40	GACTTCCCAG	GAGACGATGT	TCCTGTAATC	GCTGGTTCCTG	CATTAAAAGC	200
	TTTAGAAGGC	GACCCTGCTT	ACGAAGAAAA	AATCTTAGAA	TTAATGGCTG	250
	CAGTTGACGA	ATACATCCCA	ACTCCAGAAC	GTGACAACGA	CAAACCATTC	300
	ATGATGCCAG	TTGAAGACGT	GTTCTCAATT	ACTGGTCGTG	GTACTGTTGC	350
	TACAGGTCGT	GTTGAACGTG	GACAAGTTCG	TGTTGGTGAC	GAAGTTGAAA	400
45	TCGTTGGTAT	CGCTGACGAA	ACTTCTAAAA	CAACAGTTAC	TGGTGTTGAA	450
	ATGTTCCGTA	AATTATTAGA	TTACGCTGAA	GCTGGAGACA	ACATCGGTGC	500
	ATTATTACGT	GGTGTGGCTC	GTGAAGACAT	CCAACGTGGT	CAAGTATTAG	550
	CTAAACCAGG	TTCAATCACT	CCACATACAA	AATTCAGTGC	TGAAGTGTAC	600
	GTTTTAACTA	AAGAAGAAGG	TGGACGTCAT	ACTCCAT		637

50

2) INFORMATION FOR SEQ ID NO: 970

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 634 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

60

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus flavescens*
 5 (B) STRAIN: ATCC 49997

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 970

	TATGCCTCAA	ACACGTGAAC	ACATCTTGTT	ATCACGTAAC	GTTGGTGTAC	50
10	CATACATCGT	TGTTTTCTTA	AACAAAATGG	ATATGGTTGA	TGACGAAGAA	100
	TTACTAGAAT	TAGTTGAAAT	GGAAGTTCGT	GACTTATTGT	CAGAATATGA	150
	CTTCCCAGGC	GACGATGTTT	CTGTAATCGC	TGGTTCGTCT	TTGAAAGETC	200
	TTGAAGGCGA	TGCTTCATAC	GAAGAAAAAA	TCATGGAATT	AATGGCTGCA	250
	GTTGACGAAT	ACGTTCCAAC	TCCAGAACGT	GACACTGACA	AACCATTTCAT	300
15	GATGCCAGTC	GAAGACGTAT	TCTCAATCAC	TGGACGTGGT	ACTGTTGCTA	350
	CAGGCCGTGT	TGAACGTGGA	CAAGTTCGCG	TTGGTGACGA	AGTTGAAATC	400
	GTTGGTATTG	CTGAAGAAAC	TGCTAAAACA	ACTGTAAGTG	GTGTTGAAAT	450
	GTTCCGTAAA	TTGTTAGACT	ATGCTGAAGC	AGGGGATAAC	ATTGGTGCAT	500
	TGCTACGTGG	GGTTGCTCGT	GAAGACATCC	AACGTGGACA	AGTATTAGCT	550
20	AAAGCTGGTA	CAATCACACC	TCATACAAAA	TTTAAAGCTG	AAGTTTACGT	600
	TTTAACAAAA	GAAGAAGGTG	GACGTCACAC	TCCA		634

25 2) INFORMATION FOR SEQ ID NO: 971

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 787 bases
 (B) TYPE: Nucleic acid
 30 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

35 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
 (B) STRAIN: StrR-55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 971

40	GGACCAATGC	CACAAACTCG	TGAGCACATC	CTTCTTTCAC	GTCAGGTTGG	50
	TGTTAAACAC	CTTATCGTCT	TCATGAACAA	AGTTGACTTG	GTTGACGACG	100
	AAGAATTGCT	TGAATTGGTT	GAAATGGAAA	TCCGTGACCT	ATTGTCAGAA	150
	TACGACTTCC	CAGGTGACGA	TCTTCCAGTT	ATCCAAGGTT	CAGCACTTAA	200
45	AGCTCTTGAA	GGTGACTCTA	AATACGAAGA	CATCGTTATG	GAATTGATGA	250
	ACACAGTTGA	TGAGTATATC	CCAGAACCAG	AACGTGACAC	TGACAAACCA	300
	TTGCTTCTTC	CAGTCGAGGA	CGTATTCTCA	ATCACTGGAC	GTGGTACAGT	350
	TGCTTCAGGA	CGTATCGACC	GTGGTATCGT	TAAAGTCAAC	GACGAAATCG	400
	AAATCGTTGG	TATCAAAGAA	GAAACTCAAA	AAGCAGTTGT	TACTGGTGTG	450
50	GAAATGTTCC	GTAAACAAC	TGACGAAGGT	CTTGCTGGAG	ATAACGTAGG	500
	TGTCCTTCTT	CGTGGTGTTT	AACGTGATGA	AATCGAACGT	GGACAAGTTA	550
	TCGCTAAACC	AGGTTCAATC	AACCCACACA	CTAAATTCAA	AGGTGAAGTC	600
	TACATCCTTA	CTAAAGAAGA	AGGTGGACGT	CACACTCCAT	TCTTCAACAA	650
	CTACCGTCCA	CAATTCTACT	TCCGTACTAC	TGACGTTACA	GGTTCAATCG	700
55	AACTTCCAGC	AGGTACTGAA	ATGGTAATGC	CTGGTGATAA	CGTGACAATC	750
	GACGTTGAGT	TGATTACCCC	AATCGCCGTA	GAACAAG		787

60 2) INFORMATION FOR SEQ ID NO: 972

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 803 bases
 (B) TYPE: Nucleic acid
 5 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

- 10 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Escherichia coli*
 (B) STRAIN: ATCC 35401

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 972

15	TAGTTGCTGC	GACTGACGGC	CCGATGCCGC	AGACTCGTGA	GCACATCCTG	50
	CTGGGTCGTC	AGGTAGGCGT	TCCGTACATC	ATCGTGTTCC	TGAACAAATG	100
	CGACATGGTT	GATGACGAAG	AGCTGCTGGA	ACTGGTTGAA	ATGGAAGTTC	150
	GTGAACTTCT	GTCTCAGTAC	GACTTCCCGG	GCGACGACAC	TCCGATCGTT	200
20	CGTGGTTCTG	CTCTGAAAGC	GCTGGAAGGC	GACGCAGAGT	GGGAAGCGAA	250
	AATCCTGGAA	CTGGCTGGCT	TCCTGGATTG	TTACATTCCG	GAACCAGAGC	300
	GTGCGATTGA	CAAGCCGTTT	CTGCTGCCGA	TGGAAGACGT	ATTCTCCATC	350
	TCCGGTCGTG	GTACCGTTGT	TACCGGTCGT	GTAGAACGCG	GTATCATCAA	400
	AGTTGGTGAA	GAAGTTGAAA	TCGTTGGTAT	CAAAGAGACT	CAGAAGTCTA	450
25	CCTGTACTGG	CGTTGAAATG	TTCCGCAAAC	TGCTGGACGA	AGGCCGTGCT	500
	GGTGAGAACG	TAGGTGTTCT	GCTGCGTGGT	ATCAAACGTG	AAGAAATCGA	550
	ACGTGGTCAG	GTA CTGGCTA	AGCCGGGCAC	CATCAAGCCG	CACACCAAGT	600
	TCGAATCTGA	AGTGTACATT	CTGTCCAAAG	ATGAAGGCGG	CCGTCATACT	650
	CCGTTCTTCA	AAGGCTACCG	TCCGCAGTTC	TACTTCCGTA	CTACTGACGT	700
30	GACTGGTACC	ATCGAACTGC	CGGAAGGCGT	AGAGATGGTA	ATGCCGGGCG	750
	ACAACATCAA	AATGGTTGTT	ACCCTGATCC	ACCCGATCGC	GATGGACGAC	800
	GGT					803

35 2) INFORMATION FOR SEQ ID NO: 973

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 762 bases
 40 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

- 45 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Escherichia coli*
 (B) STRAIN: ATCC 43895

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 973

	ACTGACGGCC	CGATGCCGCA	GACTCGTGAG	CACATCCTGC	TGGGTCGTCA	50
	GGTAGGCGTT	CCGTACATCA	TCGTGTTTCT	GAACAAATGC	GACATGGTTG	100
	ATGACGAAGA	GCTGCTGGAA	CTGGTTGAAA	TGGAAGTTCG	TGAACTTCTG	150
55	TCTCAGTACG	ACTTCCCGGG	CGACGACACT	CCGATCGTTC	GTGGTTCTGC	200
	TCTGAAAGCG	CTGGAAGGCG	ACGCAGAGTG	GGAAGCGAAA	ATCCTGGAAC	250
	TGGCTGGCTT	CCTGGATTCC	TACATTCCGG	AACCAGAGCG	TGCRATTGAC	300
	AAGCCGTTCC	TGCTGCCGAT	CGAAGACGTA	TTCTCCATCT	CCGGTCGTGG	350
	TACCGTTGTT	ACCGGTCGTG	TAGAACGCGG	TATCATCAAA	GTTGGTGAAG	400
60	AAGTTGAAAT	CGTTGGTATC	AAAGAGACTC	AGAAGTCTAC	CTGTACTGGC	450

	GTTGAAATGT	TCCGCAAAC	GCTGGACGAA	GGCCGTGCTG	GTGAGAACGT	500
	AGGTGTTCTG	CTGCGTGGTA	TCAAACGTGA	AGAAATCGAA	CGTGGTCAGG	550
	TACTGGCTAA	GCCGGGCACC	ATCAAGCCGC	ACACCAAGTT	CGAATCTGAA	600
	GTGTACATTC	TGTCCAAAGA	TGAAGGCGGC	CGTCATACTC	CGTTCTTCAA	650
5	AGGCTACCGT	CCGCAGTTCT	ACTTCCGTAC	TACTGACGTG	ACTGGTACCA	700
	TTGAACTGCC	GGAAGGCGTA	GAGATGGTAA	TGCCGGGCGA	CAACATCAAA	750
	ATGGTTGTTA	CC				762

10

2) INFORMATION FOR SEQ ID NO: 974

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 804 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

20 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Escherichia coli*
(B) STRAIN: ATCC 11775

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 974

	CCTGGTAGTT	GCTGCGACTG	ACGGCCCCGAT	GCCGCAGACT	CGTGAGCACA	50
	TCCTGCTGGG	TCGTCAGGTA	GGCGTTCCGT	ACATCATCGT	GTTCTGAAC	100
	AAATGCGACA	TGGTTGATGA	CGAAGAGCTG	CTGGAAGTGG	TTGAAATGGA	150
30	AGTTCGTGAA	CTTCTGTCTC	AGTACGACTT	CCCGGGCGAC	GACACTCCGA	200
	TCGTTTCGTG	TTCTGCTCTG	AAAGCGCTGG	AAGGCGACGC	AGAGTGGGAA	250
	GCGAAAATCC	TGGAAGTGGC	TGGCTTCTCTG	GATTCCTACA	TTCCGGAACC	300
	AGAGCGTCCG	ATTGACAAGC	CGTTCTCTGCT	GCCGATCGAA	GACGTATTCT	350
	CCATCTCCCG	TCGTGGTACC	GTTGTTACCG	GTCGTGTAGA	ACGCGGTATC	400
35	ATCAAAGTTG	GTGAAGAAAGT	TGAAATCGTT	GGTATCAAAG	AGACTCAGAA	450
	GTCTACCTGT	ACTGGCGTTG	AAATGTTCCG	CAAAGTCTG	GACGAAGGCC	500
	GTGCTGGTGA	GAACGTAGGT	GTTCTGCTGC	GCGGTATCAA	ACGTGAAGAA	550
	ATCGAACGTG	GTCAGGTACT	GGCTAAGCCG	GGCACCATCA	AGCCGCACAC	600
	CAAGTTCGAA	TCTGAAGTGT	ACATTCTGTC	CAAAGATGAA	GGCGGTCGTC	650
40	ATACTCCGTT	CTTCAAAGGC	TACCGTCCGC	AGTTCTACTT	CCGTACTACT	700
	GACGTGACTG	GTACCATCGA	ACTGCCGGAA	GGCGTAGAGA	TGGTAATGCC	750
	GGGCGACAAC	ATCAAAATGG	TTGTTACCCT	GATCCACCCG	ATCGCGATGG	800
	ACGA					804

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2) INFORMATION FOR SEQ ID NO: 975

(i) SEQUENCE CHARACTERISTICS:

- 50 (A) LENGTH: 804 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

55 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Escherichia coli*
(B) STRAIN: ATCC 25922

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 975

	GCGATCCTGG	TAGTTGCTGC	GACTGACGGC	CCGATGCCGC	AGACTCGTGA	50
	GCACATCCTG	CTGGGTCGTC	AGGTAGGCGT	TCCGTACATC	ATCGTGTTCC	100
5	TGAACAAATG	CGACATGGTT	GATGACGAAG	AGCTGCTGGA	ACTGGTTGAA	150
	ATGGAAGTTC	GTGAACTTCT	GTCTCAGTAC	GACTTCCCGG	GCGACGACAC	200
	TCCGATCGTT	CGTGGTTCTG	CTCTGAAAGC	GCTGGAAGGC	GACGCAGAGT	250
	GGAAGCGAA	AATCCTGGAA	CTGGCTGGCT	TCCTGGATTG	YTACATTCCG	300
	GAACCAGAGC	GTGCGATTGA	CAAGCCGTTT	CTGCTGCCGA	TCGAAGACGT	350
10	ATTCTCCATC	TCCGGTCGTG	GTACCGTTGT	TACCGGTCGT	GTAGAACGCG	400
	GTATCATCAA	AGTTGGTGAA	GAAGTTGAAA	TCGTTGGTAT	CAAAGAGACT	450
	CAGAAGTCTA	CCTGTAAGTG	CGTTGAAAATG	TTCCGCAAAC	TGCTGGACGA	500
	AGGCCGTGCT	GGTGAGAACG	TAGGTGTTCT	GCTGCGTGGT	ATCAAACGTG	550
	AAGAAATCGA	ACGTGGTCAG	GTACTGGCTA	AGCCGGGCAC	CATCAAGCCG	600
15	CACACCAAGT	TCGAATCTGA	AGTGATACAT	CTGTCCAAAG	ATGAAGGCGG	650
	TCGTCACTACT	CCGTTCTTCA	AAGGCTACCG	TCCGCAGTTC	TACTTCCGTA	700
	CTACTGACGT	GACTGGTACC	ATCGAACTGC	CGGAAGGTGT	AGAGATGGTA	750
	ATGCCGGGCG	ACAACATCAA	AATGGTTGTT	ACCCTGATCC	ACCCGATCGC	800
	GATG					804
20						

2) INFORMATION FOR SEQ ID NO: 976

25 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 825 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

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(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Mycobacterium avium*
 35 (B) STRAIN: Mavi-1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 976

	GGCGCGATCC	TGGTGGTCGC	CGCCACCGAC	GGCCCCGATGC	CGCAGACCCG	50
40	TGAGCACGTG	CTGCTCGCCC	GTCAGGTCGG	TGTGCCCTAC	ATCCTGGTGC	100
	CCCTGAACAA	GGCCGACATG	GTCGACGACG	AGGAGCTCCT	CGAGCTCGTC	150
	GAGATGGAGG	TCCGCGAGCT	GCTGGCCGCC	CAGGAGTTCG	ACGAGGACGC	200
	CCCGGTGGTG	CGGGTCTCGG	CGCTCAAGGC	GCTCGAGGGC	GACGCCAAGT	250
	GGGTCGAGTC	CGTCGAGCAG	CTGATGGAGG	CCGTCGACGA	GTCGATCCCG	300
45	GACCCGGTCC	GCGAGACGGA	GAAGCCGTTT	CTGATGCCGG	TGGAGGACGT	350
	CTTCACCATC	ACCGGGCGTG	GCACCGTGGT	CACCGGTCGT	GTCGAGCGCG	400
	GTGTGATCAA	CGTGAACGAG	GAAGTCGAGA	TCGTCGGCAT	CCGCCCCGACC	450
	AGCACCAAGA	CCACGGTCAC	CGGTGTGGAR	ATGTTCCGCA	AGCTGCTCGA	500
	CCAGGGCCAG	GCCGGTGACA	ACGTCGGTCT	GCTGCTGCGT	GGTATCAAGC	550
50	GTGAGGACGT	CGAGCGCGGC	CAGGTCGTGA	CCAAGCCCCG	CACCACCACG	600
	CCGCACACCG	AGTTCGAGGG	CCAGGTCTAC	ATCCTGTCCA	AGGACGAGGG	650
	CGGCCGGCAC	ACGCCGTTCT	TCAACAATA	CCGTCCGCAG	TTCTACTTCC	700
	GCACCACCGA	CGTGACCGGT	GTGGTGACGC	TGCCGGAGGG	CACCGAGATG	750
	GTGATGCCCG	GTGACAACAC	CAACATCTCG	GTGAAGCTGA	TCCAGCCCCG	800
55	CGCCATGGAC	GACGGTSTGC	GGTTC			825

2) INFORMATION FOR SEQ ID NO: 977

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- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 820 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus pneumoniae*
 (B) STRAIN: StrR-06

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 977

15	TATCCTTGTA	GTAGCTTCAA	CTGACGGACC	AATGCCACAA	ACTCGTGAGC	50
	ACATCCTTCT	TTCACGTCAG	GTTGGTGTGA	AACACCTTAT	CGTCTTCATG	100
	AACAAAGTTG	ACTTGGTGTA	CGACGAAGAA	TTGCTTGAAT	TGGTTGAAAT	150
	GGAAATCCGT	GACCTATTGT	CAGAATACGA	CTTCCCAGGT	GACGATCTTC	200
	CAGTTATCCA	AGGTTTCAGCA	CTTAAAGCTC	TTGAAGGTGA	CTCTAAATAC	250
20	GAAGACATCG	TTATGGAATT	GATGAACACA	GTTGATGAGT	ATATCCCAGA	300
	ACCAGAACGT	GACACTGACA	AACCATTGCT	TCTTCCAGTC	GAGGACGTAT	350
	TCTCAATCAC	TGGACGTGGT	ACAGTTGCTT	CAGGACGTAT	CGACCGTGGT	400
	ATCGTTAAAG	TCAACGACGA	AATCGAAATT	GTTGGTATCA	AAGAAGAAAC	450
	TCAAAAAGCA	GTTGTTACTG	GTGTTGAAAT	GTTCCGTAAA	CAACTTGACG	500
25	AAGGTCTTGC	TGGAGATAAC	GTAGGTGTCC	TTCTTCGTGG	TGTTCAACGT	550
	GATGAAATCG	AACGTGGACA	AGTTATCGCT	AAACCAGGTT	CAATCAACCC	600
	ACACACTAAA	TTCAAAGGTG	AAGTCTACAT	CCTTACTAAA	GAAGAAGGTG	650
	GACGTCACAC	TCCATTCTTC	AACAACCTACC	GTCCACAATT	CTACTTCCGT	700
	ACTACTGACG	TTACAGGTTC	AATCGAACTT	CCAGCAGGTA	CTGAAATGGT	750
30	AATGCCTGGT	GATAACGTGA	CAATCGACGT	TGAGTTGATT	CACCCAATCG	800
	CCGTAGAACA	AGGTACTACA				820

35 2) INFORMATION FOR SEQ ID NO: 978

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 822 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Mycobacterium gordonae*
 (B) STRAIN: M-Gor-1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 978

50	GGCGCGATCC	TGGTGGTCGC	CGCCACCGAT	GGCCCGATGC	CGCAGACCCG	50
	TGAGCACGTG	CTGCTCGCCC	GTCAGGTGGG	CGTGCCCTAC	ATCCTGGTGG	100
	CGCTGAACAA	GTCCGACGCG	GTCGACGACG	AGGAGCTGCT	CGAGCTCGTC	150
	GAGCTGGAGG	TCCGCGAGTT	GCTGGCCGCC	CAGGACTTCG	ACGAGGAAGC	200
55	TCCGGTGGTC	CGGGTCTCGG	CGCTGAAGGC	GCTCGAGGGC	GACGCCACCT	250
	GGGTGAAGTC	GGTAGAGGAC	TTGATGGACG	CGGTGACGCA	GTCGATTCCG	300
	GACCCGGTCC	GCGACACCGA	CAAGCCGTTC	CTGATGCCCG	TCGAGGACGT	350
	CTTCACCATC	ACCGGTCGTG	GCACCGTCGT	CACCGGCCGT	GTGGAGCGCG	400
	GCGTGGTGAA	CGTGAACGAG	GAAGTCGAGA	TCGTGCGCAT	CAAGCCGACC	450
60	AGCACCAAGA	CCACGGTCAC	CGGTGTGGAG	ATGTTCCGCA	AGCTGCTCGA	500

	CCAGGGTCAG	GCCGGTGACA	ACGTCGGTCT	GCTGCTGCGT	GGTGTCAAGC	550
	GTGAGGACGT	CGAGCGCGGC	CAGGTCGTCA	TCAAGCCCGG	CACCACCACT	600
	CCGCACACCG	AGTTCGAGGG	TCAGGTCTAC	ATCCTGTCCA	AGGACGAGGG	650
	CGGCCGGCAC	ACGCCGTTCT	TCAACAACCTA	CCGTCCGCAG	TTCTACTTCC	700
5	GCACCACCGA	CGTGACCGGT	GTGGTGACGC	TGCCGGAGGG	CACCGAAATG	750
	GTGATGCCCCG	GTGACAACAC	CAACATCTCG	GTGAAGCTGA	TCCAGCCCCGT	800
	CGCCATGGAC	GACGGTCTGC	GG			822

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2) INFORMATION FOR SEQ ID NO: 979

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 821 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

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(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
(B) STRAIN: StrR-11

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 979

	CTATCCTTGT	AGTAGCTTCA	ACTGACGGAC	CAATGCCACA	AACTCGTGAG	50
	CACATCCTTC	TTTCACGTCA	GGTTGGTGTT	AAACACCTTA	TCGTCTTCAT	100
	GAACAAAGTT	GACTTGTTG	ACGACGAAGA	ATTGCTTGAA	TTGGTTGAAA	150
30	TGGAAATCCG	TGACCTATTG	TCAGAATACG	ACTTCCCAGG	TGACGATCTT	200
	CCAGTTATCC	AAGGTTCAGC	ACTTAAAGCT	CTTGAAGGTG	ACTCTAAATA	250
	CGAAGACATC	GTTATGGAAT	TGATGAACAC	AGTTGATGAG	TATATCCCAG	300
	AACCAGAACG	TGACACTGAC	AAACCATTCG	TTCTTCCAGT	CGAGGACGTA	350
	TTCTCAATCA	CTGGACGTGG	TACAGTTGCT	TCAGGACGTA	TCGACCGTGG	400
35	TATCGTTAAA	GTCAACGACG	AAATCGAAAT	CGTTGGTATC	AAAGAAGAAA	450
	CTCAAAAAGC	AGTTGTTACT	GGTGTTGAAA	TGTTCCGTAA	ACAACTTGAC	500
	GAAGGTCTTG	CTGGAGATAA	CGTAGGTGTC	CTTCTTCGTG	GTGTTCAACG	550
	TGATGAAATC	GAACGTGGAC	AAGTTATCGC	TAAACCAGGT	TCAATCAACC	600
	CACACACTAA	ATTCAAAGGT	GAAGTCTACA	TCCTTACTAA	AGAAGAAGGT	650
40	GGACGTCACA	CTCCATTCTT	CAACAACCTAC	CGTCCACAAT	TCTACTTCCG	700
	TACTACTGAC	GTTACAGGTT	CAATCGAACT	TCCAGCAGGT	ACTGAAATGG	750
	TAATGCCTGG	TGATAACGTG	ACAATCGACG	TTGAGTTGAT	TCACCCAATC	800
	GCCGTAGAAC	AAGGTACTAC	A			821

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2) INFORMATION FOR SEQ ID NO: 980

(i) SEQUENCE CHARACTERISTICS:

- 50 (A) LENGTH: 828 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

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(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Mycobacterium tuberculosis*
(B) STRAIN: ATCC 25177

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 980

	GGTGCGATCC	TGGTGGTCGC	CGCCACCGAC	GGCCCGATGC	CCCAGACCCG	50
	CGAGCACGTT	CTGCTGGCGC	GTCAAGTGGG	TGTGCCCTAC	ATCCTGGTAG	100
5	CGCTGAACAA	GGCCGACGCA	GTGGACGACG	AGGAGCTGCT	CGAACTCGTC	150
	GAGATGGAGG	TCCGCGAGCT	GCTGGCTGCC	CAGGAATTCT	ACGAGGACGC	200
	CCCGGTTGTG	CGGGTCTCGG	CGCTCAAGGC	GCTCGAGGGT	GACGCGAAGT	250
	GGGTTGCCTC	TGTCGAGGAA	CTGATGAACG	CGGTCGACGA	GTCGATTCCG	300
	GACCCGGTCC	GCGAGACCGA	CAAGCCGTTT	CTGATGCCGG	TCGAGGACGT	350
10	CTTCACCAT	ACCGGCCGCG	GAACCGTGGT	CACCGACGCT	GTGGAGCGCG	400
	GCGTGATCAA	CGTGAACGAG	GAAGTTGAGA	TCGTCGGCAT	TCGCCCATCG	450
	ACCACCAAGA	CGACCGTCAC	CGGTGTGGAG	ATGTTCCGGA	AGCTGCTEGA	500
	CCAGGGCCAG	GCGGGCGACA	ACGTTGGTTT	GCTGCTGCGG	GGCGTCAAGC	550
	GCGAGGACGT	CGAGCGTGGC	CAGGTTGTCA	CCAAGCCCGG	CACCACCACG	600
15	CCGCACACCG	AGTTCGAAGG	CCAGGTCTAC	ATCCTGTCCA	AGGACGAGGG	650
	CGGCCGGCAC	ACGCCGTTCT	TCAACAATA	CCGTCCGCAG	TTCTACTTCC	700
	GCACCACCGA	CGTGACCGGT	GTGGTGACAC	TGCCGGAGGG	CACCGAGATG	750
	GTGATGCCCG	GTGACAACAC	CAACATCTCG	GTGAAGTTGA	TCCAGCCCGT	800
	CGCCATGGAC	GAAGGTNTGC	GTTTCGCG			828

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2) INFORMATION FOR SEQ ID NO: 981

25 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 819 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

30

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus warneri*
 (B) STRAIN: CSG 144

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 981

	CGGCCGTATC	TTAGTAGTAT	CTGCTGCAGA	TGGCCCAATG	CCACAAACTC	50
40	GTGAACACAT	CTTATTATCA	CGTAACGTTG	GTGTACCAGC	TTTAGTTGTA	100
	TTCTTAAACA	AAGCTGACAT	GGTTGACGAC	GAAGAATTAT	TAGAATTAGT	150
	TGAAATGGAA	GTTTCGTGACT	TATTATCTGA	ATACGACTTC	CCTGGTGACG	200
	ATGTACCAGT	TATCGTTGGT	TCTGCATTAA	AAGCTTTAGA	AGGCGACCCA	250
	GAATACGAAC	AAAAAATCTT	AGACTTAATG	CAAGCTGTAG	ATGACTACAT	300
45	CCCAACTCCA	GAACGTGACT	CTGATAAACC	ATTCATGATG	CCAGTTGAGG	350
	ACGTATTCTC	AATCACTGGT	CGTGGTACTG	TAGCAACAGG	CCGTGTTGAA	400
	CGTGGTCAAA	TCAAAGTCGG	TGAAGAAGTT	GAAATCATCG	GTATCACTGA	450
	AGAAAGCAAG	AAAACAACAG	TTACAGGTGT	AGAAATGTTC	CGTAAATTAT	500
	TAGACTACGC	TGAAGCTGGT	GACAACATCG	GTGCTTTATT	ACGTGGTGTG	550
50	GCACGTGAAG	ACGTACAACG	TGGACAAGTA	TTAGCAGCTC	CTGGCTCTAT	600
	TACTCCACAC	ACAAAATTCA	AAGCTGATGT	TTACGTTTTA	TCTAAAGAAG	650
	AAGGTGGACG	TCATACTCCA	TTCTTCACTA	ACTACCGCCC	ACAATTCTAC	700
	TTCCGTACTA	CTGACGTAAC	TGGCGTTGTT	CACTTACCAG	AAGGTACTGA	750
	AATGGTTATG	CCTGGCGATA	ACGTAGAAAT	GACTGTTGAA	TTAATCGCTC	800
55	CAATCGCGAT	TGAAGACGG				819

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2) INFORMATION FOR SEQ ID NO: 982

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 814 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus mitis*
 (B) STRAIN: LSPQ 2583

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 982

15	CTATCCTTGT	AGTAGCTTCA	ACTGACGGAC	CAATGCCACA	AACTCGTGAG	50
	CACATCCTTC	TTTCACGTCA	GGTTGGTGTT	AAACACCTTA	TCGTCTTCAT	100
	GAACAAGATC	GACTTGGTTG	ATGACGAAGA	ATTGCTTGAA	TTGGTTGAAA	150
	TGGAAATCCG	TGACCTCTTG	TCAGAAATACG	ACTTCCCAGG	TGACGATCTT	200
	CCAGTTATCC	AAGGTTTCAGC	TCTTAAAGCT	CTTGAAGGTG	ATACTAAGTA	250
20	CGAAGACATC	ATCATGGAAT	TGATGAACAC	TGTTGATGAG	TACATCCAG	300
	AACCAGAACG	TGATACTGAC	AAACCTCTTC	TTCTTCCAGT	CGAAGACGTA	350
	TTCTCAATCA	CTGGTCGTGG	TACAGTTGCT	TCAGGACGTA	TCGACCGTGG	400
	TACTGTTCGT	GTCAACGATG	AAATCGAAAT	CGTTGGTATC	AAAGAAGAAA	450
	TCCAAAAAGC	AGTTGTTACT	GGTGTGAAA	TGTTCCGTAA	ACAGCTTGAC	500
25	GAAGGTCTTG	CAGGGGACAA	CGTAGGTGTA	CTTCTTCGTG	GTATCCAACG	550
	TGATGAAATC	GAACGTGGTC	AAGTTATCGC	TAAACCAGGT	TCAATCAACC	600
	CACACACTAA	ATTCAAGGGT	GAAGTTTACA	TCCTTACTAA	AGAAGAAGGT	650
	GGACGTCACA	CTCCATTCTT	CAACAACACTAC	CGTCCACAGT	TCTACTTCCG	700
	TACAACCTGAC	GTTACAGGTT	CAATCGAACT	TCCAGCAGGT	ACTGAAATGG	750
30	TAATGCCTGG	TGATAACGTA	ACTATCGACG	TTGAGTTGAT	CCACCCAATC	800
	GCCGTTGAAC	AAGG				814

35 2) INFORMATION FOR SEQ ID NO: 983

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 810 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus mitis*
 (B) STRAIN: ATCC 49456

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 983

50	CTATCCTTGT	AGTAGCTTCA	ACTGACGGAC	CAATGCCACA	AACTCGTGAG	50
	CACATCCTTC	TTTCACGTCA	GGTTGGTGTT	AAACACCTTA	TCGTCTTCAT	100
	GAACAAAGTT	GACTTGGTTG	ACGACGAAGA	ATTGCTTGAA	TTGGTTGAAA	150
	TGGAAATCCG	TGACCTATTG	TCAGAAATACG	ACTTCCCAGG	TGACGATCTT	200
55	CCAGTTATCC	AAGGTTTCAGC	TCTTAAAGCC	CTTGAAGGTG	ACACTAAATA	250
	CGAAGACATC	GTTATGGAAT	TGATGAACAC	AGTTGATGAG	TACATCCAG	300
	AACCAGAACG	TGACACTGAC	AAACCATTCG	TTCTTCCAGT	CGAAGACGTA	350
	TTCTCAATCA	CTGGTCGTGG	TACAGTTGCT	TCAGGACGTA	TCGACCGTGG	400
	TATCGTTAAA	GTCAACGACG	AAATCGAAAT	CGTTGGTATC	AAAGAAGAAA	450
60	CTCAAAAAGC	AGTTGTTACT	GGTGTGAAA	TGTTCCGTAA	ACAACCTTGAC	500

	GAAGGTCTTG	CCGGAGATAA	TGTAGGTGTC	CTTCTTCGTG	GTGTTCAACG	550
	TGATGAAATC	GAACGTGGAC	AAGTTATTGC	TAAACCAGGT	TCAATCAACC	600
	CACACACTAA	ATTCAAAGGT	GAAGTTTACA	TCCTTACTAA	AGAAGAAGGT	650
	GGACGTCACA	CTCCATTCTT	CAACAACACTAC	CGTCCACAAT	TCTACTTCCG	700
5	TACTACTGAC	GTTACAGGTT	CAATCGAACT	TCCAGCAGGT	ACTGAAATGG	750
	TAATGCCTGG	TGATAACGTG	ACAATCGACG	TTGAGTTGAT	CCACCCAATC	800
	GCCGTAGAAC					810

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2) INFORMATION FOR SEQ ID NO: 984

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 817 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Streptococcus mitis*
- (B) STRAIN: ATCC 903
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 984

	TCCTTGTAGT	AGCTTCAACT	GACGGACCAA	TGCCACAAAC	TCGTGAGCAC	50
	ATCCTTCTTT	CACGTCAGGT	TGGTGTTAAA	CACCTTATCG	TCTTCATGAA	100
	CAAGATCGAC	TTGGTTGATG	ACGAAGAATT	GCTTGAATTG	GTTGAAATGG	150
30	AAATCCGTGA	CCTCTTGTC	GAATACGACT	TCCCAGGTGA	CGATCTTCCA	200
	GTTATCCAAG	GTTTCAGCTCT	TAAAGCTCTT	GAAGGTGATA	CTAAGTACGA	250
	AGACATCATC	ATGGAATTGA	TGAACACTGT	TGATGAGTAC	ATCCCAGAAC	300
	CAGAACGTGA	TACTGACAAA	CCTCTTCTTC	TTCCAGTCGA	AGACGTATTC	350
	TCAATCACTG	GTCGTGGTAC	AGTTGCTTCA	GGACGTATCG	ACCGTGGTAC	400
35	TGTTTCGTGTC	AACGATGAAA	TCGAAATCGT	TGGTATCAAA	GAAGAAATCC	450
	AAAAAGCAGT	TGTTACTGGT	GTTGAAATGT	TCCGTAAACA	GCTTGACGAA	500
	GGTCTTGACG	GGGACAACGT	AGGTGTA	CTTCGTGGTA	TCCAACGTGA	550
	TGAAATCGAA	CGTGGTCAAG	TTATCGCTAA	ACCAGGTTCA	ATCAACCCAC	600
	ACACTAAATT	CAAGGGTGAA	GTTTACATCC	TTACTAAAGA	AGAAGGTGGA	650
40	CGTCACACTC	CATTCTTCAA	CAACTACCGT	CCACAGTTCT	ACTTCCGTAC	700
	AACTGACGTT	ACAGGTTCAA	TCGAACTTCC	AGCAGGTACT	GAAATGGTAA	750
	TGCCTGGTGA	TAACGTA	ATCGACGTTG	AGTTGATCCA	CCCAATCGCC	800
	GTTGAACAAG	GTACTAC				817

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2) INFORMATION FOR SEQ ID NO: 985

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 798 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Streptococcus oralis*
- (B) STRAIN: ATCC 35037

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 985

	GACGGACCAA	TGCCACAAAC	TCGTGAGCAC	ATCCTTCTTT	CACGTCAGGT	50
	TGGTGTAAAA	CACCTTATTG	TCTTCATGAA	CAAAATTGAC	TTGGTAGACG	100
5	ACGAAGAATT	GCTTGAATTG	GTTGAAATGG	AAATCCGTGA	CCTCTTGTC	150
	GAATACGACT	TCCCAGGTGA	CGATCTTCCA	GTTATCCAAG	GTTTACGCTCT	200
	TAAAGCTCTT	GAAGGTGACT	CTAAATACGA	AGACATCATT	ATGGAATTGA	250
	TGAACACTGT	TGATGAGTAC	ATCCCAGAAC	CAGAACGTGA	CACTGAAAAA	300
	CCATTGCTTC	TTCCAGTCGA	AGACGTATTC	TCAATCACTG	GACGTGGTAC	350
10	AGTTGCTTCA	GGACGTATCG	ACCGTGGTAC	TGTTCTGTGC	AACGACGAAA	400
	TCGAAATCGT	TGGTATCAAA	GAAGAACTC	AAAAAGCAGT	TGTTACTGGT	450
	GTTGAAATGT	TCCGTAAACA	ACTTGACGAA	GGTCTTGCCG	GAGATAACGT	500
	AGGTGTCCTT	CTTCGTGGTG	TTCAACGTGA	CGAAATCGAA	CGTGGACAAG	550
	TTATCGCTAA	ACCAGGTTCA	ATCAACCCAC	ACACTAAATT	TAAAGGTGAA	600
15	GTCTACATCC	TTACTAAAGA	AGAAGGTGGA	CGTCACACTC	CATTCTTCAA	650
	CAACTACCGT	CCACAATTCT	ACTTCCGTAC	TACTGACGTT	ACAGGTTCAA	700
	TCGAACTTCC	TGCAGGTACT	GAAATGGTAA	TGCCTGGTGA	TAACGTGACT	750
	ATCGACGTTG	AGTTGATCCA	CCCAATCGCC	GTAGAACAAG	GTACTACA	798

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2) INFORMATION FOR SEQ ID NO: 986

- (i) SEQUENCE CHARACTERISTICS:
- 25 (A) LENGTH: 815 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear
- 30 (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Streptococcus pneumoniae*
(B) STRAIN: StrR-05
- 35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 986

	TTGTAGTAGC	TTCAACTGAC	GGACCAATGC	CACAACTCG	TGAGCACATC	50
	CTTCTTTCAC	GTCAGGTTGG	TGTTAAACAC	CTTATCGTCT	TCATGAACAA	100
40	AGTTGACTTG	GTTGACGACG	AAGAATTGCT	TGAATTGGTT	GAAATGGAAA	150
	TCCGTGACCT	ATTGTCAGAA	TACGACTTCC	CAGGTGACGA	TCTTCCAGTT	200
	ATCCAAGGTT	CAGCACTTAA	AGCTCTTGAA	GGTGACTCTA	AATACGAAGA	250
	CATCGTTATG	GAATTGATGA	ACACAGTTGA	TGAGTATATT	CCAGAACCAG	300
	AACGTGACAC	TGACAAACCA	TTGCTTCTTC	CAGTCGAGGA	CGTATTCTCA	350
45	ATCACTGGAC	GTGGTACAGT	TGCTTCAGGA	CGTATCGACC	GTGGTATCGT	400
	TAAAGTCAAC	GACGAAATCG	AAATCGTTGG	TATCAAAGAA	GAAACTCAAA	450
	AAGCAGTTGT	TACTGGTGTT	GAAATGTTCC	GTAAACAAC	TGACGAAGGT	500
	CTTGCTGGAG	ATAACGTAGG	TGTCCTTCTT	CGTGGTGTTT	AACGTGATGA	550
	AATCGAACGT	GGACAAGTTA	TCGCTAAACC	AGGTTCAATC	AACCCACACA	600
50	CTAAATTCAA	AGGTGAAGTC	TACATCCTTA	CTAAAGAAGA	AGGTGGACGT	650
	CACACTCCAT	TCTTCAACAA	CTACCGTCCA	CAATTCTACT	TCCGTACTAC	700
	TGACGTTACA	GGTTCAATCG	AACTTCCAGC	AGGTACTGAA	ATGGTAATGC	750
	CTGGTGATAA	CGTGACAATC	GACGTTGAGT	TGATTACCC	AATCGCCGTA	800
	GAACAAGGTA	CTACA				815

55

2) INFORMATION FOR SEQ ID NO: 987

- 60 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 832 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

5

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus hirae*
 (B) STRAIN: ATCC 8043

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 987

	CGGACAATCT	TGGTTGTTTC	TGCTACGGAT	GGCCCAATGC	CTCAAACCTCG	50
15	TGAACACATT	TTACTTTCTC	GCCAAGTAGG	CGTGAAATAT	TTGATTGTTT	100
	TCTTGAACAA	AACAGATTTA	GTCGATGATG	AAGAATTAAT	TGATCTAGTA	150
	GAAATGGAAG	TTCGTGAACT	ATTAAGCGAA	TATGGATTTC	CAGGTGATGA	200
	TACACCTGTT	ATCAAAGGAT	CAGCATTAAG	AGCATTACAA	GGTGATCCTG	250
	ATGCAGAAGC	AGCTATCATG	GAATTGATGG	ACACAGTCGA	TGAATACATC	300
20	CCAACACCAG	AACGTGATAC	GGACAAACCA	TTATTGTTAC	CCGCCGAAGA	350
	TGTATTTTCA	ATTACTGGAC	GTGGAACAGT	AGCATCTGGT	CGGATTGACC	400
	GTGGGGCTGT	TAGAGTCGGT	GACGAAATCG	AAATCGTAGG	GATCAAACCA	450
	GAAACGCAAA	GAGCCGTAGT	AACAGGAGTT	GAAATGTTCC	GCAAAACGCT	500
	TGATTACGGT	GAAGCAGGGG	ATAACGTAGG	TGTGTTATTA	CGTGGGATTC	550
25	AAAGAGAAGA	CATCGAACGT	GGCCAAGTGA	TTGCCAAACC	TGGTTCAATT	600
	ACACCTCATA	CTAAATTCAA	AGCAGAAGTT	TAGGTTTGA	CTAAAGAAGA	650
	AGCGGGACGT	CATACACCAT	TCTTCAATAA	TTATCGACCA	CAATTTTATT	700
	TCCGCACAAC	TGACGTAACA	GGAACAATTG	TTTTGCCAGA	AGGAACGGAA	750
	ATGGTCATGC	CTGGCGACAA	CGTAACGATC	GATGTAGAAT	TGATTCATCC	800
30	TGTTGCTATT	GAAAACGGGA	CGACTTTCTC	CA		832

2) INFORMATION FOR SEQ ID NO: 988

35

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 835 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

40

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus mundtii*
 (B) STRAIN: ATCC 43186

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 988

50	TGGTGCGATC	TTAGTTGTTT	CTGCGACAGA	TGGACCAATG	CCTCAAACCTC	50
	GCGAGCATAT	CCTTTTATCA	CGTCAAGTTG	GTGTAAAATA	TTTGATTGTA	100
	TTTTTGAATA	AAGTTGATTT	GGTCGATGAT	GAAGAATTGA	TCGATCTTGT	150
	AGAAATGGAA	GTTTCGTGAAT	TACTGAATGA	ATATGGTTTC	CCAGGTGATG	200
	ACACACCTGT	CATCAAAGGC	TCTGCATTGA	AAGCATTGCA	AGGTGACCCA	250
55	GAAGCAGAAG	CTGCGATCAA	TGAATTGATG	GAAACAGTGG	ATGACTATAT	300
	CCCAACACCA	GAACGTGATA	CCGACAAACC	ATTGCTTTTA	CCAGTTGAAG	350
	ATGTTTTTCTC	AATCACTGGT	CGCGGAACGG	TAGCATCTGG	TCGTATCGAC	400
	CGTGGAGCCG	TTCGTGTCGG	TGATGAAATC	GAGATCATCG	GAATCAAACC	450
	TGAAACGAAA	AAAGCGGTTG	TGACAGGGGT	AGAGATGTTT	CGTAAAACGT	500
60	TAGATTATGG	CGAAGCTGGA	GATAACGTAG	GAATCTTGTT	ACGTGGTATC	550

550

	CAAAGAGAAG	ATATTGAACG	TGGACAAGTA	ATTGCGAAAC	CTGGTTCAAT	600
	CACACCACAT	ACAAAATTCA	AAGCGGAAGT	TTATGTATTG	ACGAAAGAAG	650
	AAGGCGGACG	TCATACACCA	TTCTTCAATA	ACTACCGCCC	ACAATTTTAT	700
	TTCCGCACAA	CAGATGTAAC	AGGTACGATC	GTGTTGCCAG	AAGGAACAGA	750
5	AATGGTCATG	CCTGGAGACA	ACGTAACCAT	CGAGGTAGAG	TTGATCCATC	800
	CAGTGGCAAT	CGAACAAGGA	ACGACTTTCT	CTATT		835

10 2) INFORMATION FOR SEQ ID NO: 989

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 832 bases
 (B) TYPE: Nucleic acid
 15 (C) STRANDEDNESS: Double,
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

20 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus raffinosus*
 (B) STRAIN: ATCC 49427

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 989

25	TGCGATCTTA	GTAATATCTA	CTACTGATGG	ACCAATGCCT	CAAACACGTG	50
	AGCACATTTT	GTTATCACGC	CAAGTAGGTG	TTAAATACTT	GATCGTCTTC	100
	TTGAACAAAG	TTGATTTAGT	CGACGATGAA	GAATTGATTG	ATTTAGTTGA	150
	AATGGAAGTA	CGTGAGTTAC	TTTCAGAATA	TGGTTTCCCA	GGCGATGATA	200
30	TTCTGTCTCT	TAAAGGTTCA	GCTCTGAAAG	CTTTAGAAGG	CGATCCTGAA	250
	CAAGAACAAG	TAATCATGGA	CCTAATGGAT	ACGGTTGACG	AATATATCCC	300
	AACACCAGAA	CGTGACACTG	ACAAACCATT	CTTGTTACCA	GTGGAAGATG	350
	TTTTCTCAAT	CACAGGACGT	GGGACTGTTG	CATCTGGTCG	TATTGATCGT	400
	GGGGAAGTTA	AAGTCGGTGA	CGAAGTTGAA	ATTATCGGGA	TCAAACCTGA	450
35	AGTTCAAAAG	GCTGTCGTAA	CTGGACTTGA	AATGTTCCGT	AAAACATTGG	500
	ATTATGGTGA	AGCTGGAGAT	AACGTTGGGG	TTCTATTACG	TGGTATTACA	550
	CGTGATGAAA	TCGAACGTGG	TCAAGTATTA	GCTAAACCAG	GTTCAATTAC	600
	ACCACATACG	AAATTCAGTG	CAGAAGTTTA	TGTGTTGACG	AAAGAAGAAG	650
	GTGGACGTCA	TACACCATTG	TTTAACAAC	ATCGTCCTCA	ATTCTACTTC	700
40	CGTACAACAG	ACGTTACCGG	TAATATCGTG	TTGCCAGAAG	GTACTGAAAT	750
	GGTCATGCCT	GGCGATAACG	TAACAATCGA	CGTTGAATTA	ATCCATCCAA	800
	TCGCCGTAGA	AAAAGGAACA	ACTTTCTCTA	TT		832

45

2) INFORMATION FOR SEQ ID NO: 990

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 154 bases
 50 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

55

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacillus anthracis*
 (B) STRAIN: CIP 9440

60 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 990

GGATCCTGTA TATGCACAAA AACTAGGTGT TAACATCGAT GAATTACTAT 50
 TATCACAACC TGATACAGGG GAGCAAGGTT TAGAAATCGC AGAAGCACTT 100
 GTACGAAGTG GTGCGGTTGA TATTATCGTA ATTGACTCTG TAGCAGCTCT 150
 5 TGTA 154

2) INFORMATION FOR SEQ ID NO: 991

10

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 384 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 15 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

20 (A) ORGANISM: *Prevotella melaninogenica*
 (B) STRAIN: ATCC 25845

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 991

25 GCCATTGCAG AGGCACAGAA GCAGGGCGGT ATTGCAGCCT TCATTGATGC 50
 TGAGCACGCC TTCGACCGTT TCTATGCAGA GAAGTTAGGT GTGGATGTTG 100
 ATAACCTTTG GGTTCACAG CCAGACAATG GTGAGCAGGC TTTAGAGATT 150
 GCCGACCAGC TGATTGCTC TTCCGCTATT GACATTCTCG TTGTCGACTC 200
 AGTTGCAGCC TTGACTCCAA AGAAGGAGAT TGAGGGTGAC ATGGGTGACT 250
 30 CTGCAGTAGG TTTACAAGCA CGACTGATGA GTCAGGCATT GCGTAAACTT 300
 ACCTCAACAA TCGCAAAAAC TAATACTTGC TGCATCTTCA TCAACCAGTT 350
 GCGTGAGAAG ATTGGTGTGA TGTTTGGTAA TCCA 384

35

2) INFORMATION FOR SEQ ID NO: 992

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 624 bases
 40 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

45

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Enterococcus casseliflavus*
 (B) STRAIN: R760

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 992

ACACGTGAAC ACATCTTGTT ATCACGTAAC GTTGGTGTAC CATAATCGT 50
 TGTTTTCTTA AACAAAATGG ATATGGTTGA TGACGAAGAA TTAGTAGAAT 100
 TAGTTGAAAT GGAAGTTCGT GACTTATTGT CAGAATATGA CTTCCCAGGC 150
 55 GACGATGTTT CTGTAATCGC TGGTTCGTCT TTGAAAGCTC TTGAAGGCCA 200
 TGCTTCATAC GAAGAAAAAA TCATGGAATT AATGGCTGCA GTTGACGAAT 250
 ACGTTCCAAC TCCAGAACGT GACACTGACA AACCATTTCAT GATGCCAGTC 300
 GAAGACGTAT TCTCAATCAC TGGACGTGGT ACTGTTGCTA CAGGCCGTGT 350
 TGAACGTGGA CAAGTTCGCG TTGGTGACGA AGTTGAAATC GTTGGTATTG 400
 60 CTGAAGAAAC TGCTAAAACA ACTGTAACGT GTGTTGAAAT GTTCCGTAAA 450

TTGTTAGACT	ATGCTGAAGC	AGGGGATAAC	ATTGGTGCAT	TGCTACGTGG	500
TGTTGCTCGT	GAAGACATCC	AACGTGGACA	AGTATTGGCT	AAAGCTGGTA	550
CAATCACACC	TCATACAAAA	TTTAAAGCTG	AAGTTTACGT	TTTAACAAAA	600
GAAGAAGGTG	GACGTCATAC	ACCA			624

5

2) INFORMATION FOR SEQ ID NO: 993

10 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 756 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

15

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pyogenes*
 (C) ACCESSION NUMBER: extracted from U40453

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 993

ATGGAACA	ATAAAAAGT	ATTGAAGAA	ATGGTATTTT	TTGTTTTAGT	50
GACATTTCTT	GGACTAACAA	TCTCGCAAGA	GGTATTTGCT	CAACAAGACC	100
CCGATCCAAG	CCAACCTCAC	AGATCTAGTT	TAGTTAAAAA	CCTTCAAAAT	150
ATATATTTTC	TTTATGAGGG	TGACCCGTGT	ACTCACGAGA	ATGTGAAATC	200
TGTTGATCAA	CTTTTATCTC	ACGATTTAAT	ATATAATGTT	TCAGGGCCAA	250
ATTATGATAA	ATTAAAAACT	GAACCTAAGA	ACCAAGAGAT	GGCAACTTTA	300
TTTAAGGATA	AAAACGTTGA	TATTTATGGT	GTAGAATATT	ACCATCTCTG	350
TTATTTATGT	GAAAATGCAG	AAAGGAGTGC	ATGTATCTAC	GGAGGGGTAA	400
CAAATCATGA	AGGGAATCAT	TTAGAAATTC	CTAAAAAGAT	AGTCGTTAAA	450
GTATCAATCG	ATGGTATCCA	AAGCCTATCA	TTTGATATTG	AAACAAATAA	500
AAAAATGGTA	ACTGCTCAAG	AATTAGACTA	TAAAGTTAGA	AAATATCTTA	550
CAGATAATAA	GCAACTATAT	ACTAATGGAC	CTTCTAAATA	TGAAACTGGA	600
TATATAAAGT	TCATACCTAA	GAATAAAGAA	AGTTTTTGGT	TTGATTTTTT	650
CCCTGAACCA	GAATTTACTC	AATCTAAATA	TCTTATGATA	TATAAAGATA	700
ATGAAACGCT	TGACTCAAAC	ACAAGCCAAA	TTGAAGTCTA	CCTAACCAACC	750
AAGTAA					756

40

2) INFORMATION FOR SEQ ID NO: 994

45 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 994

55 TGGACTAACA ATCTCGCAAG AGG

23

2) INFORMATION FOR SEQ ID NO: 995

60

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 22 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
5 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 995

10 ACATTCTCGT GAGTAACAGG GT 22

- 15 2) INFORMATION FOR SEQ ID NO: 996

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 25 bases
 (B) TYPE: Nucleic acid
20 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

- 25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 996

 ACAAATCATG AAGGGAATCA TTTAG 25

- 30 2) INFORMATION FOR SEQ ID NO: 997

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 23 bases
35 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

- 40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 997

 CTAATTCTTG AGCAGTTACC ATT 23

- 45 2) INFORMATION FOR SEQ ID NO: 998

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 23 bases
50 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

55 (ii) MOLECULE TYPE: DNA

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 998

60 GGAGGGGTAA CAAATCATGA AGG 23

2) INFORMATION FOR SEQ ID NO: 999

- 5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
10 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 999

15 TTGACCTTGT TGATGACGAA GAG

23

2) INFORMATION FOR SEQ ID NO: 1000

- 20 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
25 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1000

30 TTAGTGTGTG GGTGATTGA ACT

23

35 2) INFORMATION FOR SEQ ID NO: 1001

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 bases
(B) TYPE: Nucleic acid
40 (C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1001

AAGAGTTGCT TGAATTAGTT GAG

23

50

2) INFORMATION FOR SEQ ID NO: 1002

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 894 bases
55 (B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

60

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pyogenes*

(B) STRAIN: ATCC 700294

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1002

	AACATGATCA	CTGGTGCCGC	TCAAATGGAC	GGAGCTATCC	TTGTAGTTGC	50
	TTCAACTGAT	GGACCAATGC	CACAACTCG	TGAGCACATC	CTTCTTTTCAC	100
	GTCAGGTTGG	TGTTAAACAC	CTTATCGTGT	TCATGAACAA	AGTTGACCTT	150
10	GTTGATGACG	AAGAGTTGCT	TGAATTAGTT	GAGATGGAAA	TTCGTGACCT	200
	TCTTTTCAGAA	TACGATTTCC	CAGGTGATGA	CCTTCCAGTT	ATCCAAGGTT	250
	CAGCTCTTAA	AGCTCTTGAA	GGCGACACTA	AATTGGAAGA	CATCATCATG	300
	GAATTGATGG	ATACTGTTGA	TTCATACATT	CCAGAACCAG	AACGCGACAC	350
	TGACAAACCA	TTGCTTCTTC	CAGTCGAAGA	CGTATTCTCA	ATTACAGGTC	400
15	GTGGTACAGT	TGCTTCAGGA	CGTATCGACC	GTGGTACTGT	TCGTGTCAAC	450
	GACGAAATCG	AAATCGTTGG	TATCAAAGAA	GAAACTAAAA	AAGCTGTTGT	500
	TACTGGTGTT	GAAATGTTCC	GTAAACAAC	TGACGAAGGT	CTTGCAGGAG	550
	ACAACGTAGG	TATCCTTCTT	CGTGGTGTTT	AACGTGACGA	AATCGAACGT	600
	GGTCAAGTTA	TTGCTAAACC	AAGTTCAATC	AACCCACACA	CTAAATTCAA	650
20	AGGTGAAGTA	TATATCCTTT	CTAAAGACGA	AGGTGGACGT	CACACTCCAT	700
	TCTTCAACAA	CTACCGTCCA	CAATTCTACT	TCCGTACAAC	TGACGTAACA	750
	GGTTCAATCG	AACCTCCAGC	AGGTACAGAA	ATGGTTATGC	CTGGTGATAA	800
	CGTGACAATC	AACGTTGAGT	TGATCCACCC	AATCGCCGTA	GAACAAGGTA	850
	CTACTTTCTC	AATCCGTGAA	GGTGGACGTA	CTGTTGGTTC	AGGT	894

25

2) INFORMATION FOR SEQ ID NO: 1003

30 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 332 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Bacillus cereus*

40

(B) STRAIN: ATCC 14579

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1003

	AATGGATCCT	GTATATGCAC	AAAAATTAGG	CGTTAACATA	GATGAATTAC	50
45	TATTATCACA	GCCTGATACA	GGGGAGCAAG	GATTAGAAAT	CGCGGAAGCA	100
	CTTGACGAA	GTGGTGCGGT	TGACATTATC	GTAATTGACT	CTGTAGCAGC	150
	TCTTGACCG	AAAGCAGAGA	TTGAAGGCCA	CATGGGTGAC	TCACACGTAG	200
	GTTTACAAGC	ACGTTTAATG	TCACAAGCAC	TTCGTAAGCT	TTCAGGAGCA	250
	ATCAACAAAT	CAAAAACAAT	TGCAATCTTT	ATTAACCAAA	TTCGTGAAAA	300
50	AGTTGGGGTT	ATGTTTCGAA	ACCCAGAAAC	AA		332

55

2) INFORMATION FOR SEQ ID NO: 1004

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1212 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

60

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 5 (A) ORGANISM: *Streptococcus pneumoniae*
(B) STRAIN: StrR-01

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1004

10	ACCAAGAAGC	TCAAAAACAT	CTGTGGGATA	TCTACAACTC	CGATCAATAC	50
	GTCTCTTACC	CTGACGATGA	TTTGCAAGTC	GCATCTACGG	TCGTAGATGT	100
	TTCAAATGGT	AAAGTCATCG	CCCAACTTGG	AGCTCGTCAC	CAAGCAAGTA	150
	ACGTTTCATT	TGGTACCAAC	CAAGCTGTGG	AAACCAATCG	TGACTGGGGT	200
	TCTGCTATGA	AACCAATCAC	CGATTATGCA	CCTGCCATAG	AATACGGTGT	250
15	TTATGATTCC	ACTGCAACTA	TGGTTAATGA	TATTCCTTAT	AACTATCCGG	300
	GAACAAGCAC	ACCTGTCTAC	AACTGGGATA	GAGCATATTT	CGGTAATATT	350
	ACTCTGCAAT	ATGCTCTTCA	ACAATCACGA	AATGTCACAG	CCGTTGAGAC	400
	TTTGAATAAG	GTCGGTCTAG	ATAGAGCTAA	AACCTTCCTT	AATGGTCTTG	450
	GTATCGACTA	TCCAAGCATG	CATTATGCAA	ACGCCATTTT	AAGTAATACA	500
20	ACAGAATCTA	ATAAACAATA	CGGAGCAAGT	AGTGAAAAAA	TGGCTGCTGC	550
	TTATGCTGCC	TTTGCAATG	GTGGCACTTA	CTATAAACCA	ATGTATATCC	600
	ATAAAGTCGT	CTTCAGTGAT	GGAAGTAAAA	AAGAGTTCTC	TAATGTCGGA	650
	ACTCGTGCCA	TGAAGGAAAC	GACAGCCTAT	ATGATGACCG	ACATGATGAA	700
	AACAGTCTTG	ACTTATGGAA	CTGGGCGTGG	AGCCTATCTT	CCTTGGCTTC	750
25	CTCAAGCTGG	TAAAACAGGA	ACCTCTAACT	ATACAGATGA	GGAAGTTGAA	800
	AACCACATCA	AGAACACTGG	CTATGTAGCT	CCAGATGAAA	TGTTTGTTGG	850
	TTATACTCGT	AAGTATTCTA	TGGCTGTATG	GACAGGTTAT	TCGAATCGTT	900
	TAACTCCTAT	CGTTGGAGAT	GGTTTCCTAG	TTGCAGCTAA	AGTTTATCGC	950
	TCAATGATAA	CGTATCTATC	AGAAGATACT	CATCCAGAAG	ACTGGACGAT	1000
30	GCCAGACGGA	CTTTTCAGAA	ACGGGGAATT	TGTATTCAAA	AATGGAGCTC	1050
	GCCCAATATG	GACTGAACCC	TCTACTCAAC	AATCCTCAAC	AGCTGAAAGT	1100
	TCAAGCTCAT	CATCAGATAG	TTCAACTTCA	CAGTCTAGCT	CAACCACTCC	1150
	AAGCACAAAT	AATAGTACGA	CTACCAATCC	TAACAATAAT	ACGCAACAAT	1200
	CAAATACAAC	CC				1212

2) INFORMATION FOR SEQ ID NO: 1005

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1212 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 50 (A) ORGANISM: *Streptococcus pneumoniae*
(B) STRAIN: StrR-02

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1005

	AAGCTCAAAA	ACATCTGTGG	GATATCTACA	ACTCCGATCA	ATACGTCTCT	50
55	TACCCTGACG	ATGATTTGCA	AGTCGCATCT	ACGGTCGTAG	ATGTTTCAAA	100
	TGGTAAAGTC	ATCGCCCAAC	TTGGAGCTCG	TCACCAAGCA	AGTAACGTTT	150
	CATTTGGTAC	CAACCAAGCT	GTGGAAACCA	ATCGTGACTG	GGGTTCTGCT	200
	ATGAAACCAA	TCACCGATTA	TGCACCTGCC	ATAGAATACG	GTGTTTATGA	250
	TTCCACTGCA	ACTATGGTTA	ATGATATTCC	TTATAACTAT	CCGGGAACAA	300
60	GCACACCTGT	CTACAACTGG	GATAGAGCAT	ATTTCCGTAA	TATTACTCTG	350

	CAATATGCTC	TTCAACAATC	ACGAAATGTC	ACAGCCGTTG	AGACTTTGAA	400
	TAAGGTCGGT	CTAGATAGAG	CTAAAACCTT	CCTTAATGGT	CTTGGTATCG	450
	ACTATCCAAG	CATGCATTAT	GCAAACGCCA	TTTCAAGTAA	TACAACAGAA	500
	TCTAATAAAC	AATACGGAGC	AAGTAGTGAA	AAAATGGCTG	CTGCTTATGC	550
5	TGCCTTTGCC	AACGGTGGAA	TTTACCACAA	ACCCATGTAT	ATCAATAAGG	600
	TCGTCTTCAG	TGACGGTAGT	AAAAAAGAAT	TTTCAGATGT	AGGTACACGA	650
	GCTATGAAAG	AAACAACCTG	TTACATGATG	ACCGAAATGA	TGAAAACCTGT	700
	CTTGGCATA	GGAACCTGGT	GTGGAGCCTA	TCTCCCATGG	TTAGCGCAAG	750
	CTGGTAAGAC	AGGTACTTCT	AACTACACAG	ATGATGAAAT	TGAAAAACAC	800
10	ATCAAGAACA	CTGGCTATGT	AGCTCCAGAT	GAAATGTTTG	TTGGTTATAC	850
	TCGTAAGTAT	TCTATGGCTG	TATGGACAGG	TTATTCTGAAT	CGTTTAACTC	900
	CTATCGTTGG	AGATGGTTTC	CTAGTTGCAG	CTAAAGTTTA	TCGCTCAATG	950
	ATAACGTATC	TGTCTGAAGG	AAGCAATCCA	GAGGATTGGA	ATATACCAGA	1000
	GGGGCTCTAC	AGAAATGGAG	AATTCGTATT	TAAAAATGGT	GCTCGTTCTA	1050
15	CGTGGAGCTC	ACCTGCTCCA	CAACAACCCC	CATCAACTGA	AAGTTCAAGC	1100
	TCATCATCAG	ATAGTTCAAC	TTCACAGTCT	AACTCAACCA	CTCCAAGCAC	1150
	AAATAATAGT	ACGACTACCA	ATCCTAACAA	TAATACGCAA	CAATCAAATA	1200
	CAACCCCTGA	TC				1212

20

2) INFORMATION FOR SEQ ID NO: 1006

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 1213 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

30 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
 (B) STRAIN: StrR-03

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1006

	ACCAAGAAGC	TCAAAAACAT	CTGTGGGATA	TCTACAACTC	CGATCAATAC	50
	GTCTCTTACC	CTGACGATGA	TTTGCAAGTC	GCATCTACGG	TCGTAGATGT	100
40	TTCAAATGGT	AAAGTCATCG	CCCAACTTGG	AGCTCGTCAC	CAAGCAAGTA	150
	ACGTTTCATT	TGGTACCAAC	CAAGCTGTGG	AAACCAATCG	TGACTGGGGT	200
	TCTGCTATGA	AACCAATCAC	CGATTATGCA	CCTGCCATAG	AATACGGTGT	250
	TTATGATTCC	ACTGCAACTA	TGGTTAATGA	TATTCCTTAT	AACTATCCGG	300
	GAACAAGCAC	ACCTGTCTAC	AACTGGGATA	GAGCATATTT	CGGTAATATT	350
45	ACTCTGCAAT	ATGCTCTTCA	ACAATCACGA	AATGTCACAG	CCGTTGAGAC	400
	TTTGAATAAG	GTCGGTCTAG	ATAGAGCTAA	AACCTTCCTT	AATGGTCTTG	450
	GTATCGACTA	TCCAAGCATG	CATTATGCAA	ACGCCATTTC	AAGTAATACA	500
	ACAGAATCTA	ATAAACAATA	CGGAGCAAGT	AGTGAAAAAA	TGGCTGCTGC	550
	TTATGCTGCC	TTTGCCAACG	GTGGAATTTA	CCACAAACCC	ATGTATATCA	600
50	ATAAGGTCGT	CTTCAGTGAC	GGTAGTAAAA	AAGAATTTTC	AGATGTAGGT	650
	ACACGAGCTA	TGAAAGAAAC	AACTGCTTAC	ATGATGACCG	AAATGATGAA	700
	AACTGTCTTG	GCATACGGAA	CTGGTCTGTG	AGCCTATCTC	CCATGGTTAG	750
	CGCAAGCTGG	TAAGACAGGT	ACTTCTAACT	ACACAGATGA	TGAAATTGAA	800
	AAACACATCA	AGAACACTGG	CTATGTAGCT	CCAGATGAAA	TGTTTGTGTTG	850
55	TTATACTCGT	AAGTATTCTA	TGGCTGTATG	GACAGGTAT	TCGAATCGTT	900
	TAACTCCTAT	CGTTGGAGAT	GGTTTCCTAG	TTGCAGCTAA	AGTTTATCGC	950
	TCAATGATAA	CGTATCTGTC	TGAAGGAAGC	AATCCAGAGG	ATTGGAATAT	1000
	ACCAGAGGGG	CTCTACAGAA	ATGGAGAATT	CGTATTTAAA	AATGGTGTCTC	1050
	GTTCTACGTG	GAGCTCACCT	GCTCCACAAC	AACCCCATC	AACTGAAAGT	1100
60	TCAAGCTCAT	CATCAGATAG	TTCAACTTCA	CAGTCTAACT	CAACCACTCC	1150

AAGCACAAAT AATAGTACGA CTACCAATCC TAACAATAAT ACGCAACAAT 1200
 CAAATACAAC CCC 1213

5

2) INFORMATION FOR SEQ ID NO: 1007

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1218 bases
 10 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

- 15 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
 (B) STRAIN: StrR-04

- 20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1007

	ACCAAGAAGC	TCAAAAACAT	CTGTGGGATA	TCTACAACCTC	CGATCAATAC	50
	GTCTCTTACC	CTGACGATGA	TTTGCAAGTC	GCATCTACGG	TCGTAGATGT	100
	TTCAAATGGT	AAAGTCATCG	CCCAACTTGG	AGCTCGTCAC	CAAGCAAGTA	150
25	ACGTTTCATT	TGGTACCAAC	CAAGCTGTGG	AAACCAATCG	TGACTGGGGT	200
	TCTGCTATGA	AACCAATCAC	CGATTATGCA	CCTGCCATAG	AATACGGTGT	250
	TTATGATTCC	ACTGCAACTA	TGGTTAATGA	TATTCCTTAT	AACTATCCGG	300
	GAACAAGCAC	ACCTGTCTAC	AACTGGGATA	GAGCATATTT	CGGTAATATT	350
	ACTCTGCAAT	ATGCTCTTCA	ACAATCACGA	AATGTCACAG	CCGTTGAGAC	400
30	TTTGAATAAG	GTCGGTCTAG	ATAGAGCTAA	AACCTTCCTT	AATGGTCTTG	450
	GTATCGACTA	TCCAAGCATG	CATTATGCAA	ACGCCATTTC	AAGTAATACA	500
	ACAGAATCTA	ATAAACAATA	CGGAGCAAGT	AGTGAAAAAA	TGGCTGCTGC	550
	TTATGCTGCC	TTTGCAAATG	GTGGCACTTA	CTATAAACCA	ATGTATATCC	600
	ATAAAGTCGT	CTTCAGTGAT	GGAAGTAAAA	AAGAGTTCTC	TAATGTCGGA	650
35	ACTCGTGCCA	TGAAGGAAAC	GACAGCCTAT	ATGATGACCG	ACATGATGAA	700
	AACAGTCTTG	ACTTATGGAA	CTGGGCGTGG	AGCCTATCTT	CCTTGGCTTC	750
	CTCAAGCTGG	TAAACAGGA	ACCTCTAACT	ATACAGATGA	GGAAGTTGAA	800
	AACCACATCA	AGAACACTGG	CTATGTAGCT	CCAGATGAAA	TGTTTGTGG	850
	TTATACTCGT	AAGTATTCTA	TGGCTGTATG	GACAGGTTAT	TCGAATCGTT	900
40	TAACTCCTAT	CGTTGGAGAT	GGTTTCCTAG	TTGCAGCTAA	AGTTTATCGC	950
	TCAATGATAA	CGTATCTATC	AGAAGATACT	CATCCAGAAG	ACTGGACGAT	1000
	GCCAGACGGA	CTTTTCAGAA	ACGGGGAATT	TGTATTCAAA	AATGGAGCTC	1050
	GCCCAATATG	GACTGAACCC	TCTACTCAAC	AATCCTCAAC	AGCTGAAAGT	1100
	TCAAGCTCAT	CATCAGATAG	TTCAACTTCA	CAGTCTAGCT	CAACCACTCC	1150
45	AAGCACAAAT	AATAGTACGA	CTACCAATCC	TAACAATAAT	ACGCAACAAT	1200
	CAAATACAAC	CCCTGATC				1218

50 2) INFORMATION FOR SEQ ID NO: 1008

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1223 bases
 55 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

- (ii) MOLECULE TYPE: Genomic DNA

- 60 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(B) STRAIN: StrR-05

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1008

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5   GTAGACCAAG AAGCTCAAAA ACATCTGTGG GATATCTACA ACTCCGATCA      50
    ATACGTCTCT TACCCTGACG ATGATTGCA AGTCGCATCT ACGGTCGTAG      100
    ATGTTTCAAA TGGTAAAGTC ATCGCCCAAC TTGGAGCTCG TCACCAAGCA      150
    AGTAACGTTT CATTTGGTAC CAACCAAGCT GTGGAAACCA ATCGTGA CTG      200
10  GGGTTCTGCT ATGAAACCAA TCACCGATTA TGCACCTGCC ATAGAATACG      250
    GTGTTTATGA TTCCACTGCA ACTATGGTTA ATGATATTCC TTATAACTAT      300
    CCGGGAACAA GCACACCTGT CTACAACCTGG GATAGAGCAT ATTTCCGGTAA      350
    TATTACTCTG CAATATGCTC TTCAACAATC ACGAAATGTC ACAGCCGTTG      400
    AGACTTTGAA TAAGGTCGGT CTAGATAGAG CTAAAACCTT CCTTAATGGT      450
15  CTTGGTATCG ACTATCCAAG CATGCATTAT GCAAACGCCA TTTCAAGTAA      500
    TACAACAGAA TCTAATAAAC AATACGGAGC AAGTAGTGAA AAAATGGCTG      550
    CTGCTTATGC TGCCTTTGCA AATGGTGGCA CTTACTATAA ACCAATGTAT      600
    ATCCATAAAG TCGTCTTCAG TGATGGAAGT AAAAAAGAGT TCTCTAATGT      650
    CGGAACCTCG GCCATGAAGG AAACGACAGC CTATATGATG ACCGACATGA      700
20  TGAAAACAGT CTTGACTTAT GGAACCTGCG GTGGAGCCTA TCTTCCTTGG      750
    CTTCTCAAG CTGGTAAAAC AGGAACCTCT AACTATACAG ATGAGGAAGT      800
    TGAAAACCAC ATCAAGAACA CTGGCTATGT AGCTCCAGAT GAAATGTTTG      850
    TTGGTTATAC TCGTAAGTAT TCTATGGCTG TATGGACAGG TTATTCTGAAT      900
    CGTTTAACTC CTATCGTTGG AGATGGTTTC CTAGTTGCAG CTAAAGTTTA      950
25  TCGCTCAATG ATAACGTATC TATCAGAAGA TACTCATCCA GAAGACTGGA      1000
    CGATGCCAGA CGGACTTTTC AGAAACGGGG AATTGTATT CAAAAATGGA      1050
    GCTCGCCCAA TATGGACTGA ACCCTCTACT CAACAATCCT CAACAGCTGA      1100
    AAGTTCAAGC TCATCATCAG ATAGTTCAAC TTCACAGTCT AGCTCAACCA      1150
    CTCCAAGCAC AAATAATAGT ACGACTACCA ATCCTAACAA TAATACGCAA      1200
30  CAATCAAATA CAACCCCTGA TCA                                1223

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2) INFORMATION FOR SEQ ID NO: 1009

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35  (i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 1214 bases
    (B) TYPE: Nucleic acid
    (C) STRANDEDNESS: Double
40  (D) TOPOLOGY: Linear

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(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

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45  (A) ORGANISM: Streptococcus pneumoniae
    (B) STRAIN: StrR-06

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1009

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50  ACCAAGAAGC TCAAAAACAT CTGTGGGATA TCTACAACTC CGATCAATAC      50
    GTCTCTTACC CTGACGATGA TTTGCAAGTC GCATCTACGG TCGTAGATGT      100
    TTCAAATGGT AAAGTCATCG CCAACTTGG AGCTCGTCAC CAAGCAAGTA      150
    ACGTTTCATT TGGTACCAAC CAAGCTGTGG AAACCAATCG TGA CTGGGGT      200
    TCTGCTATGA AACCAATCAC CGATTATGCA CCTGCCATAG AATACGGTGT      250
55  TTATGATTCC ACTGCAACTA TGGTTAATGA TATTCCTTAT AACTATCCGG      300
    GAACAAGCAC ACCTGTCTAC AACTGGGATA GAGCATATTT CCGTAATATT      350
    ACTCTGCAAT ATGCTCTTCA ACAATCACGA AATGTCACAG CCGTTGAGAC      400
    TTTGAATAAG GTCGGTCTAG ATAGAGCTAA AACCTTCCTT AATGGTCTTG      450
    GTATCGACTA TCCAAGCATG CATTATGCAA ACGCCATTTT AAGTAATACA      500
60  ACAGAATCTA ATAAACAATA CGGAGCAAGT AGTGAAAAAA TGGCTGCTGC      550

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	TTATGCTGCC	TTTGCAAATG	GTGGCACTTA	CTATAAACCA	ATGTATATCC	600
	ATAAAGTCGT	CTTCAGTGAT	GGAAGTAAAA	AAGAGTTCTC	TAATGTCGGA	650
	ACTCGTGCCA	TGAAGGAAAC	GACAGCCTAT	ATGATGACCG	ACATGATGAA	700
	AACAGTCTTG	ACTTATGGAA	CTGGGCGTGG	AGCCTATCTT	CCTTGGCTTC	750
5	CTCAAGCTGG	TAAAACAGGA	ACCTCTAACT	ATACAGATGA	GGAAGTTGAA	800
	AACCACATCA	AGAACACTGG	CTATGTAGCT	CCAGATGAAA	TGTTTGTGG	850
	TTATACTCGT	AAGTATTCTA	TGGCTGTATG	GACAGGTTAT	TCGAATCGTT	900
	TAACTCCTAT	CGTTGGAGAT	GGTTTCCTAG	TTGCAGCTAA	AGTTTATCGC	950
	TCAATGATAA	CGTATCTATC	AGAAGATACT	CATCCAGAAG	ACTGGACGAT	1000
10	GCCAGACGGA	CTTTTCAGAA	ACGGGGAATT	TGTATTCAAA	AATGGAGCTC	1050
	GCCCAATATG	GACTGAACCC	TCTACTCAAC	AATCCTCAAC	AGCTGAAAGT	1100
	TCAAGETCAT	CATCAGATAG	TTCAACTTCA	CAGTCTAGCT	CAACCACTCC	1150
	AAGCACAAAT	AATAGTACGA	CTACCAATCC	TAACAATAAT	ACGCAACAAT	1200
	CAAATACAAC	CCCT				1214
15						

2) INFORMATION FOR SEQ ID NO: 1010

20 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1223 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

25 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
 30 (B) STRAIN: StrR-07

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1010

	CCAAGAAGCT	CAAAAACATC	TGTGGGATAT	CTACAACTCC	GATCAATACG	50
35	TCTCTTACCC	TGACGATGAT	TTGCAAGTCG	CATCTACGGT	CGTAGATGTT	100
	TCAAATGGTA	AAGTCATCGC	ACAACCTGGT	GCTCGTCATC	AAGCAAGTAA	150
	TGTTTCATTC	GGTACCAACC	AGGCCGTAGA	AACCAATCGT	GACTGGGGAT	200
	CATCAATGAA	ACCAATCACT	GACTATGCTC	CCGCTTTAGA	ATATGGAGTC	250
	TATGACTCTA	CTGCTTCTAT	TGTACATGAT	GTCCCTTATA	ACTATCCTGG	300
40	CACTGATACT	CCACTCTACA	ACTGGGATCA	TGTCTACTTT	GGAAACATTA	350
	CAATCCAGTA	TGCTCTTCAA	CAATCACGAA	ATGTCACAGC	CGTTGAGACT	400
	TTGAATAAGG	TCGGTCTAGA	TAGAGCTAAA	ACCTTCCTTA	ATGGTCTTGG	450
	TATCGACTAT	CCAAGCATGC	ATTATGCAAA	CGCCATTTCA	AGTAACACAA	500
	CTGAATCCAA	CAAAAAATAT	GGTGCAAGTA	GTGAAAAAAT	GGCTGCTGCC	550
45	TACGCTGCTT	TTGCTAATGG	TGGTATTTAT	CACAAACCAA	TGTATATCAA	600
	TAAAATCGTC	TTTAGTGATG	GTAGCGAAAA	AGAATTTTCT	GATGCTGGTA	650
	CACGAGCTAT	GAAAGAGACT	ACTGCCCTATA	TGATGACTGA	AATGATGAAA	700
	ACTGTTTTAA	CTTACGGAAC	AGGACGTGGA	GCCTACCTAC	CATGGCTTCC	750
	ACAAGCAGGT	AAGACAGGTA	CTTCTAACTA	TACTGACGAA	GAAATTGAAA	800
50	AGTATATCAA	GAACACTGGT	TACGTAGCTC	CAGATGAAAT	GTTTGTAGGG	850
	TATACCCGTA	AATATGCAAT	GGCTGTTTGG	ACAGGATACT	CAAATCGTCT	900
	AACTCCAATC	ATCGGAGATG	GTTTCCTTGT	TGCTGGTAAA	GTCTATCGTT	950
	CAATGATAAC	TTACCTTTCT	GAAGATGACC	AACCTGGAGA	TTGGACAATG	1000
	CCAGATGGCT	TGTATAGAAA	TGGAGAATTC	GTATTTAAAA	ATGGTGCTCG	1050
55	TTCTACGTGG	AGCTCACCTG	CTCCACAACA	ACCCCATCA	ACTGAAAGTT	1100
	CAAGCTCATC	ATCAGATAGT	TCAACTTCAC	AGTCTAACTC	AACCACTCCA	1150
	AGCACAAATA	ATAGTACGAC	TACCAATCCT	AACAATAATA	CGCAACAATC	1200
	AAATACAACC	CCTGATCAAC	AAA			1223

2) INFORMATION FOR SEQ ID NO: 1011

- (i) SEQUENCE CHARACTERISTICS:
- 5 (A) LENGTH: 1207 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

10 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
- (B) STRAIN: StrR-08

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1011

	AAGCTCAAAA	ACATCTGTGG	GATATCTACA	ACTCCGATCA	ATACGTCTCT	50
	TACCCTGACG	ATGATTGCA	AGTCGCATCT	ACGGTCGTAG	ATGTTTCAAA	100
20	TGGTAAAGTC	ATCGCCCAAC	TTGGAGCTCG	TCACCAAGCA	AGTAACGTTT	150
	CATTTGGTAC	CAACCAAGCT	GTGGAAACCA	ATCGTGACTG	GGGTTCTGCT	200
	ATGAAACCAA	TCACCGATTA	TGCACCTGCC	ATAGAATACG	GTGTTTATGA	250
	TTCCACTGCA	ACTATGGTTA	ATGATATTCC	TTATAACTAT	CCGGGAACAA	300
	GCACACCTGT	CTACAACCTG	GATAGAGCAT	ATTTTCGGTAA	TATTACTCTG	350
25	CAATATGCTC	TTCAACAATC	ACGAAATGTC	ACAGCCGTTG	AGACTTTGAA	400
	TAAGGTCGGT	CTAGATAGAG	CTAAACCTT	CCTTAATGGT	CTTGGTATCG	450
	ACTATCCAAG	CATGCATTAT	GCAAACGCCA	TTTCAAGTAA	TACAACAGAA	500
	TCTAATAAAC	AATACGGAGC	AAGTAGTGAA	AAAATGGCTG	CTGCTTATGC	550
	TGCCTTTGCA	AATGGTGGCA	CTTACTATAA	ACCAATGTAT	ATCCATAAAG	600
30	TCGTCTTCAG	TGATGGAAGT	AAAAAAGAGT	TCTCTAATGT	CGGAACTCGT	650
	GCCATGAAGG	AAACGACAGC	CTATATGATG	ACCGACATGA	TGAAAACAGT	700
	CTTGACTTAT	GGAACCTGGC	GTGGAGCCTA	TCTTCCTTGG	CTTCCTCAAG	750
	CTGGTAAAAC	AGGAACCTCT	AACTATACAG	ATGAGGAAGT	TGAAAACCAC	800
	ATCAAGAACA	CTGGCTATGT	AGCTCCAGAT	GAAATGTTTG	TTGGTTATAC	850
35	TCGTAAGTAT	TCTATGGCTG	TATGGACAGG	TTATTCGAAT	CGTTTAACTC	900
	CTATCGTTGG	AGATGGTTTC	CTAGTTGCAG	CTAAAGTTTA	TCGCTCAATG	950
	ATAACGTATC	TATCAGAAGA	TACTCATCCA	GAAGACTGGA	CGATGCCAGA	1000
	CGGACTTTTC	AGAAACGGGG	AATTTGTATT	CAAAAATGGA	GCTCGCCCAA	1050
	TATGGACTGA	ACCCTCTACT	CAACAATCCT	CAACAGCTGA	AAGTTCAAGC	1100
40	TCATCATCAG	ATAGTTCAAC	TTCACAGTCT	AGCTCAACCA	CTCCAAGCAC	1150
	AAATAATAGT	ACGACTACCA	ATCCTAACAA	TAATACGCAA	CAATCAAATA	1200
	CAACCCC					1207

45

2) INFORMATION FOR SEQ ID NO: 1012

- (i) SEQUENCE CHARACTERISTICS:
- 50 (A) LENGTH: 1201 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

55

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
- (B) STRAIN: StrR-09

60 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1012

	AAGCTCAAAA	ACATCTGTGG	GATATCTACA	ACTCCGATCA	ATACGTCTCT	50
	TACCCTGACG	ATGATTGCA	AGTCGCATCT	ACGGTCGTAG	ATGTTTCAAA	100
	TGGTAAAGTC	ATCGCCCAAC	TTGGAGCTCG	TCACCAAGCA	AGTAACGTTT	150
5	CATTTGGTAC	CAACCAAGCT	GTGGAAACCA	ATCGTGACTG	GGGTTCTGCT	200
	ATGAAACCAA	TCACCGATTA	TGCACCTGCC	ATAGAATACG	GTGTTTATGA	250
	TTCCACTGCA	ACTATGGTTA	ATGATATTCC	TTATAACTAT	CCGGGAACAA	300
	GCACACCTGT	CTACAACCTGG	GATAGAGCAT	ATTTTCGGTAA	TATTACTCTG	350
	CAATATGCTC	TTCAACAATC	ACGAAATGTC	ACAGCCGTTG	AGACTTTGAA	400
10	TAAGGTCGGT	CTAGATAGAG	CTAAAACCTT	CCTTAATGGT	CTTGGTATCG	450
	ACTATCCAAG	CATGCATTAT	GCAAACGCCA	TTTCAAGTAA	TACAACAGAA	500
	TCTAATAAAC	AATACGGAGC	AAGTAGTGAA	AAAATGGCTG	CTGCTTATGC	550
	TGCCTTTGCC	AACGGTGGAA	TTTACCACAA	ACCCATGTAT	ATCAATAAGG	600
	TCGTCTTCAG	TGACGGTAGT	AAAAAAGAAT	TTTCAGATGT	AGGTACACGA	650
15	GCTATGAAAG	AAACAACCTGC	TTACATGATG	ACCGAAATGA	TGAAAACCTGT	700
	CTTGGCATA	GGAACCTGGTC	GTGGAGCCTA	TCTCCCATGG	TTAGCGCAAG	750
	CTGGTAAGAC	AGGTACTTCT	AACTACACAG	ATGATGAAAT	TGAAAAACAC	800
	ATCAAGAACA	CTGGCTATGT	AGCTCCAGAT	GAAATGTTTG	TTGGTTATAC	850
	TCGTAAGTAT	TCTATGGCTG	TATGGACAGG	TTATTCTGAAT	CGTTTAACTC	900
20	CTATCGTTGG	AGATGGTTTC	CTAGTTGCAG	CTAAAGTTTA	TCGCTCAATG	950
	ATAACGTATC	TATCAGAAGA	TACTCATCCA	GAAGACTGGA	CGATGCCAGA	1000
	CGGACTTTTC	AGAAACGGGG	AATTTGTATT	CAAAAATGGA	GCTCGTTCTA	1050
	CGTGGAACCTC	ACCTGCTCCA	CAACAACCCC	CATCAACTGA	AAGTTC AAGC	1100
	TCATCATCAG	ATAGTTCAAC	TTCACAGTCT	AGCTCAACCA	CTCCAAGCAC	1150
25	AAATAATAGT	ACGACTACCG	ATCCTAACAA	TAATACGCAA	CAATCAAATA	1200
	C					1201

30 2) INFORMATION FOR SEQ ID NO: 1013

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1220 bases
 (B) TYPE: Nucleic acid
 35 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

40 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
 (B) STRAIN: StrR-10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1013

45	TGTAGACCAA	GAAGCTCAAA	AACATCTGTG	GGATATCTAC	AACTCCGATC	50
	AATACGTCTC	TTACCCTGAC	GATGATTGTC	AAGTCGCATC	TACGGTCGTA	100
	GATGTTTCAA	ATGGTAAAGT	CATCGCACAA	CTTGGTGCTC	GTCATCAAGC	150
	AAGTAATGTT	TCATTTCGTA	CCAACCAGGC	CGTAGAAACC	AATCGTGACT	200
50	GGGGATCATC	AATGAAACCA	ATCACTGACT	ATGCTCCCGC	TTTAGAATAT	250
	GGAGTCTATG	ACTCTACTGC	TTCTATTGTA	CATGATGTCC	CTTATAACTA	300
	TCCTGGCACT	GATACTCCAC	TCTACAACCTG	GGATCATGTC	TACTTTGGAA	350
	ACATTACAAT	CCAGTATGCT	CTTCAACAAT	CACGAAATGT	CACAGCCGTT	400
	GAGACTTTGA	ATAAGGTCGG	TCTAGATAGA	GCTAAAACCT	TCCTTAATGG	450
55	TCTTGGTATC	GACTATCCAA	GCATGCATTA	TGCAAAACGCC	ATTTCAAGTA	500
	ACACAACCTGA	ATCCAACAAA	AAATATGGTG	CAAGTAGTGA	AAAAATGGCT	550
	GCTGCCTACG	CTGCTTTTGC	TAATGGTGGT	ATTTATCACA	AACCAATGTA	600
	TATCAATAAAA	ATCGTCTTTA	GTGATGGTAG	CGAAAAAGAA	TTTTCTGATG	650
	CTGGTACACG	AGCTATGAAA	GAGACTACTG	CCTATATGAT	GACTGAAATG	700
60	ATGAAAACCTG	TTTTAACTTA	CGGAACAGGA	CGTGGAGCCT	ACCTACCATG	750

	GCTTCCACAA	GCAGGTAAGA	CAGGTACTTC	TAACATACT	GACGAAGAAA	800
	TTGAAAAGTA	TATCAAGAAC	ACTGGCTACG	TAGCTCCAGA	TGAAATGTTT	850
	GTGGGTTATA	CTCGTAAGTA	TTCTATGGCT	GTATGGACAG	GTTATTTCGAA	900
	TCGTTTAACT	CCTATCGTTG	GAGATGGTTT	CCTAGTTGCA	GCTAAAGTTT	950
5	ATCGCTCTAT	GATGACCTAC	CTGTCTGAAG	GAAGCAATCC	AGAGGATTGG	1000
	AATATACCAG	AGGGGCTCTA	CAGAAATGGA	GAATTCGTAT	TTAAAAATGG	1050
	TGCTCGTTCT	ACGTGGAGCT	CACCTGCTCC	ACAACAACCC	CCATCAACTG	1100
	AAAGTTCAAG	CTCATCATCA	GATAGTTCAA	CTTCACAGTC	TAGCTCAACC	1150
	ACTCCAAGCA	CAAATAATAG	TACGACTACC	AATCCTAACA	ATAATACGCA	1200
10	ACAATCAAAT	ACAACCCCTG				1220

2) INFORMATION FOR SEQ ID NO: 1014

15

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1199 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

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(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

25

- (A) ORGANISM: *Streptococcus pneumoniae*
 (B) STRAIN: StrR-11

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1014

30	CAAAAACATC	TGTGGGATAT	TTACAATACA	GACGAATACG	TTGCCTATCC	50
	AGACGATGAA	TTGCAAGTCG	CTTCTACCAT	TGTTGATGTT	TCTAACGGTA	100
	AAGTCATTGC	CCAGCTAGGA	GCACGCCATC	AGTCAAGTAA	TGTTTCCTTC	150
	GGAATTAACC	AAGCAGTAGA	AACAAACCGC	GACTGGGGAT	CAACTATGAA	200
	ACCGATCACA	GACTATGCTC	CTGCCTTGGA	GTACGGTGTC	TACGATTCAA	250
35	CTGCTACTAT	CGTTCACGAT	GAGCCCTATA	ACTACCCTGG	GACAAATACC	300
	CCTGTTTATA	ACTGGGATAG	GGGCTACTTT	GGCAACATCA	CCTTGCAATA	350
	CGCCCTGCAA	CAATCGCGAA	ACGTCCCAGC	CGTGGAAACT	CTAAACAAGG	400
	TCGGACTCAA	CCGCGCCAAG	ACTTTCCTAA	ATGGTCTCGG	AATCGACTAC	450
	CCAAGTATTC	ACTACTCAAA	TGCCATTTCA	AGTAACACAA	CCGAATCAGA	500
40	CAAAAAATAT	GGAGCAAGTA	GTGAAAAGAT	GGCTGCTGCT	TACGCTGCCT	550
	TTGCAAATGG	TGGAACCTAC	TATAAACCAA	TGTATATCCA	TAAAGTCGTC	600
	TTTAGTGATG	GGAGTGAAAA	AGAGTTCTCT	AATGTCGGAA	CTCGTGCCAT	650
	GAAGGAAACG	ACAGCCTATA	TGATGACCSA	CATGATGAAA	ACTGTCTTAG	700
	TATACGGAAT	CGGACGTGGA	GCCTACCTAC	CTTGCTTCC	ACAAGCAGGT	750
45	AAAACAGGTA	CTTCTAACTA	TACTGACGAA	GAAATTGAAA	AGTATATCAA	800
	GAACACTGGT	TACGTAGCTC	CAGATGAAAT	GTTTGTAGGG	TATACCCGCA	850
	AATATGCAAT	GGCTGTATGG	ACAGGCTATT	CTAACCGTCT	GACACCACTT	900
	GTAGGCGATG	GCCTTACGGT	CGCTGCTAAA	GTTTACCGCT	CTATGATGAC	950
	CTACCTGTCT	GAAGGAAGCA	ATCCAGAGGA	TTGGAATATA	CCAGAGGGGC	1000
50	TCTACAGAAA	TGGAGAATTC	GTATTTAAAA	ATGGTGCTCG	TTCTACGTGG	1050
	AACTCACCTG	CTCCACAACA	ACCCCATCA	ACTGAAAGTT	CAAGCTCATC	1100
	ATCAGATAGT	TCAACTTCAC	AGTCTAGCTC	AACCACTCCA	AGCACAAATA	1150
	ATAGTACGAC	TACCAATCCT	AACAATAATA	CGCAACAATC	AAATACAAC	1199

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2) INFORMATION FOR SEQ ID NO: 1015

(i) SEQUENCE CHARACTERISTICS:

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- (A) LENGTH: 1211 bases

- (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

5 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
 (B) STRAIN: StrR-12

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1015

	AAGCTCAAAA	ACATCTGTGG	GATATCTACA	ACTCCGATCA	ATACGTCTCT	50
	TACCCTGACG	ATGATTTGCA	AGTCGCATCT	ACGGTCGTAG	ATGTTTCAAA	100
15	TGGTAAAGTC	ATCGCCCAAC	TTGGAGCTCG	TCACCAAGCA	AGTAACGTTT	150
	CATTTGGTAC	CAACCAAGCT	GTGGAAACCA	ATCGTGACTG	GGGTTCTGCT	200
	ATGAAACCAA	TCACCGATTA	TGCACCTGCC	ATAGAATACG	GTGTTTATGA	250
	TTCCACTGCA	ACTATGGTTA	ATGATATTCC	TTATAACTAT	CCGGGAACAA	300
	GCACACCTGT	CTACAACCTG	GATAGAGCAT	ATTTCCGTAA	TATTACTCTG	350
20	CAATATGCTC	TTCAACAATC	ACGAAATGTC	ACAGCCGTTG	AGACTTTGAA	400
	TAAGGTCGGT	CTAGATAGAG	CTAAAACCTT	CCTTAATGGT	CTTGGTATCG	450
	ACTATCCAAG	CATGCATTAT	GCAAACGCCA	TTTCAAGTAA	TACAACAGAA	500
	TCTAATAAAC	AATACGGAGC	AAGTAGTGAA	AAAATGGCTG	CTGCTTATGC	550
	TGCCTTTGCC	AACGGTGGAA	TTTACCACAA	ACCCATGTAT	ATCAATAAGG	600
25	TCGTCTTCAG	TGACGGTAGT	AAAAAAGAAT	TTTCAGATGT	AGGTACACGA	650
	GCTATGAAAG	AAACAACCTG	TTACATGATG	ACCGAAATGA	TGAAAACTGT	700
	CTTGGCATA	GGAACCTGGT	GTGGAGCCTA	TCTCCCATGG	TTAGCGCAAG	750
	CTGGTAAGAC	AGGTACTTCT	AACTACACAG	ATGATGAAAT	TGAAAAACAC	800
	ATCAAGAACA	CTGGCTATGT	AGCTCCAGAT	GAAATGTTTG	TTGGTTATAC	850
30	TCGTAAGTAT	TCTATGGCTG	TATGGACAGG	TTATTCCAAT	CGTTTAACTC	900
	CTATCGTTGG	AGATGGTTTC	CTAGTTGCAG	CTAAAGTTTA	TCGCTCAATG	950
	ATAACGTATC	TGTCTGAAGG	AAGCAATCCA	GAGGATTGGA	ATATACCAGA	1000
	GGGGCTCTAC	AGAAATGGAG	AATTCGTATT	TAAAAATGGT	GCTCGTTCTA	1050
	CGTGGAGCTC	ACCTGCTCCA	CAACAACCCC	CATCAACTGA	AAGTTCAAGC	1100
35	TCATCATCAG	ATAGTTCAAC	TTACAGTCT	AACTCAACCA	CTCCAAGCAC	1150
	AAATAATAGT	ACGACTACCA	ATCCTAACAA	TAATACGCAA	CAATCAAATA	1200
	CAACCCCTGA	T				1211

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2) INFORMATION FOR SEQ ID NO: 1016

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1222 bases
 45 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

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(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
 (B) STRAIN: StrR-13

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1016

	GTAGACCAAG	AAGCTCAAAA	ACATCTGTGG	GATATCTACA	ACTCCGATCA	50
	ATACGTCTCT	TACCCTGACG	ATGATTTGCA	AGTCGCATCT	ACGGTCGTAG	100
	ATGTTTCAAA	TGGTAAAGTC	ATCGCACAAC	TTGGTGCTCG	TCATCAAGCA	150
60	AGTAATGTTT	CATTCGGTAC	CAACCAGGCC	GTAGAAACCA	ATCGTGACTG	200

	GGGATCATCA	ATGAAACCAA	TCACTGACTA	TGCTCCCGCT	TTAGAATATG	250
	GAGTCTATGA	CTCTACTGCT	TCTATTGTAC	ATGATGTCCC	TTATAACTAT	300
	CCTGGCACTG	ATACTCCACT	CTACAACCTGG	GATCATGTCT	ACTTTGGAAA	350
	CATTACAATC	CAGTATGCTC	TTCAACAATC	ACGAAATGTC	ACAGCCGTTG	400
5	AGACTTTGAA	TAAGGTCGGT	CTAGATAGAG	CTAAAACCTT	CCTTAATGGT	450
	CTTGGTATCG	ACTATCCAAG	CATGCATTAT	GCAAACGCCA	TTTCAAGTAA	500
	CACAACTGAA	TCCAACAAAA	AATATGGTGC	AAGTAGTGAA	AAAATGGCTG	550
	CTGCCTACGC	TGCTTTTGCT	AATGGTGGTA	TTTATCACAA	ACCAATGTAT	600
	ATCAATAAAA	TCGTCTTTAG	TGATGGTAGC	GAAAAAGAAT	TTTCTGATGC	650
10	TGGTACACGA	GCTATGAAAG	AGACTACTGC	CTATATGATG	ACTGAAATGA	700
	TGAAAACCTGT	TTTAACTTAC	GGAACAGGAC	GTGGAGCCTA	CCTACCATGG	750
	CTTCCACAAG	CAGGTAAGAC	AGGTACTTCT	AACATACTG	ACGAAGAAAT	800
	TGAAAAGTAT	ATCAAGAACA	CTGGCTACGT	AGCTCCAGAT	GAAATGTTTG	850
	TGGGTATATAC	TCGTAAGTAT	TCTATGGCTG	TATGGACAGG	TTATTCTGAAT	900
15	CGTTTAACTC	CTATCGTTGG	AGATGGTTTC	CTAGTTGCAG	CTAAAGTTTA	950
	TCGCTCTATG	ATGACCTACC	TGTCTGAAGG	AAGCAATCCA	GAGGATTGGA	1000
	ATATAACCAGA	GGGGCTCTAC	AGAAATGGAG	AATTCGTATT	TAAAAATGGT	1050
	GCTCGTTCTA	CGTGGAGCTC	ACCTGCTCCA	CAACAACCCC	CATCAACTGA	1100
	AAGTTCAAGC	TCATCATCAG	ATAGTTCAAC	TTCACAGTCT	AGCTCAACCA	1150
20	CTCCAAGCAC	AAATAATAGT	ACGACTACCA	ATCCTAACAA	TAATACGCAA	1200
	CAATCAAATA	CAACCCCTGA	TC			1222

25 2) INFORMATION FOR SEQ ID NO: 1017

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1229 bases
 (B) TYPE: Nucleic acid
 30 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

35 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
 (B) STRAIN: StrR-14

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1017

40	TGTAGACCAA	GAAGCTCAAA	AACATCTGTG	GGATATTTAC	AATACAGACG	50
	AATACGTTGC	CTATCCAGAC	GATGAATTGC	AAGTCGCTTC	TACCATTGTT	100
	GATGTTTCTA	ACGGTAAAGT	CATTGCCAG	CTAGGAGCAC	GCCATCAGTC	150
	AAGTAATGTT	TCCTTCGGAA	TTAACCAAGC	AGTAGAAACA	AACCGCGACT	200
45	GGGGATCAAC	TATGAAACCG	ATCACAGACT	ATGCTCCTGC	CTTGGAGTAC	250
	GGTGTCTACG	ATTCAACTGC	TACTATCGTT	CACGATGAGC	CCTATAACTA	300
	CCCTGGGACA	AATACCCCTG	TTTATAACTG	GGATAGGGGC	TACTTTGGCA	350
	ACATCACCTT	GCAATACGCC	CTGCAACAAT	CGCGAAACGT	CCCAGCCGTG	400
	GAAACTCTAA	ACAAGGTCGG	ACTCAACCGC	GCCAAGACTT	TCCTAAATGG	450
50	TCTCGGAATC	GACTACCCAA	GTATTCACTA	CTCAAAATGCC	ATTTCAAGTA	500
	ACACAACCGA	ATCAGACAAA	AAATATGGAG	CAAGTAGTGA	AAAGATGGCT	550
	GCTGCTTACG	CTGCCTTTGC	AAATGGTGGA	ACTTACTATA	AACCAATGTA	600
	TATCCATAAA	GTCGTCTTTA	GTGATGGGAG	TGAAAAAGAG	TTCTCTAATG	650
	TCGGAACCTG	TGCCATGAAA	GAAACAACCTG	CTTACATGAT	GACCGAAATG	700
55	ATGAAAACCTG	TCCTGGCATA	CGGAAGTGGT	CGTGGAGCCT	ATCTCCCATG	750
	GTTAGCGCAA	GCTGGTAAGA	CAGGTACTTC	TAACTACACA	GATGATGAAA	800
	TTGAAAACATA	CATCAAGAAC	ACTGGCTATG	TAGCTCCAGA	TGAAATGTTT	850
	GTTGGTTATA	CTCGTAAGTA	TTCTATGGCT	GTATGGACAG	GTTATTCTGAA	900
	TCGTTTAACT	CCTATCGTTG	GAGATGGTTT	CCTAGTTGCA	GCTAAAGTTT	950
60	ATCGCTCAAT	GATAACGTAT	CTATCAAAAAG	ATACTCATCC	AGAAGACTGG	1000

	ACGATGCCAG	ACGGACTTTT	CAGAAACGGG	GAATTTGTAT	TCAAAAATGG	1050
	AGCTCGTTCT	ACGTGGAAC	CACCTGCTCC	ACAACAACCC	CCATCAACTG	1100
	AAAGTTCAAG	CTCATCATCA	GATAGTTCAA	CTTCACAGTC	TAACTCAACC	1150
	ACTCCAAGCA	CAAATAATAG	TACGACTACC	AATCCTAACA	ATAATACGCA	1200
5	ACAATCAAAT	ACAACCCCTG	ATCAACAAA			1229

2) INFORMATION FOR SEQ ID NO: 1018

10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1225 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 15 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 20 (A) ORGANISM: *Streptococcus pneumoniae*
 (B) STRAIN: StrR-15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1018

25	ATGTAGACCA	AGAGGCTCAA	AAACGTCTGT	GGGATATCTA	CAACTCCGAT	50
	CAATACGTCT	CTTACCCTGA	CGATGATTG	CAAGTCGCAT	CTACGGTCGT	100
	AGATGTTTCA	AATGGTAAAG	TCATCGCCCA	ACTTGGAGCT	CGTCACCAAG	150
	CAAGTAACGT	TTCATTTGGT	ACCAACCAAG	CTGTGGAAAC	CAACCGTGAC	200
	TGGGGATCAA	GCATGAAACC	AATCACTGAT	TATGCCCCAG	CCTTAGAATA	250
30	TGGTGTATAT	GATTCCACTG	CAACTATGGT	TAATGATATT	CCTTATAACT	300
	ATCCGGGCAC	AAGCACACCT	GTCTACAAC	GGGATCGAGC	ATATTTTGGT	350
	AATATTAGCC	TGCAATATGC	CCTTCAACAA	TCTCGTAACG	TGCCTGCCGT	400
	TGAAACACTA	AACAAGGTTG	GTTTAGATAG	AGCCAAAAC	TTCCTAAATG	450
	GTTTGGGAAT	TGACTATCCA	AGTATTTACT	ACTCAAATGC	TATTTCAAGT	500
35	AATACAACCTG	AATCTAGTAA	ACAGTACGGG	GCAAGCAGTG	AGAAAATGGC	550
	TGCGGCTTAC	GCTGCATTCT	CTAATGGCGG	TATTTACCAC	AAACCAATGT	600
	ACATCAATAA	AGTTGTCTTT	AGTGATGGTA	GCGAAAAAGA	ATTTTCTGAT	650
	GCTGGTACAC	GAGCTATGAA	AGAGACTACT	GCCTATATGA	TGACTGAAAT	700
	GATGAAAAC	GTTTAACTT	ACGGAACAGG	ACGTGGAGCC	TACCTACCAT	750
40	GGCTTCCACA	AGCAGGTAAG	ACAGGTACTT	CTAACTATAC	TGACGACGAA	800
	ATTGAAAAGT	ATATCAAGAA	CACTGGCTAC	GTAGCTCCAG	ATGAAATGTT	850
	TGTGGGTTAT	ACTCGTAAGT	ATTCTATGGC	TGTATGGACT	GGATACTCAA	900
	ATCGTTTAAC	TCCAATCATT	GGAGATGGTT	TCCTAGTTGC	TGCCAAAGTT	950
	TATCGCTCAA	TGATATCGTA	TCTATCAGAA	GATGACCATC	CTGGAGATTG	1000
45	GACAATGCCT	GAGGGAGTAT	ACAGAAGTGG	AGAATTCGTA	TTTAAAAATG	1050
	GTGCTCGTTC	TACGTGGAGC	TCCCCTGCTC	CACAACAACC	CCCATCAACT	1100
	GAAAGTTCAA	GCTCATCATC	AGATAGTTCA	ACTTCACAGT	CTAGCTTAAC	1150
	CACTCCAAGC	ACAAATAATA	GTACGACTAC	CAATCCTAAC	AACAATACGC	1200
50	AACAATCAAA	TACAACCCCT	GATCA			1225

2) INFORMATION FOR SEQ ID NO: 1019

55 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1439 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 60 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 5 (A) ORGANISM: *Streptococcus pneumoniae*
(B) STRAIN: StrR-01

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1019

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10 GCCTCTATTT CAAAGGAGAT GCCTGGCATT AGTATTTCTA CTTCTTGGGA      50
   TCGAAAGGTT TTGGAAACTT CCCTTTCTTC TATAGTAGGG AGTGTATCCA      100
   GTGAAAAAGC TGGTCTCCCA GCGGAAGAAG CAGAATCCTA TCTTAAAAAA      150
   GGCTATTCTC TAAATGACCG TGTGGAACCC TCCTATTTGG AAAAGCAATA      200
   TGAAGAGACC TTACAAGGAA AACGCTCGGT AAAAGAAATC CATCTGGATA      250
   AATATGGCAA TATGGAAAGC GTGGACACAA TTGAGGAAGG TAGTAAGGGA      300
15 AACAAATATCA AACTGACCAT TGATTTGGCC TTCCAAGATA GCGTGGATGC      350
   TTTGCTGAAA AGTTATTTCA ATTCCGAGCT AGGAAATGGT GGAGCTAAAT      400
   ATTCTGAAGG TGTCTATGCA GTCGCCCTTA ACCCAAAAAC AGGTGCTGTT      450
   TTATCCATGT CAGGGATCAA ACATGACCTG AAAACGGGAG AGTTGACTCC      500
   TGATTCCTTG GGAACGGTAA CCAATGTCTT TGTCCCAGGT TCGGTTGTCA      550
20 AGGCTGCGAC CATCAGCTCA GGTGCGGAAA ATGGTGTTTT ATCAGGAAAC      600
   CAAACCTTAA CAGATCAGCC TATTGTTTTT CAAGGTTTCA CTCCAATTTA      650
   TTCTTGGTAT AAATTGGCAT ATGGATCTTT TCCTATTACA GCTGTGGAAG      700
   CCTTGGAGTA TTCATCCAAT GCTTACATGG TTCAAACCGC TCTTGAATC      750
   ATGGGCCAGA CCTATCAACC AAATATGTTT GTTGAACCA GCAATTTGGA      800
25 AACAGCTATG GGAAACTTC GTGCGACCTT TGGCGAATAT GGCTTGGGGG      850
   CTGCGACCGG AATTGACCTA CCAGATGAAT CTACTGGATT TGTTCCTCAA      900
   GAGTATAGCT TTGCTAATTA CATCACCAAT TCCTTTGGGC AGTTTGATAA      950
   CTATACGCCC ATGCAGTTGG CTCAGTATGT AGCAACTATT GCAAATAATG     1000
   GTGTTTCGTG GGCTCCTCGT ATTGTTGAAG GCATTTATGG TAATAATGAT     1050
30 AAGGGAGGAC TGGGTGACTT GATTCAGCAA CTGCAACCGA CAGAGATGAA     1100
   TAAGGTCAAT ATATCCGACT CCGATATGAG CATCTTGCAC CAAGGTTTTT     1150
   ATCAGGTTGC CCATGGTACT AGTGGATTGA CAACTGGACG TGCTTTTTC      1200
   AATGGTGCCT TGGTATCCAT TAGCGGAAAA ACAGGTACAG CCGAAAGCTA     1250
   TGTGGCAGAT GGTGAGCAAG CAACCAATAC CAATGCGGTG GCCTATGCCC     1300
35 CATCTGATAA TCCCCAAATC GCTGTGCGAG TGGTCTTTCC TCATAATACC     1350
   AATCTAACAA ATGGTGTAGG ACCTTCCATT GCGCGTGACA TTATCAATCT     1400
   GTATCAAAAA TACCATCCAA TGAAGTAGAA AGGAAATTA      1439

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2) INFORMATION FOR SEQ ID NO: 1020

(i) SEQUENCE CHARACTERISTICS:

- 45 (A) LENGTH: 1441 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

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(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
(B) STRAIN: StrR-02

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1020

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60 GCCTCTATTT CAAAGGAGAT GCCTGGCATT AGTATTTCTA CTTCTTGGGA      50
   TCGAAAGGTT TTGGAAACTT CCCTTTCTTC TATAGTAGGG AGTGTATCCA      100
   GTGAAAAAGC TGGTCTCCCA GCGGAAGAAG CAGAATCCTA TCTTAAAAAA      150
   GGCTATTCTC TAAATGACCG TGTGGAACCC TCCTATTTGG AAAAGCAATA      200

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1	TGAAGAGACC	TTACAAGGAA	AACGCTCGGT	AAAAGAAATC	CATCTGGATA	250
	AATATGGCAA	TATGGAAAAGC	GTGGACACAA	TTGAGGAAGG	TAGTAAGGGA	300
	AACAATATCA	AACTGACCAT	TGATTTGGCC	TTCCAAGATA	GCGTGGATGC	350
	TTTGCTGAAA	AGTTATTTCA	ATTCCGAGCT	AGGAAATGGT	GGAGCTAAAT	400
5	ATTCTGAAGG	TGTCTATGCA	GTCGCCCTTA	ACCCAAAAAC	AGGTGCTGTT	450
	TTATCCATGT	CAGGGATCAA	ACATGACCTG	AAAACGGGAG	AGTTGACTCC	500
	TGATTCCTTG	GGAACGGTAA	CCAATGTCTT	TGTCCCAGGT	TCGGTTGTCA	550
	AGGCTGCGAC	CATCAGCTCA	GGTTGGGAAA	ATGGTGTTTT	ATCAGGAAAC	600
	CAAACCTTAA	CAGATCAGCC	TATTGTTTTT	CAAGGTTTCA	CTCCAATTTA	650
10	TTCTTGGTAT	AAATTGGCAT	ATGGATCTTT	TCCTATTACA	GCTGTGGAAG	700
	CCTTGGAGTA	TTCATCCAAT	GCTTACATGG	TTCAAACCGC	TCTTGAATC	750
	ATGGGCCAGA	CCTATCAACC	AAATATGTTT	GTTGGAACCA	GCAATTTGGA	800
	AACAGCTATG	GGAAAACCTC	GTGCGACCTT	TGGCGAATAT	GGCTTGGGGG	850
	CTGCGACCGG	AATTGACCTA	CCAGATGAAT	CTACTGGATT	TGTTCCCAAA	900
15	GAGTATAGCT	TTGCTAATTA	CATCACCAAT	TCCTTTGGGC	AGTTTGATAA	950
	CTATACGCCC	ATGCAGTTGG	CTCAGTATGT	AGCAACTATT	GCAAATAATG	1000
	GTGTTTCGTG	GGCTCCTCGT	ATTGTTGAAG	GCATTTATGG	TAATAATGAT	1050
	AAGGGAGGAC	TGGGTGACTT	GATTCAGCAA	CTGCAACCGA	CAGAGATGAA	1100
	TAAGGTCAAT	ATATCCGACT	CCGATATGAG	CATCTTGAC	CAAGGTTTTT	1150
20	ATCAGGTTGC	CCATGGTACT	AGTGGATTGA	CAACTGGACG	TGCCCTTTCA	1200
	AATGGTGCCT	TGGTATCCAT	TAGCGGAAAA	ACAGGTACAG	CCGAAAGCTA	1250
	TGTGGCAGAT	GGTCAGCAAG	CAACCAATAC	CAATGCGGTG	GCCTATGCCC	1300
	CATCTGATAA	TCCCCAAATC	GCTGTGCGAG	TGGTCTTTCC	TCATAATACC	1350
	AATCTAACAA	ATGGTGTAGG	ACCTTCCATT	GCGCGTGACA	TTATCAATCT	1400
25	GTATCAAAAA	TACCATCCAA	TGAAC TAGAA	AGGAAATTAT	G	1441

2) INFORMATION FOR SEQ ID NO: 1021

30

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1396 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
 (B) STRAIN: StrR-03

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1021

45	TATTGCCTCT	ATTTCAAAGG	AGATGCCTGG	CATTAGTATT	TCTACTTCTT	50
	GGGATCGAAA	GGTTTTGGAA	ACTTCCCTTT	CTTCTATAGT	AGGGAGTGTA	100
	TCCAGTGAAA	AAGCTGGTCT	CCCAGCGGAA	GAAGCAGAAT	CCTATCTTAA	150
	AAAAGGCTAT	TCTCTAAATG	ACCGTGTTGG	AACCTCCTAT	TTGGAAAAGC	200
	AATATGAAGA	GACCTTACAA	GGAAAACGCT	CGGTAAAAGA	AATCCATCTG	250
50	GATAAATATG	GCAATATGGA	AAGCGTGGAC	ACAATTGAGG	AAGGTAGTAA	300
	GGGAAACAAT	ATCAAACCTGA	CCATTGATTT	GGCCTTCCAA	GATAGCGTGG	350
	ATGCTTTGCT	GAAAAGTTAT	TTCAATTCCG	AGCTAGGAAA	TGGTGGAGCT	400
	AAATATTCTG	AAGGTGTCTA	TGCAGTCGCC	CTTAACCCAA	AAACAGGTGC	450
	TGTTTTATCC	ATGTCAGGGA	TCAAACATGA	CCTGAAAACG	GGAGAGTTGA	500
55	CTCCTGATTC	CTTGGGAACG	GTAACCAATG	TCTTTGTCCC	AGGTTTCGGTT	550
	GTCAAGGCTG	CGACCATCAG	CTCAGGTTGG	GAAAATGGTG	TTTTATCAGG	600
	AAACCAAACC	TTAACAGATC	AGCCTATTGT	TTTCCAAGGT	TCAGCTCCAA	650
	TTTATTCTTG	GTATAAATTG	GCATATGGAT	CTTTTCCTAT	TACAGCTGTG	700
	GAAGCCTTGG	AGTATTCATC	CAATGCTTAC	ATGGTTCAAA	CCGCTCTTGG	750
60	AATCATGGGC	CAGACCTATC	AACCAAATAT	GTTTGTGTTGA	ACCAGCAATT	800

	TGGAAACAGC	TATGGGAAAA	CTTCGTGCGA	CCTTTGGCGA	ATATGGCTTG	850
	GGGGCTGCGA	CCGGAATTGA	CCTACCAGAT	GAATCTACTG	GATTGTGTTCC	900
	CAAAGAGTAT	AGCTTTGCTA	ATTACATCAC	CAATTCCTTT	GGGCAGTTTG	950
	ATAACTATAC	GCCCATGCAG	TTGGCTCAGT	ATGTAGCAAC	TATTGCAAAT	1000
5	AATGGTGTTC	GTGTGGCTCC	TCGTATTGTT	GAAGGCATTT	ATGGTAATAA	1050
	TGATAAGGGA	GGACTGGGTG	ACTTGATTCA	GCAACTGCAA	CCGACAGAGA	1100
	TGAATAAGGT	CAATATATCC	GACTCCGATA	TGAGCATCTT	GCACCAAGGT	1150
	TTTTATCAGG	TTGCCCATGG	TACTAGTGGA	TTGACAACTG	GACGTGCCTT	1200
	TTCAAATGGT	GCCTTGGTAT	CCATTAGCGG	AAAAACAGGT	ACAGCCGAAA	1250
10	GCTATGTGGC	AGATGGTCAG	CAAGCAACCA	ATACCAATGC	GGTGGCCTAT	1300
	GCCCCATCTG	ATAATCCCCA	AATCGCTGTC	GCAGTGGTCT	TTCCTCATAA	1350
	TACCAATCTA	ACAAATGGTG	TAGGACCTTC	CATTGCGCGT	GACATT	1396

15

2) INFORMATION FOR SEQ ID NO: 1022

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1428 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Streptococcus pneumoniae*
- (B) STRAIN: StrR-04

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1022

	AAAGGAGATG	CCTGGCATTG	GTATTTCTAC	TTCTTGGGAT	CGAAAGGTTT	50
	TGGAAACTTC	CCTTTCTTCT	ATAGTAGGGA	GTGTATCCAG	TGAAAAAGCT	100
	GGTCTCCCAG	CGGAAGAAGC	AGAATCCTAT	CTTAAAAAAG	GCTATTCTCT	150
35	AAATGACCGT	GTTGGAACCT	CCTATTGGA	AAAGCAATAT	GAAGAGACCT	200
	TACAAGGAAA	ACGCTCGGTA	AAAGAAATCC	ATCTGGATAA	ATATGGCAAT	250
	ATGGAAAGCG	TGGACACAAT	TGAGGAAGGT	AGTAAGGGAA	ACAATATCAA	300
	ACTGACCATT	GATTTGGCCT	TCCAAGATAG	CGTGGATGCT	TTGCTGAAAA	350
	GTTATTTCAA	TTCCGAGCTA	GGAAATGGTG	GAGCTAAATA	TTCTGAAGGT	400
40	GTCTATGCAG	TCGCCCTTAA	CCCCAAAACA	GGTGCTGTTT	TATCCATGTC	450
	AGGGATCAAA	CATGACCTGA	AAACGGGAGA	GTTGACTCCT	GATTCCTTGG	500
	GAACGGTAAC	CAATGTCTTT	GTCCCGGTT	CGGTTGTCAA	GGCTGCGACC	550
	ATCAGCTCAG	GTTGGGAAAA	TGGTGTTTTA	TCAGGAAACC	AAACCTTAAC	600
	AGATCAGCCT	ATTGTTTTCC	AAGGTCAGC	TCCAATTTAT	TCTTGGGTATA	650
45	AATTGGCATA	TGGATCTTTT	CCTATTACAG	CTGTGGAAGC	CTTGGAGTAT	700
	TCATCCAATG	CTTACATGGT	TCAAACCGCT	CTTGGAATCA	TGGGCCAGAC	750
	CTATCAACCA	AATATGTTTG	TTGGAACAG	CAATTGGA	ACAGCTATGG	800
	GAAAACTTCG	TGCGACCTTT	GGCGAATATG	GCTTGGGGGC	TGCGACCGGA	850
	ATTGACCTAC	CAGATGAATC	TACTGGATTT	GTTCCCAAAG	AGTATAGCTT	900
50	TGCTAATTAC	ATCACCAATT	CCTTTGGGCA	GTTTGATAAC	TATACGCCCA	950
	TGCAGTTGGC	TCAGTATGTA	GCAACTATTG	CAAATAATGG	TGTTCTGTGTG	1000
	GCTCCTCGTA	TTGTTGAAGG	CATTTATGGT	AATAATGATA	AGGGAGGACT	1050
	GGGTGACTTG	ATTCAGCAAC	TGCAACCGAC	AGAGATGAAT	AAGGTCAATA	1100
	TATCCGACTC	CGATATGAGC	ATCTTGACCC	AAGGTTTTTA	TCAGGTTGCC	1150
55	CATGGTACTA	GTGGATTGAC	AACTGGACGT	GCCTTTTCAA	ATGGTGCCTT	1200
	GGTATCCATT	AGCGGAAAAA	CAGGTACAGC	CGAAAGCTAT	GTGGCAGATG	1250
	GTCAGCAAGC	AACCAATACC	AATGCGGTGG	CCTATGCCCC	ATCTGATAAT	1300
	CCCCAAATCG	CTGTCGCAGT	GGTCTTTCCT	CATAATACCA	ATCTAACAAA	1350
	TGGTGTAGGA	CCTTCCATTG	CGCGTGACAT	TATCAATCTG	TATCAAAAAT	1400
60	ACCATCCAAT	GAAC TAGAAA	GGAAATTA			1428

2) INFORMATION FOR SEQ ID NO: 1023

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1442 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

10

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
 (B) STRAIN: StrR-05

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1023

20	TGCCTCTATT TCAAAGGAGA TGCCTGGCAT TAGTATTTCT ACTTCTTGGG	50
	ATCGAAAGGT TTTGGAAACT TCCCTTTCTT CTATAGTAGG GAGTGTATCC	100
	AGTGAAAAG CTGGTCTCCC AGCGGAAGAA GCAGAATCCT ATCTTAAAAA	150
	AGGCTATTCT CTAAATGACC GTGTTGGAAC CTCCTATTTG GAAAAGCAAT	200
	ATGAAGAGAC CTTACAAGGA AAACGCTCGG TAAAAGAAAT CCATCTGGAT	250
25	AAATATGGCA ATATGGAAAG CGTGGACACA ATTGAGGAAG GTAGTAAGGG	300
	AAACAATATC AAACGACCA TTGATTGGC CTCCAAGAT AGCGTGGATG	350
	CTTTGCTGAA AAGTTATTTT AATTCCGAGC TAGGAAATGG TGGAGCTAAA	400
	TATTCTGAAG GTGTCTATGC AGTCGCCCTT AACCCAAAAA CAGGTGCTGT	450
	TTTATCCATG TCAGGGATCA AACATGACCT GAAAACGGGA GAGTTGACTC	500
30	CTGATTCCCT GGGAACGGTA ACCAATGTCT TTGTCCCAGG TTCGGTTGTC	550
	AAGGCTGCGA CCATCAGCTC AGGTTGGGAA AATGGTGTTC TATCAGGAAA	600
	CCAAACCTTA ACAGATCAGC CTATTGTTTT CCAAGGTTCA GCTCCAATTT	650
	ATTCTTGGA TAAATTGGCA TATGGATCTT TTCCTATTAC AGCTGTGGAA	700
	GCCTTGAGT ATTCATCCAA TGCTTACATG GTTCAAACCG CTCTTGGAAT	750
35	CATGGGCCAG ACCTATCAAC CAAATATGTT TGTGGAACC AGCAATTTGG	800
	AAACAGCTAT GGGAAAACCT CGTGCGACCT TTGGCGAATA TGGCTTGGGG	850
	GCTGCGACCG GAATTGACCT ACCAGATGAA TCTACTGGAT TTGTTCCCAA	900
	AGAGTATAGC TTTGCTAATT ACATCACCAA TTCCTTTGGG CAGTTTGATA	950
	ACTATACGCC CATGCAGTTG GCTCAGTATG TAGCAACTAT TGCAAATAAT	1000
40	GGTGTTCGTG TGGCTCCTCG TATTGTTGAA GGCATTTATG GTAATAATGA	1050
	TAAGGGAGGA CTGGGTGACT TGATTCAGCA ACTGCAACCG ACAGAGATGA	1100
	ATAAGGTCAA TATATCCGAC TCCGATATGA GCATCTTGCA CCAAGGTTTT	1150
	TATCAGGTTG CCCATGGTAC TAGTGGATTG ACAACTGGAC GTGCCTTTTC	1200
	AAATGGTGCC TTGGTATCCA TTAGCGGAAA AACAGGTACA GCCGAAAGCT	1250
45	ATGTGGCAGA TGGTCAGCAA GCAACCAATA CCAATGCGGT GGCCTATGCC	1300
	CCATCTGATA ATCCCCAAAT CGCTGTGCGA GTGGTCTTTC CTCATAATAC	1350
	CAATCTAACA AATGGTGTAG GACCTTCCAT TGC GCGTGAC ATTATCAATC	1400
	TGTATCAAAA ATACCATCCA ATGAAC TAGA AAGGAAATTA TG	1442

50

2) INFORMATION FOR SEQ ID NO: 1024

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1445 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

55

(ii) MOLECULE TYPE: Genomic DNA

60

571

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(B) STRAIN: StrR-06

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1024

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TTGCCTCTAT TTCAAAGGAG ATGCCTGGCA TTAGTATTTT TACTTCTTGG      50
GATCGAAAGG TTTTGGAAAC TTCCCTTTCT TCTATAGTAG GGAGTGTATC      100
10 CAGTGAAAAA GCTGGTCTCC CAGCGGAAGA AGCAGAAATCC TATCTTAAAA      150
AAGGCTATTC TCTAAATGAC CGTGTGGGAA CCTCCTATTT GGAAAAGCAA      200
TATGAAGAGA CCTTACAAGG AAAACGCTCG GTAAAAGAAA TCCATCTGGA      250
TAAATATGGC AATATGGAAA GCGTGGACAC AATTGAGGAA GGTAAGTAAGG      300
GAAACAATAT CAAACTGACC ATTGATTGCG CCTTCCAAGA TAGCGTGGAT      350
15 GCTTTGCTGA AAAGTTATTT CAATTCCGAG CTAGGAAATG GTGGAGCTAA      400
ATATTCTGAA GGTGTCTATG CAGTCGCCCT TAACCCAAAA ACAGGTGCTG      450
TTTTATCCAT GTCAGGGATC AAACATGACC TGAAAACGGG AGAGTTGACT      500
CCTGATTCCT TGGGAACGGT AACCAATGTC TTTGTCCCAG GTTCGGTTGT      550
CAAGGCTGCG ACCATCAGCT CAGGTTGGGA AAATGGTGTT TTATCAGGAA      600
20 ACCAAACCTT AACAGATCAG CCTATTGTTT TCCAAGGTTT AGCTCCAATT      650
TATTCTTGGT ATAAATTGGC ATATGGATCT TTTCTTATTA CAGCTGTGGA      700
AGCCTTGGAG TATTCATCCA ATGCTTACAT GGTTCAAACC GCTCTTGGAA      750
TCATGGGCCA GACCTATCAA CCAAATATGT TTGTTGGAAC CAGCAATTTG      800
GAAACAGCTA TGGGAAACT TCGTGCGACC TTTGGCGAAT ATGGCTTGGG      850
25 GGCTGCGACC GGAATTGACC TACCAGATGA ATCTACTGGA TTTGTTCCCA      900
AAGAGTATAG CTTTGCTAAT TACATACCA ATTCCTTTGG GCAGTTTGAT      950
AACTATACAC CCATGCAGTT GGCTCAGTAT GTAGCAACTA TTGCAAATAA      1000
TGGTGTTTCG GTGGCTCCTC GTATTGTTGA AGGCATTTAT GGTAATAATG      1050
ATAAGGGAGG ACTGGGTGAC TTGATTCAGC AACTGCAACC GACAGAGATG      1100
30 AATAAGGTCA ATATATCCGA CTCCGATATG AGCATCTTGC ACCAAGGTTT      1150
TTATCAGGTT GCCCATGGTA CTAGTGGATT GACAACTGGA CGTGCCTTTT      1200
CAAATGGTGC CTTGGTATCC ATTAGCGGAA AACAGGTAC AGCCGAAAGC      1250
TATGTGGCAG ATGGTCAGCA AGCAACCAAT ACCAATGCGG TGGCCTATGC      1300
CCCATCTGAT AATCCCCAAA TCGCTGTCGC AGTGGTCTTT CCTCATAATA      1350
35 CCAATCTAAC AAATGGTGTA GGACCTTCCA TTGCGCGTGA CATTATCAAT      1400
CTGTATCAAA AATACCATCC AATGAACTAG AAAGGAAATT ATGCT          1445

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40 2) INFORMATION FOR SEQ ID NO: 1025

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1441 bases

(B) TYPE: Nucleic acid

45 (C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

50 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(B) STRAIN: StrR-07

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1025

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55 TTGCCTCTAT TTCAAAGGAG ATGCCTGGCA TTAGTATTTT TACTTCTTGG      50
GATCGAAAGA TTTTGGAAAC TTCCCTTTCT TCTATAGTAG GGAGTGTATC      100
CAGTGAAAAA GCTGGTCTCC CAGCGGAAGA AGCAGAAATCC TATCTTAAAA      150
AAGGCTATTC TCTAAATGAC CGTGTGGGAA CCTCGTATTT GGAAAAGCAA      200
60 TATGAAGAGA CCTTACAAGG AAAACGCTCG GTAAAAGAAA TCCATCTGGA      250

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	TAAATATGGC	AATATGGAAA	GCGTGGACAC	AATTGAGGAA	GGTAGTAAGG	300
	GAAACAATAT	CAAACCTGACC	ATTGATTG	CCTTCCAAGA	TAGCGTGGAT	350
	GCTTTGCTGA	AAAGTTATTT	CAATTCCGAG	CTAGGAAATG	GTGGAGCCAA	400
	GTATTCTGAG	GGTGTGTATG	CAGTCGCCCT	TAACCCCAAA	ACAGGTGCTG	450
5	TTTTGTCTAT	GTCAGGACTC	AAACATGACC	TGAAAACGGG	AGAGTTGACT	500
	CCTGATTCCCT	TGGGAACGGT	AACCAATGTC	TTTGTCCTCAG	GTTCCGTTGT	550
	CAAGGCTGCG	ACCATCAGCT	CTGGCTGGGA	AAATGGTGTT	TTATCAGGAA	600
	ACCAAACCTT	AACAGATCAG	CCTATTGTTT	TCCAAGGTTC	AGCTCCAATT	650
	TATTCTTGGT	ATAAATTGGC	ATATGGATCT	TTTCCTATTA	CAGCTGTGGA	700
10	AGCCTTGGAG	TATTCATCCA	ATGCTTACAT	GGTTCAAACC	GCTCTTGGAA	750
	TCATGGGCCA	GACCTATCAA	CCAAATATGT	TTGTTGGAAC	CAGCAATTTG	800
	GAAACAGCTA	TGGGAAAAC	TCGTGCGACC	TTTGGCGAAT	ATGGCTTGGG	850
	GGCTGCGACC	GGAATTGACC	TACCAGATGA	ATCTACTGGA	TTTGTTCCCA	900
	AAGACTATAG	CTTTGCTAAT	TACATCACCA	ATGCCTTTGG	GCAGTTTGAT	950
15	AAC TATACGC	CCATGCAGTT	GGCTCAGTAT	GTAGCAACTA	TTGCAAATGA	1000
	TGGTGTTTCGT	GTGGCTCCTC	GTATTGTTGA	AGGCATTAT	GGTAATAATG	1050
	ATAAGGGAGG	ACTGGGTGAC	TTGATTACAGC	AACTGCAACC	GACAGAGATG	1100
	AATAAGGTGA	ATATATCCGA	CTCCGATATG	AGTATCTTGC	ACCAAGGATT	1150
	TTACCAAGTA	TCGCATGGAA	CTAGTCCCCT	TACGACAGGA	CGGGCGTTTT	1200
20	CAGATGGCGC	CACTGTTTCT	ATCAGTGGTA	AGACCGGTAC	AGGTGAAAGC	1250
	TATGTAGCTG	GTGGTCAAGA	AGCTAATAAT	ACCAATGCCG	TGGCCTATGC	1300
	TCCAACAGAA	AATCCTCAA	TTGCAGTTGC	AGTAGTCTTT	CCTCATAATA	1350
	CCAATTTAAC	CAAAAATGTT	GGGCCAGCAA	TTGCTCGCGA	CATTATCAAT	1400
	TTATATAACC	AACACCATCC	AATGAATTAG	AAAGGAAGCC	A	1441
25						

2) INFORMATION FOR SEQ ID NO: 1026

- 30 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1443 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Double
 - (D) TOPOLOGY: Linear
- 35 (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Streptococcus pneumoniae*
 - 40 (B) STRAIN: StrR-08

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1026

	TATTGCCTCT	ATTTCAAAGG	AGATGCCTGG	CATTAGTATT	TCTACTTCTT	50
45	GGGATCGAAA	GGTTTTGGAA	ACTTCCCTTT	CTTCTATAGT	AGGGAGTGTA	100
	TCCAGTGAAA	AAGCTGGTCT	CCCAGCGGAA	GAAGCAGAAT	CCTATCTTAA	150
	AAAAGGCTAT	TCTCTAAATG	ACCGTGTTGG	AACCTCCTAT	TTGGAAAAGC	200
	AATATGAAGA	GACCTTACAA	GGAAAACGCT	CGGTAAAAGA	AATCCATCTG	250
	GATAAATATG	GCAATATGGA	AAGCGTGGAC	ACAATTGAGG	AAGGTAGTAA	300
50	GGGAAACAAT	ATCAAACCTGA	CCATTGATTT	GGCCTTCCAA	GATAGCGTGG	350
	ATGCTTTGCT	GAAAAGTTAT	TTCAATTCCG	AGCTAGGAAA	TGGTGGAGCT	400
	AAATATTCTG	AAGGTGTCTA	TGCAGTCGCC	CTTAACCCAA	AAACAGGTGC	450
	TGTTTTATCC	ATGTCAGGGA	TCAAACATGA	CCTGAAAACG	GGAGAGTTGA	500
	CTCCTGATTC	CTTGGGAACG	GTAACCAATG	TCTTTGTCCC	AGGTTCGGTT	550
55	GTCAAGGCTG	CGACCATCAG	CTCAGGTTGG	GAAAATGGTG	TTTTATCAGG	600
	AAACCAAACC	TTAACAGATC	AGCCTATTGT	TTTCCAAGGT	TCAGCTCCAA	650
	TTTATTCTTG	GTATAAATTG	GCATATGGAT	CTTTTCCTAT	TACAGCTGTG	700
	GAAGCCTTGG	AGTATTCATC	CAATGCTTAC	ATGGTTCAAA	CCGCTCTTGG	750
	AATCATGGGC	CAGACCTATC	AACCAAATAT	GTTTGTGGA	ACCAGCAATT	800
60	TGGAAACAGC	TATGGGAAAA	CTTCGTGCGA	CCTTTGGCGA	ATATGGCTTG	850

	GGGGCTGCGA	CCGGAATTGA	CCTACCAGAT	GAATCTACTG	GATTGTGTTCC	900
	CAAAGAGTAT	AGCTTTGCTA	ATTACATCAC	CAATTCCTTT	GGGCAGTTTG	950
	ATAACTATAC	GCCCATGCAG	TTGGCTCAGT	ATGTAGCAAC	TATTGCAAAT	1000
	AATGGTGTTC	GTGTGGCTCC	TCGTATTGTT	GAAGGCATTT	ATGGTAATAA	1050
5	TGATAAGGGA	GGACTGGGTG	ACTTGATTCA	GCAACTGCAA	CCGACAGAGA	1100
	TGAATAAGGT	CAATATATCC	GACTCCGATA	TGAGCATCTT	GCACCAAGGT	1150
	TTTTATCAGG	TTGCCCATGG	TACTAGTGGA	TTGACAACGT	GACGTGCCTT	1200
	TTCAAATGGT	GCCTTGGTAT	CCATTAGCGG	AAAAACAGGT	ACAGCCGAAA	1250
	GCTATGTGGC	AGATGGTCAG	CAAGCAACCA	ATACCAATGC	GGTGGCCTAT	1300
10	GCCCCATCTG	ATAATCCCCA	AATCGCTGTC	GCAGTGGTCT	TTCCTCATAA	1350
	TACCAATCTA	ACAAATGGTG	TAGGACCTTC	CATTGCGCGT	GACATTATCA	1400
	ATCTGTATCA	AAAATACCAT	CCAATGAAC	AGAAAGGAAA	TTA	1443

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2) INFORMATION FOR SEQ ID NO: 1027

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1443 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Streptococcus pneumoniae*
- (B) STRAIN: StrR-09

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1027

	TATTGCCTCT	ATTTCAAAGG	AGATGCCTGG	CATTAGTATT	TCTACTTCTT	50
	GGGATAGAAA	GGTTTTGGAA	ACTTCCCTTT	CTTCTATAGT	TGGGAGTGTA	100
	TCCAGTGAAA	AAGCTGGTCT	CCCAGCGGAA	GAAGCAGAAG	CCTATCTTAA	150
35	AAAAGGCTAT	TCTCTAAATG	ATCGTGTAGG	AACCTCCTAT	TTGGAAAAGC	200
	AATATGAAGA	GACCTTACAA	GGAAAACGCT	CGGTAAAAGA	AATCCATCTG	250
	GATAAATATG	GCAATATGGA	AAGCGTGGAT	ACAATTGAGG	AAGGTAGTAA	300
	GGGAAACAAT	ATCAAACCTGA	CCATTGATTT	GGCTTTCCAA	GATAGCGTGG	350
	ATGCTTTACT	GAAAAGTTAT	TTCAATTCCG	AGCTAGAAAA	TGGTGGAGCC	400
40	AAGTATTCTG	AAGGTGTCTA	TGCAGTCGCC	CTTAACCCAA	AAACAGGTGC	450
	TGTTTTGTCT	ATGTCAGGGA	TTAAACATGA	CTTGAAAACG	GGAGATTTAA	500
	CACCTGATTC	CTTGGAACA	GTAACCAATG	TCTTTGTCCC	GGGTTCTGTT	550
	GTCAAGGCGG	CGACCATCAG	CTCTGGTTGG	GAGAATGGAG	TCTTATCAGG	600
	AAATCAGACC	TTGACAGACC	AACCGATTGT	CTTCCAAGGT	TCAGCTCCGA	650
45	TTAATTCTTG	GTACACTCAG	GCTTACGATT	CATTTCCGAT	TACAGCGGTG	700
	GAAGCCTTGG	AGTATTCTTC	TAATGCCTAT	ATGGTCCAA	CAGCTCTAGG	750
	TCTTATGGGG	CAGACCTACC	AACCCAATAT	GTTTGTGCGC	ACCAGCAATC	800
	TAGAGTCTGC	TATGGGGAAA	TTGCGTTCAA	CCTTTGGTGA	ATATGGCTTG	850
	GGCTCTGCGA	CTGGGATTGA	CCTACCAGAT	GAATCTACTG	GATTGTGTTCC	900
50	CAAAGAGTAT	AGCTTTGCTA	ATTACATTAC	TAATGCCTTT	GGGCAGTTTG	950
	ATAACTATAC	GCCGATGCAG	TTGGCTCAGT	ATGTAGCAAC	TATTGCAAAT	1000
	GATGGTGTTC	GTGTGGCTCC	TCGTATTGTG	GAAGGCATTT	ATGGCAATAA	1050
	TGATAAGGGA	GGACTGGGTG	ACTTGATTCA	GCAACTGCAA	CCGACAGAGA	1100
	TGAATAAGGT	CAATATATCC	GACTCCGATA	TGAGTATCTT	GCACCAAGGT	1150
55	TTTTATCAGG	TTGCTCATGG	GACTAGCGGA	TTGACAACAG	GTCGTGCCTT	1200
	TTCCAATGGT	GCAGCTGTAT	CCATTAGTGG	AAAAACAGGT	ACCGCCGAAA	1250
	GTTATGTAGC	AGGTGGCCAA	GAAGCCAACA	ATACTAATGC	TGTAGCCTAT	1300
	GCACCATCAG	ATAATCCTCA	AATAGCTGTT	GCTGTTGTCT	TCCCTCATAA	1350
	CACCAATCTA	ACAAATGGTG	TAGGACCTTC	CATTGCGCGT	GATATTATCA	1400
60	ATCTGTATCA	AAAATACCAT	CCAATGAAC	AGAAAGGAAT	TTA	1443

2) INFORMATION FOR SEQ ID NO: 1028

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1446 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

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(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
 (B) STRAIN: StrR-10

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1028

20	TATTGCCTCT	ATTTCAAAGG	AGATGCCTGG	CATTAGTATT	TCTACCTCTT	50
	GGGATAGAAA	GGTTTTGGAA	ACTTCTCTTT	CTTCTATAGT	AGGGAGTGTA	100
	TCCAGTGAAA	AAGCTGGTCT	CCCAGCGGAA	GAAGCAGAAG	CCTATCTTAA	150
	AAAAGGCTAT	TCTCTAAATG	ACCGTGTTGG	GACTTCTTAC	CTGGAAAAAC	200
	AATACGAGGA	AACCTTACAA	GGAAAACGCT	CGGTAAAAGA	AATCCATCTG	250
25	GATAAATATG	GCAATATGGA	AAGCGTGGAT	ACAATTGAGG	AAGGTAGTAA	300
	GGGAAACAAT	ATCAAACCTGA	CCATTGATTT	GGCCTTCCAA	GATAGCGTGG	350
	ATGCTTTGCT	GAAAAGTTAT	TTCAATTCCG	AGCTAGGAAA	TGGTGGAGCT	400
	AAGTATTCTG	AAGGCGTGTA	TGCAGTCGCC	CTTAACCCCA	AAACAGGTGC	450
	TGTTTTGTCT	ATGTCAGGAC	TCAAACATGA	CCTGAAAACG	GGAGACTTGA	500
30	CGCCTGATTC	CTTGGAACG	GTAACCAATG	TCTTTGTCCC	AGGGTCAGTA	550
	GTTAAGGCCG	CTACCATCAG	CTCAGGTGG	GAAAATGGTG	TTTTATCAGG	600
	AAACCAAACC	TTAACAGATC	AGCCTATTGT	TTTCCAAGGT	TCAGCTCCAA	650
	TTTATTCTTG	GTATAAATTG	GCATATGGAT	CTTTTCCTAT	TACAGCTGTG	700
	GAAGCCTTGG	AGTATTCATC	TAATGCTTAC	ATGGTTCAAA	CCGCTCTTGG	750
35	AATCATGGGC	CAGACCTATC	AACCAAATAT	GTTTGTGGA	ACCAGCAATT	800
	TGGAAACAGC	TATGGGAAAA	CTTCGTGCGA	CCTTTGGCGA	ATATGGCTTG	850
	GGGGCTGCGA	CCGGAATTGA	CCTACCAGAT	GAATCTACTG	GATTGTGTTCC	900
	CAAAGAGTAT	AGCTTTGCTA	ATTACATTAC	TAATGCCTTT	GGGCAGTTTG	950
	ATAACTATAC	GCCGATGCAG	TTGGCTCAGT	ATGTAGCAAC	TATTGCAAAAT	1000
40	GATGGTGTTC	GTGTGGCTCC	TCGTATTGTT	GAAGGCATTT	ATGGTAATAA	1050
	TGATAAGGGA	GGACTGGGTG	ACTTGATTCA	GCAACTGCAA	CCGACAGAGA	1100
	TGAATAAGGT	CAATATATCC	GACTCCGATA	TGAGCATCTT	GCACCAAGGT	1150
	TTTTATCAGG	TTGCCCATGG	TACTAGTGGA	TTGACAACCTG	GACGTGCCTT	1200
	TTCAAATGGC	GCCTTGGTAT	CCATTAGCGG	AAAAACAGGT	ACAGCCGAAA	1250
45	GCTATGTGGC	AGATGGTCAG	CAAGCAACCA	ATACCAATGC	GGTGGCCTAT	1300
	GCCCCATCTG	ATAATCCCCA	AATCGCTGTT	GCAGTGGTCT	TTCTCATATA	1350
	TACCAATCTA	ACAAATGGTG	TAGGACCTTC	CATTGCGCGT	GACATTATCA	1400
	ATCTGTATCA	AAAATACCAT	CCAATGAAC	AGAAAGGAAA	TTATGC	1446

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2) INFORMATION FOR SEQ ID NO: 1029

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1423 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

55

(ii) MOLECULE TYPE: Genomic DNA

60

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
 (B) STRAIN: StrR-11

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1029

	TTGCCTCTAT	TTCAAAGGAG	ATGCCTGGCA	TTAGTATTTT	TACTTCTTGG	50
	GATAGAAAGG	TTTTGGAAAC	TTCCCTTTCT	TCTATAGTTG	GGAGTGTATC	100
10	CAGTGAAAAA	GCTGGTCTCC	CAGCGGAAGA	AGCAGAAGCC	TATCTTAAAA	150
	AAGGCTATTC	TCTAAATGAC	CGTGTAGGAA	CCTCCTATTT	GGAAAAGCAA	200
	TATGAAGAGA	CCTTACAAGG	AAAACGCTCG	GTAAAAGAAA	TCCATCTGGA	250
	TAAATATGGC	AATATGGAAA	GCGTGGATAC	AATTGAGGAA	GGTAGTAAGG	300
	GAAACAATAT	CAAAC TGACC	ATTGATTTGG	CCTTCCAAGA	TAGCGTGGAT	350
15	GCTTTACTGA	AAAGTTATTT	CAATTCTGAG	CTAGAAAATG	GTGGAGCCAA	400
	GTATTCTGAA	GGTGTCTATG	CAGTCGCCCT	TAACCCAAAA	ACAGGTGCGG	450
	TTTTGTCTAT	GTCAGGGATT	AAACATGACT	TGAAAACGGG	AGAGTTGACG	500
	CCTGATTCTT	TGGGAACGGT	AACCAATGTC	TTTGTTCCAG	GTTTCGGTTGT	550
	CAAGGCGGCG	ACCATCAGCT	CAGGTTGGGA	AAATGGAGTC	TTGTCAGGAA	600
20	ACCAGACCTT	GACAGACCAG	TCCATTGTCT	TCCAAGGTTT	AGCTCCCATC	650
	AATTCTTGGT	ATACTCAGGC	TTACGGTTCA	TTCCCTATCA	CAGCGGTCCA	700
	AGCTCTGGAG	TATTCATCCA	ATGCTTATAT	GGTCCAAACA	GCCTTAGGTC	750
	TTATGGGGCA	GACCTATCAA	CCCAATATGT	TTGTCGGCAC	CAGCAATCTA	800
	GAGTCTGCTA	TGGGTAAATT	GCGTTCAACC	TTTGGCGAAT	ATGGCTTGGG	850
25	GGCTGCGACT	GGGATTGATC	TACCAGATGA	ATCTACTGGA	TTTGTTCCCA	900
	AAGACTATAA	CTTTGCCAAT	TTCATTACCA	ATGCCTTTGG	GCAGTTTGAT	950
	AACTATACCC	CAATGCAATT	GGCTCAGTAT	GTAGCAACTA	TTGCAAATGA	1000
	TGGTGTTTCG	GTGGCTCCTC	GTATTGTTGA	AGGCATTTAT	GGTAATAATG	1050
	ATAAGGGAGG	ACTGGGTGAC	TTGATTCAGC	AACTGCAACC	GACAGAGATG	1100
30	AATAAGGTCA	ATATATCCGA	CTCCGATATG	AGTGTCTTGC	ACCAAGGTTT	1150
	TTATCAGGTT	GCTCATGGGA	CTAGTGGGTT	GACAACTGGC	CGTGCCTTTT	1200
	CAAATGGTGC	CTTGGTATCC	ATTAGCGGAA	AAACGGGTAC	AGCCGAAAGC	1250
	TATGTGGCAG	ATGGTCAGGA	AGCAACCAAT	ACCAATGCGG	TGGCCTATGC	1300
	CCCATCTGAT	AATCCCCAAA	TCGCTGTCGC	AGTGGTCTTT	CCTCATAATA	1350
35	CCAATCTAAC	AAATGGTGTA	GGACCTTCCA	TTGCGCGTGA	CATTATCAAT	1400
	CTGTATCAAA	AATACCATCC	AAT			1423

40 2) INFORMATION FOR SEQ ID NO: 1030

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1447 bases
 (B) TYPE: Nucleic acid
 45 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

50 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
 (B) STRAIN: StrR-12

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1030

55	TATTGCCTCT	ATTTCAAAGG	AGATGCCTGG	CATTAGTATT	TCTACTTCTT	50
	GGGATCGAAA	GGTTTTGGAA	ACTTCCCTTT	CTTCTATAGT	AGGGAGTGTA	100
	TCCAGTGAAA	AAGCTGGTCT	CCCAGCGGAA	GAAGCAGAAT	CCTATCTTAA	150
	AAAAGGCTAT	TCTCTAAATG	ACCGTGTGTT	AACCTCCTAT	TTGGAAAAGC	200
60	AATATGAAGA	GACCTTACAA	GGAAAACGCT	CGGTAAAAGA	AATCCATCTG	250

	GATAAATATG	GCAATATGGA	AAGCGTGGAC	ACAATTGAGG	AAGGTAGTAA	300
	GGGAAACAAT	ATCAAACCTGA	CCATTGATTT	GGCCTTCCAA	GATAGCGTGG	350
	ATGCTTTGCT	GAAAAGTTAT	TTCAATTCCG	AGCTAGGAAA	TGGTGGAGCT	400
	AAATATTCTG	AAGGTGTCTA	TGCAGTCGCC	CTTAACCCAA	AAACAGGTGC	450
5	TGTTTTATCC	ATGTCAGGGA	TCAAACATGA	CCTGAAAACG	GGAGAGTTGA	500
	CTCCTGATTC	CTTGGGAACG	GTAACCAATG	TCTTTGTCCC	AGGTTTCGGTT	550
	GTCAAGGCTG	CGACCATCAG	CTCAGGTTGG	GAAAATGGTG	TTTTATCAGG	600
	AAACCAAACC	TTAACAGATC	AGCCTATTGT	TTTCCAAGGT	TCAGCTCCAA	650
	TTTATTCTTG	GTATAAATTG	GCATATGGAT	CTTTTCCTAT	TACAGCTGTG	700
10	GAAGCCTTGG	AGTATTCATC	CAATGCCTTAC	ATGGTTCAAA	CCGCTCTTGG	750
	AATCATGGGC	CAGACCTATC	AACCAAATAT	GTTTGTGGGA	ACCAGCAATT	800
	TGGAAACAGC	TATGGGAAAA	CTTCGTGCGA	CCTTTGGCGA	ATATGGCTTG	850
	GGGGCTGCGA	CCGGAATTGA	CCTACCAGAT	GAATCTACTG	GATTTGTTCC	900
	CAAAGAGTAT	AGCTTTGCTA	ATTACATCAC	CAATTCCTTT	GGGCAGTTTG	950
15	ATAACTATAC	GCCCATGCAG	TTGGCTCAGT	ATGTAGCAAC	TATTGCAAAT	1000
	AATGGTGTTC	GTGTGGCTCC	TCGTATTGTT	GAAGGCATTT	ATGGTAATAA	1050
	TGATAAGGGA	GGACTGGGTG	ACTTGATTCA	GCAACTGCAA	CCGACAGAGA	1100
	TGAATAAGGT	CAATATATCC	GACTCCGATA	TGAGCATCTT	GCACCAAGGT	1150
	TTTTATCAGG	TTGCCCATGG	TACTAGTGGA	TTGACAACTG	GACGTGCCTT	1200
20	TTCAAATGGT	GCCTTGGTAT	CCATTAGCGG	AAAAACAGGT	ACAGCCGAAA	1250
	GCTATGTGGC	AGATGGTCAG	CAAGCAACCA	ATACCAATGC	GGTGGCCTAT	1300
	GCCCCATCTG	ATAATCCCCA	AATCGCTGTC	GCAGTGGTCT	TTCCTCATAA	1350
	TACCAATCTA	ACAAATGGTG	TAGGACCTTC	CATTGCGCGT	GACATTATCA	1400
	ATCTGTATCA	AAAATACCAT	CCAATGAAC	AGAAAGGAAA	TTATGCT	1447
25						

2) INFORMATION FOR SEQ ID NO: 1031

30 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1446 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
 (B) STRAIN: StrR-13

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1031

	ATTGCCTCTA	TTTCAAAGGA	GATGCCTGGC	ATTAGTATTT	CTACCTCTTG	50
45	GGATAGAAAG	GTTTTGGAAA	CTTCTCTTTC	TTCTATAGTA	GGGAGTGTAT	100
	CCAGTGAAAA	AGCTGGTCTC	CCAGCGGAAG	AAGCAGAAGC	CTATCTTAAA	150
	AAAGGCTATT	CTCTAAATGA	CCGTGTTGGG	ACTTCTTACC	TGGAAAAACA	200
	ATACGAGGAA	ACCTTACAAG	GAAAACGCTC	GGTAAAAGAA	ATCCATCTGG	250
	ATAAATATGG	CAATATGGAA	AGCGTGGATA	CAATTGAGGA	AGGTAGTAAG	300
50	GGAAACAATA	TCAAACCTGAC	CATTGATTTG	GCCTTCCAAG	ATAGCGTGGA	350
	TGCTTTGCTG	AAAAGTTATT	TCAATTCCGA	GCTAGGAAAT	GGTGGAGCTA	400
	AGTATTCTGA	AGGCGTGTAT	GCAGTCGCCC	TTAACCCCAA	AACAGGTGCT	450
	GTTTTGTCTA	TGTCAGGACT	CAAACATGAC	CTGAAAACGG	GAGACTTGAC	500
	GCCTGATTCC	TTGGGAACGG	TAACCAATGT	CTTTGTCCCA	GGGTCAGTAG	550
55	TTAAGGCCGC	TACCATCAGC	TCAGGTTGGG	AAAATGGTGT	TTTATCAGGA	600
	AACCAAACCT	TAACAGATCA	GCCTATTGTT	TTCCAAGGTT	CAGCTCCAAT	650
	TTATTCTTGG	TATAAATTGG	CATATGGATC	TTTTCTTATT	ACAGCTGTGG	700
	AAGCCTTGGA	GTATTCATCT	AATGCTTACA	TGGTTCAAAC	CGCTCTTGGA	750
	ATCATGGGCC	AGACCTATCA	ACCAAATATG	TTTGTGGGAA	CCAGCAATTT	800
60	GGAAACAGCT	ATGGGAAAAC	TTCGTGCGAC	CTTTGGCGAA	TATGGCTTGG	850

	GGGCTGCGAC	CGGAATTGAC	CTACCAGATG	AATCTACTGG	ATTTGTTCCC	900
	AAAGAGTATA	GCTTTGCTAA	TTACATTACT	AATGCCTTTG	GGCAGTTTGA	950
	TAACATACG	CCGATGCAGT	TGGCTCAGTA	TGTAGCAACT	ATTGCAAATG	1000
	ATGGTGTTCG	TGTGGCTCCT	CGTATTGTTG	AAGGCATTTA	TGGTAATAAT	1050
5	GATAAGGGAG	GACTGGGTGA	CTTGATTGAG	CAACTGCAAC	CGACAGAGAT	1100
	GAATAAGGTC	AATATATCCG	ACTCCGATAT	GAGCATCTTG	CACCAAGGTT	1150
	TTTATCAGGT	TGCCCATGGT	ACTAGTGGAT	TGACAACTGG	ACGTGCCTTT	1200
	TCAAATGGCG	CCTTGGTATC	CATTAGCGGA	AAAACAGGTA	CAGCCGAAAG	1250
	CTATGTGGCA	GATGGTCAGC	AAGCAACCAA	TACCAATGCG	GTGGCCTATG	1300
10	CCCCATCTGA	TAATCCCCAA	ATCGCTGTTG	CAGTGGTCTT	TCCTCATAAT	1350
	ACCAATCTAA	CAAATGGTGT	AGGACCTTCC	ATTGCGCGTG	ACATTATCAA	1400
	TCTGTATCAA	AAATACCATC	CAATGAACATA	GAAAGGAAAT	TATGCT	1446

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2) INFORMATION FOR SEQ ID NO: 1032

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1446 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Streptococcus pneumoniae*
- (B) STRAIN: StrR-14

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1032

	ATTGCCTCTA	TTTCAAAGGA	GATGCCTGGC	ATTAGTATTT	CTACTTCTTG	50
	GGATAGAAAG	GTTTTGGAAA	CTTCCCTTTC	TTCTATAGTT	GGGAGTGTAT	100
	CCAGTGAAAA	AGCTGGTCTC	CCAGCGGAAG	AAGCAGAAGC	CTATCTTAAA	150
35	AAAGGCTATT	CTCTAAATGA	TCGTGTTGGA	ACCTCCTATT	TGGAAAAGCA	200
	ATATGAAGAG	ACCTTACAAG	GGAAACGCTC	GGTAAAAGAA	ATCCATCTGG	250
	ATAAATATGG	CAATATGGAA	AGTGTGGATA	CAATTGAGGA	AGGTAGTAAG	300
	GGAAACAATA	TCAAGCTGAC	CATTGATTTG	GCCTTCCAAG	ATAGCGTGGA	350
	TGCTTTGCTG	AAAAGTTATT	TCAATTCCGA	GCTAGGAAAT	GGTGGAGCCA	400
40	AGTATTCTGA	GGGTGTGTAT	GCAGTCGCCC	TTAACCCCAA	AACAGGTGCT	450
	GTTTTGTCTA	TGTCAGGACT	CAAACATGAC	CTGAAAACGG	GAGAGTTGAC	500
	TCCTGATTCC	TTGGGAACGG	TAACCAATGT	CTTTGTCCCA	GGTTCGGTTG	550
	TCAAGGCTGC	GACCATCAGC	TCTGGCTGGG	AAAATGGAGT	CTTATCAGGA	600
	AACCAGACCT	TGACAGACCA	GTCCATTGTC	TTTCAAGGTT	CAGCTCCCAT	650
45	CAATTCTTGG	TATACTCAGG	CTTACGGTTC	ATTCCCTATC	ACAGCAGTCC	700
	AAGCTCTGGA	GTATTGATCT	AATGCCTATA	TGGTCCAAAC	AGCTTTAGGT	750
	CTTATGGGGC	AGACCTACCA	ACCTAATATG	TTTGTGCGCA	CCAGCAACCT	800
	AGAGTCTGCT	ATGGGGAAAT	TGCGTTCAAC	CTTTGGTGAA	TATGGTTTGG	850
	GTTCTGCGAC	CGGGATTGAC	CTACCAGATG	AATCTACTGG	ATTTGTTCCC	900
50	AAAGACTATA	GCTTTGCTAA	TTACATCACC	AATGCCTTTG	GGCAGTTTGA	950
	TAACATACG	CCGATGCAGT	TGGCTCAGTA	TGTAGCAACT	ATTGCAAATG	1000
	ATGGTGTTCG	TGTGGCTCCT	CGTATTGTTG	AAGGCATTTA	TGGAAATAAT	1050
	GATAAGGGAG	GCCTAGGCGA	CTTGATTGAG	CAACTGCAAC	CGACAGAGAT	1100
	GAATAAGGTC	AATATATCCG	ACTCTGATAT	GAGTATTTTG	CACCAAGGTT	1150
55	TTTATCAGGT	TGCTCATGGG	ACTAGTGGAT	TGACAACTGG	ACGTGCCTTT	1200
	TCAAATGGCG	CAGCGGTATC	CATTAGTGGA	AAAACAGGTA	CTGCCGAAAG	1250
	TTATGTTGAG	GGTGGTCAAG	AAGCTAACAA	TACTAATGCT	GTGGCCTATG	1300
	CACCATCAGA	TAATCCTCAA	ATCGCTGTAG	CTGTTGTCTT	CCCTCATAAC	1350
	ACCAACCTTA	CAAATGGTGT	CGGACCTTCC	ATTGCGCGCG	ATATTATCAA	1400
60	CCTCTATAAC	CAACATCATC	CAATGAATTA	GAAAGGAACA	TATGCT	1446

2) INFORMATION FOR SEQ ID NO: 1033

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1446 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

10

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
 (B) STRAIN: StrR-15

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1033

20	TATTGCCTCT	ATTTCAAAGG	AGATGCCTGG	CATTAGTATT	TCTACTTCTT	50
	GGGATAGAAA	GGTTTTGGAA	ACTTCCCTTT	CTTCTATAGT	TGGGAGTGTA	100
	TCCAGTGAAA	AAGCTGGTCT	CCCAGCGGAA	GAAGCAGAAG	CCTATCTTAA	150
	AAAAGGCTAT	TCTCTAAATG	ACCGTGTTGG	AACCTCGTAT	TTGGAAAAGC	200
	AATATGAAGA	GACCTTACAA	GGAAAACGCT	CGGTAAAAGA	AATCCATCTG	250
25	GATAAATATG	GCAATATGGA	AAGCGTGGAT	ACAATTGAGG	AAGGTAGTAA	300
	GGGAAACAAT	ATCAAGCTGA	CCATTGATTT	GGCCTTCCAA	GATAGCGTGG	350
	ATGCTTTGCT	GAAAAGTTAT	TTCAATTCCG	AGCTAGGAAA	TGGTGGAGCC	400
	AAGTATTCTG	AGGGTGTGTA	TGCAGTCGCC	CTTAACCCCA	AAACAGGTGC	450
	TGTTTTGTCT	ATGTCAGGAC	TCAAACATGA	CCTGAAAACG	GGAGAGTTGA	500
30	CTCCTGATTC	CTTGGAACG	GTAACCAATG	TCTTTGTCCC	AGGTTCGGTT	550
	GTTAAGGCCG	CTACCATCAG	CTCAGGTTGG	GAAAATGGTG	TTTTATCAGG	600
	AAACCAAACC	TTAACAGATC	AGCCTATTGT	TTTCCAAGGT	TCAGCTCCAA	650
	TTTATTCTTG	GTATAAATTG	GCATATGGAT	CTTTTCCTAT	TACAGCTGTG	700
	GAAGCCTTGG	AGTATTCATC	CAATGCTTAC	ATGGTTCAAA	CCGCTCTTGG	750
35	AATCATGGGC	CAGACCTATC	AACCAAATAT	GTTTGTGTTGA	ACCAGCAATT	800
	TGGAAACAGC	TATGGGAAAA	CTTCGTGCGA	CCTTTGGCGA	ATATGGCTTG	850
	GGGGCTGCGA	CCGGAATTGA	CCTACCAGAT	GAATCTACTG	GATTGTGTTCC	900
	CAAAGAGTAT	AGCTTTGCTA	ATTACATCAC	CAATGCCTTT	GGGCAGTTTG	950
	ATAACTATAC	GCCCATGCAG	TTGGCTCAGT	ATGTAGCAAC	TATTGCAAAT	1000
40	GATGGTGTTC	GTGTGGCTCC	TCGTATTGTT	GAAGGCATTT	ATGGTAATAA	1050
	TGATAAGGGA	GGACTGGGTG	ACTTGATTCA	GCAACTGCAA	CCGACAGAGA	1100
	TGAATAAGGT	CAATATATCC	GACTCCGATA	TGAGTATCTT	GCACCAAGGT	1150
	TTTTATCAGG	TTGCTCATGG	GACTAGTGGA	TTGACAACCTG	GACGTGCTTT	1200
	TTCAAATGGT	GCCTTGGTAT	CCATTAGTGG	GAAAACAGGT	ACTGCCGAAA	1250
45	GTTATGTTGC	AGGTGGTCAA	GAAGCCAACA	ATACCAACGC	GGTGGCCTAT	1300
	GCCCCATCAG	ATAATCCTCA	AATCGCTGTT	GCCGTTGTCT	TCCCTCATAA	1350
	CACCAATCTA	ACAAATGGTG	TTGGACCTTC	TATTGCACGC	GATATTATCA	1400
	ACCTCTATAA	CCAACACCAT	CCAATGAATT	AGAAAGGAAC	TTATGC	1446

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2) INFORMATION FOR SEQ ID NO: 1034

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1670 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

55

(ii) MOLECULE TYPE: Genomic DNA

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(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
 (B) STRAIN: StrR-01

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1034

	GGAAACTGCA	GAGGTCAAGG	GGATTGATTT	TACAACCAGT	CCCAATCGTA	50
	GTTATCCAAA	CGGACAATTT	GCTTCTAGTT	TTATCGGACT	AGCTCAGCTC	100
10	CATGAAAATG	AAGATGGCAG	CAAGAGCTTA	CTGGGAACCT	CTGGAATGGA	150
	GAGTTCCTTG	AACAGTATTC	TTGCAGGGAC	AGACGGTATT	ATTACCTATG	200
	AAAAAGACCG	TGTAGGAAAT	ATCGTACCAG	GTACAGAACT	GGTATCGCAA	250
	CAAACTGTGG	ATGGCAAGGA	TGTTTATACA	ACATTGTCTA	GTCCGCTACA	300
	ATCTTTTCATG	GAAACTCAGA	TGGATGCCCTT	TCTAGAAAAA	GTAAAAGGTA	350
15	AGTATATGAC	CGCGACCTTG	GTCAGTGCAA	AGACCGGTGA	AATCCTCGCT	400
	ACCACCCAAC	GACCTACCTT	TAATGCAGAT	ACTAAAGAAG	GAATCACTGA	450
	GGACTTTTGT	TGGCGTGATA	TTCTTTTATCA	AAGTAACTAT	GAACCAGGAT	500
	CAGCCATGAA	GGTTATGACG	TTAGCTTCTT	CTATTGATAA	TAATACCTTC	550
	CCAAGTGGAG	AATACTTCAA	TAGCAGTGAA	TTCAAAATAG	CGGATGCGAC	600
20	GACTCGAGAT	TGGGATGTTA	ATGATGGTTT	GACTACTGGT	GGGATGATGA	650
	CTTTCTTACA	AGGTTTCGCT	CACTCCAGTA	ATGTTGGAAT	GAGTCTACTT	700
	GAACAAAAAA	TGGGAGATGC	TACTTGTTTG	GATTATCTAA	AACGCTTTAA	750
	ATTTGGGGTT	CCAACCTCGCT	TTGGCTTGAC	AGATGAATAC	GCTGGTCAAC	800
	TTCCAGCTGA	TAATATTGTT	AGTATTGCTC	AAAGCTCATT	TGGGCAAGGA	850
25	ATTTTCAGTGA	CACAAACACA	AATGCTTCGT	GCCTTTACAG	CTATTGCTAA	900
	TGATGGAGTT	ATGCTGGAGC	CAAAATTTAT	AAGTGCTATT	TATGATACTA	950
	ACAATCAGTC	TGTACGTAAG	TCACAAAAAG	AAATAGTAGG	AAATCCTGTT	1000
	TCCAAAGAGG	CAGCAAGCAC	AACTCGAAAT	CACATGATCT	TAGTTGGGAC	1050
	GGACCCTCTA	TATGGAACCTA	TGTATAATCA	CTACACAGGA	AAGCCAATTA	1100
30	TAACAGTTCC	TGGACAAAAT	GTAGCAGTTA	AATCCGGTAC	GGCTCAAATC	1150
	GCTGATGAGA	AAAATGGAGG	ATACTTGTTT	GGTTCTACCA	ATTATATTTT	1200
	CTCAGTTGTG	ACTATGAATC	CTGCTGAAAA	TCCTGATTTT	ATCTTGATATG	1250
	TAACGGTTCA	ACAGCCTGAG	CATTATTTCAG	GTATCCAGTT	GGGAGAATTT	1300
	GCCACCCCAA	TCTTGGAGCG	GGCTTCAGCT	ATGAAAGAAT	CTCTCAATCT	1350
35	TCAATCTCCA	GCCAAAAATT	TAGATAAAGT	TACGACAGAA	TCTTCTTATG	1400
	CAATGCCTAG	CATCAAGGAT	ATTTACACCTG	GTGAGTTGGC	GGAAGCCTTA	1450
	CGCCGAAATA	TTGTGCAACC	AATCGTTGTA	GGTACTGGAA	CAAAGATTAA	1500
	AGACACTTCT	TAGAAGAAG	GGACCAATCT	TGCACCAAAC	CAACAAGTTC	1550
	TCCTTTTATC	GGATAAGGTA	GAAGAAATTC	CAGACATGTA	TGGCTGGAAA	1600
40	AAAGAGACTG	CCGAGACCTT	TGCTAAATGG	TTGGATATTG	AACTGGAATT	1650
	TGAAGGTTCA	GGTTCCGTTG				1670

45 2) INFORMATION FOR SEQ ID NO: 1035

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1683 bases
 (B) TYPE: Nucleic acid
 50 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

55 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
 (B) STRAIN: StrR-02

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1035

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	AAAGAATTGG	AAACTGCAGA	GGTCAAGGGG	ATTGATTTTA	CAACCAAGTCC	50
	CAATCGTAGT	TACCCAAATG	GACAATTTGC	TTCTAGTTTT	ATCGGTCTAG	100
	CTCAGCTCCA	TGAAAATGAA	GATGGAAGCA	AGAGTTTGCT	GGGAACCTCT	150
	GGAATGGAGA	GTTCTTGAA	CAGTATTCTT	GCAGGGACAG	ACGGCATTAT	200
5	TACCTATGAA	AAGGATCGTC	TGGGCAATAT	TGTACCCGGA	ACAGAACAAG	250
	TTTCCCAACA	AACGGTGGAT	GGCAAGGATG	TTTACACAAC	CATTTCAGC	300
	CCCCTCCAGT	CCTTCATGGA	AACTCAGATG	GATGCCTTTC	TAGAAAAAGT	350
	AAAAGGTAAG	TATATGACCG	CGACCTTGGT	CAGTGCAAAG	ACCGGTGAAA	400
	TCCTCGCTAC	CACCCAACGA	CCTACCTTTA	ATGCAGATAC	TAAAGAAGGA	450
10	ATCACTGAGG	ACTTTGTTTG	GCGTGATATT	CTTTATCAAA	GTAAGTATGA	500
	ACCAGGATGA	GCCATGAAGG	TTATGACGTT	AGCTTCTTCT	ATTGATAATA	550
	ATACCTTCCC	AAGTGGAGAA	TACTTCAATA	GCAGTGAATT	CAAAATAGCG	600
	GATGCGACGA	CTCGAGATTG	GGATGTTAAT	GATGGTTTGA	CTACTGGTGG	650
	GATGATGACT	TTCTTACAAG	GTTTCGCTCA	CTCCAGTAAT	GTTGGAATGA	700
15	GTCTACTTGA	ACAAAAAATG	GGAGATGCTA	CTTGGTTGGA	TTATCTAAAA	750
	CGCTTTAAAT	TTGGGGTTCC	AACTCGCTTT	GGCTTGACAG	ATGAATACGC	800
	TGGTCAACTT	CCAGCTGATA	ATATTGTTAG	TATTGCTCAA	AGCTCATTTG	850
	GGCAAGGAAT	TTCAGTGACA	CAAACACAAA	TGCTTCGTGC	CTTTACAGCT	900
	ATTGCTAATG	ATGGAGTTAT	GCTGGAGCCA	AAATTTATAA	GTGCTATTTA	950
20	TGATACTAAC	AATCAGTCTG	TACGTAAGTC	ACAAAAAGAA	ATAGTAGGAA	1000
	ATCCTGTTTC	CAAAGAGGCA	GCAAGCACAA	CTCGAAATCA	CATGATCTTA	1050
	GTTGGGACGG	ACCCTCTATA	TGGAAGTATG	TATAATCACT	ACACAGGAAA	1100
	GCCAATTATA	ACAGTTCCTG	GACAAAATGT	AGCAGTTAAA	TCCGGTACGG	1150
	CTCAAATCGC	TGATGAGAAA	AATGGAGGAT	ACTTGTTTGG	TTCTACCAAT	1200
25	TATATTTTCT	CAGTTGTGAC	TATGAATCCT	GCTGAAAATC	CTGATTTTAT	1250
	CTTGTATGTA	ACGGTTCAAC	AGCCTGAGCA	TTATTCAGGT	ATCCAGTTGG	1300
	GAGAATTTGC	CACCCCAATC	TTGGAGCGGG	CTTCAGCTAT	GAAAGAATCT	1350
	CTCAATCTTC	AATCTCCAGC	CAAAAATTTA	GATAAAGTTA	CGACAGAATC	1400
	TTCTTATGCA	ATGCCTAGCA	TCAAGGATAT	TTCACCTGGT	GAGTTGGCGG	1450
30	AAGCCTTACG	CCGAAATATT	GTGCAACCAA	TCGTTGTAGG	TACTGGAACA	1500
	AAGATTAAAG	AGACTTCTGT	AGAAGAAGGG	ACCAATCTTG	CACCAAACCA	1550
	ACAAGTTCTC	CTTTTATCGG	ATAAGGTAGA	AGAAATTCCA	GACATGTATG	1600
	GCTGGAAAAA	AGAGACTGCC	GAGACCTTTG	CTAAATGGTT	GGATATTGAA	1650
	CTGGAATTTG	AAGGTTCAAG	TTCCGTTGTT	CAG		1683
35						

2) INFORMATION FOR SEQ ID NO: 1036

- 40 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1682 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Double
 - (D) TOPOLOGY: Linear
- 45 (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Streptococcus pneumoniae*
 - 50 (B) STRAIN: StrR-03

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1036

	TCAAAAAAGA	ATTGGAAACT	GCAGAGGTCA	AGGGGATTGA	TTTTACAACC	50
55	AGTCCCAATC	GTAGTTACCC	AAATGGACAA	TTTGCTTCTA	GTTTTATCGG	100
	TCTAGCTCAG	CTCCATGAAA	ATGAAGATGG	AAGCAAGAGT	TTGCTGGGAA	150
	CCTCTGGAAT	GGAGAGTTCC	TTGAACAGTA	TTCTTGCAGG	GACAGACGGC	200
	ATTATTACCT	ATGAAAAGGA	TCGTCTGGGC	AATATTGTAC	CCGGAACAGA	250
	ACAAGTTTCC	CAACAAACGG	TGGATGGCAA	GGATGTTTAC	ACAACCATTT	300
60	CCAGCCCCCT	CCAGTCCTTC	ATGGAAACTC	AGATGGATGC	CTTTCTAGAA	350

	AAAGTAAAAG	GTAAGTATAT	GACCGCGACC	TTGGTCAGTG	CAAAGACCGG	400
	TGAAATCCTC	GCTACCACCC	AACGACCTAC	CTTTAATGCA	GATACTAAAG	450
	AAGGAATCAC	TGAGGACTTT	GTTTGGCGTG	ATATTCTTTA	TCAAAGTAAC	500
	TATGAACCAG	GATCAGCCAT	GAAGGTTATG	ACGTTAGCTT	CTTCTATTGA	550
5	TAATAATACC	TTCCCAAGTG	GAGAATACTT	CAATAGCAGT	GAATTCAAAA	600
	TAGCGGATGC	GACGACTCGA	GATTGGGATG	TTAATGATGG	TTTGACTACT	650
	GGTGGGATGA	TGACTTTCTT	ACAAGGTTTC	GCTCACTCCA	GTAATGTTGG	700
	AATGAGTCTA	CTTGAACAAA	AAATGGGAGA	TGCTACTTGG	TTGGATTATC	750
	TAAAACGCTT	TAAATTTGGG	GTTCCAACCT	GCTTTGGCTT	GACAGATGAA	800
10	TACGCTGGTC	AACCTCCAGC	TGATAATATT	GTTAGTATTG	CTCAAAGCTC	850
	ATTTGGGCAA	GGAATTTTCAG	TGACACAAAC	ACAAATGCTT	CGTGCCTTTA	900
	CAGCTATTGC	TAATGATGGA	GTTATGCTGG	AGCCAAAATT	TATAAGTGCT	950
	ATTTATGATA	CTAACAATCA	GTCTGTACGT	AAGTCACAAA	AAGAAATAGT	1000
	AGGAAATCCT	GTTTCCAAAG	AGGCAGCAAG	CACAACTCGA	AATCACATGA	1050
15	TCTTAGTTGG	GACGGACCCT	CTATATGGAA	CTATGTATAA	TCACTACACA	1100
	GGAAAGCCAA	TTATAACAGT	TCCTGGACAA	AATGTAGCAG	TTAAATCCGG	1150
	TACGGCTCAA	ATCGCTGATG	AGAAAAATGG	AGGATACTTG	GTTGGTTCTA	1200
	CCAATTATAT	TTTCTCAGTT	GTGACTATGA	ATCCTGCTGA	AAATCCTGAT	1250
	TTTATCTTGT	ATGTAACGGT	TCAACAGCCT	GAGCATTATT	CAGGTATCCA	1300
20	GTTGGGAGAA	TTTGCCACCC	CAATCTTGGA	GCGGGCTTCA	GCTATGAAAG	1350
	AATCTCTCAA	TCTTCAATCT	CCAGCCAAAA	ATTTAGATAA	AGTTACGACA	1400
	GAATCTTCTT	ATGCAATGCC	TAGCATCAAG	GATATTTTCA	CTGGTGAGTT	1450
	GGCGGAAGCC	TTACGCCGAA	ATATTGTGCA	ACCAATCGTT	GTAGGTACTG	1500
	GAACAAAGAT	TAAAGAGACT	TCTGTAGAAG	AAGGGACCAA	TCTTGCACCA	1550
25	AACCAACAAG	TTCTCCTTTT	ATCGGATAAG	GTAGAAGAAA	TTCCAGACAT	1600
	GTATGGCTGG	AAAAAAGAGA	CTGCCGAGAC	CTTTGCTAAA	TGGTTGGATA	1650
	TTGAAGTGA	ATTTGAAGGT	TCAGGTTCGG	TT		1682

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2) INFORMATION FOR SEQ ID NO: 1037

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1681 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

40

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
 (B) STRAIN: StrR-04

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1037

	CAAAAAAGAA	TTGGAAACTG	CAGAGGTCAA	GGGGATTGAT	TTTACAACCA	50
	GTCCCAATCG	TAGTTATCCA	AACGGACAAT	TTGCTTCTAG	TTTTATCGGA	100
	CTAGCTCAGC	TCCATGAAAA	TGAAGATGGC	AGCAAGAGCT	TACTGGGAAC	150
50	CTCTGGAATG	GAGAGTTCCT	TGAACAGTAT	TCTTGCAGGG	ACAGACGGTA	200
	TTATTACCTA	TGAAAAAGAC	CGTGTAGGAA	ATATCGTACC	AGGTACAGAA	250
	CTGGTATCGC	AACAAACTGT	GGATGGCAAG	GATGTTTATA	CAACATTGTC	300
	TAGTCCGCTA	CAATCTTTCA	TGGAACTCA	GATGGATGCC	TTTCTAGAAA	350
	AAGTAAAAGG	TAAGTATATG	ACCGCGACCT	TGGTCAGTGC	AAAGACCGGT	400
55	GAAATCCTCG	CTACCACCCA	ACGACCTACC	TTTAATGCAG	ATACTAAAGA	450
	AGGAATCACT	GAGGACTTTG	TTTGGCGTGA	TATTCTTTAT	CAAAGTAACT	500
	ATGAACCAGG	ATCAGCCATG	AAGGTTATGA	CGTTAGCTTC	TTCTATTGAT	550
	AATAATACCT	TCCCAAGTGG	AGAATACTTC	AATAGCAGTG	AATTCAAAAT	600
	AGCGGATCGC	ACGACTCGAG	ATTGGGATGT	TAATGATGGT	TTGACTACTG	650
60	GTGGGATGAT	GACTTTCTTA	CAAGGTTTCG	CTCACTCCAG	TAATGTTGGA	700

	ATGAGTCTAC	TTGAACAAAA	AATGGGAGAT	GCTACTTGGT	TGGATTATCT	750
	AAAACGCTTT	AAATTTGGGG	TTCCAACCTCG	CTTTGGCTTG	ACAGATGAAT	800
	ACGCTGGTCA	ACTTCCAGCT	GATAATATTG	TTAGTATTGC	TCAAAGCTCA	850
	TTTGGGCAAG	GAATTTTCAGT	GACACAAACA	CAAATGCTTC	GTGCCTTTAC	900
5	AGCTATTGCT	AATGATGGAG	TTATGCTGGA	GCCAAAATTT	ATAAGTGCTA	950
	TTTATGATAC	TAACAATCAG	TCTGTACGTA	AGTCACAAAA	AGAAATAGTA	1000
	GGAAATCCTG	TTTCCAAAGA	GGCAGCAAGC	ACAACTCGAA	ATCACATGAT	1050
	CTTAGTTGGG	ACGGACCCTC	TATATGGAAC	TATGTATAAT	CACTACACAG	1100
	GAAAGCCAAT	TATAACAGTT	CCTGGACAAA	ATGTAGCAGT	TAAATCCGGT	1150
10	ACGGCTCAAA	TCGCTGATGA	GAAAAATGGA	GGATACTTGG	TTGGTTCTAC	1200
	CAATTATATT	TTCTCAGTTG	TGACTATGAA	TCCTGCTGAA	AATCCTGATT	1250
	TTATCTTGTA	TGTAACGGTT	CAACAGCCTG	AGCATTATTC	AGGTATCCAG	1300
	TTGGGAGAAT	TTGCCACCCC	AATCTTGGAG	CGGGCTTCAG	CTATGAAAGA	1350
	ATCTCTCAAT	CTTCAATCTC	CAGCCAAAAA	TTTAGATAAA	GTTACGACAG	1400
15	AATCTTCTTA	TGCAATGCCT	AGCATCAAGG	ATATTTACC	TGGTGAGTTG	1450
	GCGGAAGCCT	TACGCCGAAA	TATTGTGCAA	CCAATCGTTG	TAGGTACTGG	1500
	AACAAAGATT	AAAGAGACTT	CTGTAGAAGA	AGGGACCAAT	CTTGCACCAA	1550
	ACCAACAAGT	TCTCCTTTTA	TCGGATAAGG	TAGAAGAAAT	TCCAGACATG	1600
	TATGGCTGGA	AAAAAGAGAC	TGCCGAGACC	TTTGCTAAAT	GGTTGGATAT	1650
20	TGAACTGGAA	TTTGAAGGTT	CAGGTTCCGT	T		1681

2) INFORMATION FOR SEQ ID NO: 1038

25

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1685 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

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(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

35

- (A) ORGANISM: *Streptococcus pneumoniae*
- (B) STRAIN: StrR-05

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1038

40	AAAAAAGAAT	TGGAAACTGC	AGAGGTCAAG	GGGATTGATT	TTACAACCAG	50
	TCCCAATCGT	AGTTATCCAA	ACGGACAATT	TGCTTCTAGT	TTTATCGGAC	100
	TAGCTCAGCT	CCATGAAAAT	GAAGATGGCA	GCAAGAGCTT	ACTGGGAACC	150
	TCTGGAATGG	AGAGTTCCTT	GAACAGTATT	CTTGCAGGGA	CAGACGGTAT	200
	TATTACCTAT	GAAAAAGACC	GTGTAGGAAA	TATCGTACCA	GGTACAGAAC	250
45	TGGTATCGCA	ACAAACTGTG	GATGGCAAGG	ATGTTTATAC	AACATTGTCT	300
	AGTCCGCTAC	AATCTTTCAT	GGAAACTCAG	ATGGATGCCT	TTCTAGAAAA	350
	AGTAAAAGGT	AAGTATATGA	CCGCGACCTT	GGTCAGTGCA	AAGACCGGTG	400
	AAATCCTCGC	TACCACCCAA	CGACCTACCT	TTAATGCAGA	TACTAAAGAA	450
	GGAATCACTG	AGGACTTTGT	TTGGCGTGAT	ATTCTTTATC	AAAGTAACTA	500
50	TGAACCAGGA	TCAGCCATGA	AGGTTATGAC	GTTAGCTTCT	TCTATTGATA	550
	ATAATACCTT	CCCAAGTGGA	GAATACTTCA	ATAGCAGTGA	ATTCAAAATA	600
	GCGGATGCGA	CGACTCGAGA	TTGGGATGTT	AATGATGGTT	TGACTACTGG	650
	TGGGATGATG	ACTTTCTTAC	AAGGTTTCGC	TCACTCCAGT	AATGTTGGAA	700
	TGAGTCTACT	TGAACAAAAA	ATGGGAGATG	CTACTTGGTT	GGATTATCTA	750
55	AAACGCTTTA	AATTTGGGGT	TCCAACCTCG	TTTGGCTTGA	CAGATGAATA	800
	CGCTGGTCAA	CTTCCAGCTG	ATAATATTGT	TAGTATTGCT	CAAAGCTCAT	850
	TTGGGCAAGG	AATTTCAAGT	ACACAAACAC	AAATGCTTCG	TGCCTTTACA	900
	GCTATTGCTA	ATGATGGAGT	TATGCTGGAG	CCAAAATTTA	TAAGTGCTAT	950
	TTATGATACT	AACAATCAGT	CTGTACGTAA	GTCACAAAAA	GAAATAGTAG	1000
60	GAAATCCTGT	TTCCAAAGAG	GCAGCAAGCA	CAACTCGAAA	TCACATGATC	1050

	TTAGTTGGGA	CGGACCCTCT	ATATGGAAC	ATGTATAATC	ACTACACAGG	1100
	AAAGCCAATT	ATAACAGTTC	CTGGACAAAA	TGTAGCAGTT	AAATCCGGTA	1150
	CGGCTCAAAT	CGCTGATGAG	AAAAATGGAG	GATACTTGGT	TGGTTCTACC	1200
	AATTATATTT	TCTCAGTTGT	GACTATGAAT	CCTGCTGAAA	ATCCTGATTT	1250
5	TATCTTGAT	GTAACGGTTC	AACAGCCTGA	GCATTATTCA	GGTATCCAGT	1300
	TGGGAGAATT	TGCCACCCCA	ATCTTGGAGC	GGGCTTCAGC	TATGAAAGAA	1350
	TCTCTCAATC	TTCAATCTCC	AGCCAAAAAT	TTAGATAAAG	TTACGACAGA	1400
	ATCTTCTTAT	GCAATGCCTA	GCATCAAGGA	TATTTACCT	GGTGAGTTGG	1450
	CGGAAGCCTT	ACGCCGAAAT	ATTGTGCAAC	CAATCGTTGT	AGGTACTGGA	1500
10	ACAAAGATTA	AAGAGACTTC	TGTAGAAGAA	GGGACCAATC	TTGCACCAAA	1550
	CCAACAAGTT	CTCCTTTTAT	CGGATAAGGT	AGAAGAAATT	CCAGACATGT	1600
	ATGGCTGGAA	AAAAGAGACT	GCCGAGACCT	TTGCTAAATG	GTTGGATATT	1650
	GAACTGGAAT	TTGAAGGTTC	AGGTTCCGTT	GTTCA		1685

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2) INFORMATION FOR SEQ ID NO: 1039

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 1679 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

25 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
 (B) STRAIN: StrR-06

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1039

	AAAAGAATTG	GAAACTGCAG	AGGTCAAGGG	GATTGATTTT	ACAACCAGTC	50
	CCAATCGTAG	TTATCCAAAC	GGACAATTG	CTTCTAGTTT	TATCGGACTA	100
35	GCTCAGCTCC	ATGAAAATGA	AGATGGCAGC	AAGAGCTTAC	TGGGAACCTC	150
	TGGAATGGAG	AGTTCCCTGA	ACAGTATTCT	TGCAGGGACA	GACGGTATTA	200
	TTACCTATGA	AAAAGACCGT	GTAGGAAATA	TCGTACCAGG	TACAGAACCTG	250
	GTATCGCAAC	AAACTGTGGA	TGGCAAGGAT	GTTTATACAA	CATTGTCTAG	300
	TCCGCTACAA	TCTTTCATGG	AAACTCAGAT	GGATGCCTTT	CTAGAAAAAG	350
40	TAAAAGGTAA	GTATATGACC	GCGACCTTGG	TCAGTGCAAA	GACCGGTGAA	400
	ATCCTCGCTA	CCACCCAACG	ACCTACCTTT	AATGCAGATA	CTAAAGAAGG	450
	AATCACTGAG	GACTTTGTTT	GGCGTGATAT	TCTTTATCAA	AGTAACTATG	500
	AACCAGGATC	AGCCATGAAG	GTTATGACGT	TAGCTTCTTC	TATTGATAAT	550
	AATACCTTCC	CAAGTGGAGA	ATACTTCAAT	AGCAGTGAAT	TCAAAATAGC	600
45	GGATGCGACG	ACTCGAGATT	GGGATGTTAA	TGATGGTTTG	ACTACTGGTG	650
	GGATGATGAC	TTTCTTACAA	GGTTTCGCTC	ACTCCAGTAA	TGTTGGAATG	700
	AGTCTACTTG	AACAAAAAAT	GGGAGATGCT	ACTTGGTTGG	ATTATCTAAA	750
	ACGCTTTAAA	TTTGGGGTTC	CAACTCGCTT	TGGCTTGACA	GATGAATACG	800
	CTGGTCAACT	TCCAGCTGAT	AATATTGTTA	GTATTGCTCA	AAGCTCATT	850
50	GGGCAAGGAA	TTTCAGTGAC	ACAAACACAA	ATGCTTCGTG	CCTTTACAGC	900
	TATTGCTAAT	GATGGAGTTA	TGCTGGAGCC	AAAATTTATA	AGTGCTATTT	950
	ATGATACTAA	CAATCAGTCT	GTACGTAAGT	CACAAAAAGA	AATAGTAGGA	1000
	AATCCTGTTT	CCAAAGAGGC	AGCAAGCACA	ACTCGAAATC	ACATGATCTT	1050
	AGTTGGGACG	GACCTCTAT	ATGGAACAT	GTATAATCAC	TACACAGGAA	1100
55	AGCCAATTAT	AACAGTTCCT	GGACAAAATG	TAGCAGTTAA	ATCCGGTACG	1150
	GCTCAAATCG	CTGATGAGAA	AAATGGAGGA	TACTTGGTTG	GTTCTACCAA	1200
	TTATATTTTC	TCAGTTGTGA	CTATGAATCC	TGCTGAAAAT	CCTGATTTTA	1250
	TCTTGATATG	AACGGTTCAA	CAGCCTGAGC	ATTATTCAGG	TATCCAGTTG	1300
	GGAGAATTTG	CCACCCAAT	CTTGAGCGG	GCTTCAGCTA	TGAAAGAATC	1350
60	TCTCAATCTT	CAATCTCCAG	CCAAAAATTT	AGATAAAGTT	ACGACAGAAT	1400

	CTTCTTATGC	AATGCCTAGC	ATCAAGGATA	TTTCACCTGG	TGAGTTGGCG	1450
	GAAGCCTTAC	GCCGAAATAT	TGTGCAACCA	ATCGTTGTAG	GTACTGGAAC	1500
	AAAGATTAAA	GAGACTTCTG	TAGAAGAAGG	GACCAATCTT	GCACCAAACC	1550
	AACAAGTTCT	CCTTTTATCG	GATAAGGTAG	AAGAAATTC	AGACATGTAT	1600
5	GGCTGGAAAA	AAGAGACTGC	CGAGACCTTT	GCTAAATGGT	TGGATATTGA	1650
	ACTGGAATTT	GAAGGTTTCA	GTTCCGTTG			1679

10 2) INFORMATION FOR SEQ ID NO: 1040

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1685 bases
 (B) TYPE: Nucleic acid
 15 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

20 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
 (B) STRAIN: StrR-07

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1040

25	TAAAAAGGAT	CTAAAAGACG	CTAGTGTGTA	AGGAATTGAC	TTCACAACCTA	50
	GCCCTAATAG	AAGCTATCCA	AATGGACAAT	TCGCTTCTAG	TTTTATTGGT	100
	TTGGCCCAAC	TCCATGAAAA	TGAGGATGGT	AGCAAGAGTT	TGCTGGGAAC	150
	TTCTGGGATG	GAGAGTTCCT	TGAACAGTAT	TCTTGCAGGG	AAAGACGGTA	200
30	TTATTACCTA	TGAAAAAGAT	CGTCTGGGTA	ATATTGTCCC	TGGAACAGAA	250
	CAAGTTTCCC	AACAAACGGT	AGATGGCAAG	GATGTTTATA	CAACATTGTC	300
	TAGTCCGCTA	CAATCTTTCA	TGGAAACTCA	GATGGATGCC	TTTCTAGAAA	350
	AAGTAAAAGG	TAAGTATATG	ACCGCGACCT	TGGTCAGTGC	AAAGACCGGT	400
	GAAATCCTCG	CTACCACCCA	ACGACCTACC	TTTAATGCAG	ATACTAAAGA	450
35	AGGAATCACT	GAGGACTTTG	TTTGGCGTGA	TATTCTTTAT	CAAAGTAACT	500
	ATGAACCAGG	ATCAGCCATG	AAGGTTATGA	CGTTAGCTTC	TTCTATTGAT	550
	AATAATACCT	TCCCAAGTGG	AGAATACTTC	AATAGCAGTG	AATTCAAAAT	600
	AGCGGATGCG	ACGACTCGAG	ATTGGGATGT	TAATGAAGGT	TTGACTACTG	650
	GTGGGATGAT	GACTTTCTTA	CAAGGTTTCG	CTCACTCCAG	TAATGTTGGA	700
40	ATGAGTCTAC	TTGAACAAAA	AATGGGAGAT	GCTACTTGGT	TGGATTATCT	750
	AAAACGCTTT	AAATTTGGGG	TTCCAACCTCG	CTTTGGCTTG	ACAGATGAAT	800
	ACGCTGGTCA	ACTTCCAGCT	GATAATATTG	TTAGTATTGC	TCAAAGCTCA	850
	TTTGGGCAAG	GAATTTCACT	GACACAAACA	CAAATGCTTC	GTGCCTTTAC	900
	AGCTATTGCT	AATGATGGAG	TTATGCTGGA	GCCAAAATTT	ATAAGTGCTA	950
45	TTTATGATAC	TAACAATCAG	TCTGTACGTA	AGTCACAAAA	AGAAATAGTA	1000
	GGAAATCCTG	TTTCCAAAGA	GGCAGCAAGC	ACAACCTCGA	ATCACATGAT	1050
	CTTAGTTGGG	ACGGACCCCT	TATATGGAAC	TATGTATAAT	CACTACACAG	1100
	GAAAGCCAAT	TATAACAGTT	CCTGGACAAA	ATGTAGCAGT	TAAATCCGGT	1150
	ACGGCTCAAA	TCGCTGATGA	GAAAAATGGA	GGATACTTGG	TTGGTTCTAC	1200
50	CAATTATATT	TTCTCAGCTG	TGACTATGAA	TCCTGCTGAA	AATCCTGATT	1250
	TTATCTTGTA	TGTAACGGTT	CAACAGCCTG	AGCATTATTC	AGGTATCCAG	1300
	TTGGGAGAAT	TTGCCACCCC	AATCTTGAGG	CGGGCTTCAG	CTATGAAAGA	1350
	ATCTCTCAAT	CTTCAATCTC	CAGCCAAAAA	TTTAGATAAA	GTTACGACAG	1400
	AATCTTCTTA	TGCAATGCCT	AGCATCAAGG	ATATTTCAAC	TGGTGAGTTG	1450
55	GCGGAAGCCT	TACGCCGAAA	TATTGTGCAA	CCAATCGTTG	TAGGTACTGG	1500
	AACAAAGATT	AAAGAGACTT	CTGTAGAAGA	AGGGACCAAT	CTTGCAACCA	1550
	ACCAACAAGT	TCTCCTTTTA	TCGGATAAGG	TAGAAGAAAT	TCCAGACATG	1600
	TATGGCTGGA	AAAAAGAGAC	TGCCGAGACC	TTTGCTAAAT	GGTTGGATAT	1650
	TGAAC TGGA	TTTGAAGGTT	CAGGTTCCGT	CGTTC		1685

2) INFORMATION FOR SEQ ID NO: 1041

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1696 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus pneumoniae*
 (B) STRAIN: StrR-08

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1041

	GTCTATCAAA	AAAGAATTGG	AAACTGCAGA	GGTCAAGGGG	ATTGATTTTA	50
20	CAACCAGTCC	CAATCGTAGT	TATCCAAACG	GACAATTTCG	TTCTAGTTTT	100
	ATCGGACTAG	CTCAGCTCCA	TGAAAATGAA	GATGGCAGCA	AGAGCTTACT	150
	GGGAACCTCT	GGAATGGAGA	GTTCTTGAA	CAGTATTCTT	GCAGGGACAG	200
	ACGGTATTAT	TACCTATGAA	AAAGACCGTG	TAGGAAATAT	CGTACCAGGT	250
	ACAGAACTGG	TATCGCAACA	AACTGTGGAT	GGCAAGGATG	TTTATACAAC	300
25	ATTGTCTAGT	CCGCTACAAT	CTTTCATGGA	AACTCAGATG	GATGCCTTTC	350
	TAGAAAAAGT	AAAAGGTAAG	TATATGACCG	CGACCTTGGT	CAGTGCAAAG	400
	ACCGGTGAAA	TCCTCGCTAC	CACCCAACGA	CCTACCTTTA	ATGCAGATAC	450
	TAAAGAAGGA	ATCACTGAGG	ACTTTGTTTG	GCGTGATATT	CTTTATCAAA	500
	GTAACATATGA	ACCAGGATCA	GCCATGAAGG	TTATGACGTT	AGCTTCTTCT	550
30	ATTGATAATA	ATACCTTCCC	AAGTGGAGAA	TACTTCAATA	GCAGTGAATT	600
	CAAAATAGCG	GATGCGACGA	CTCGAGATTG	GGATGTTAAT	GATGGTTTGA	650
	CTACTGGTGG	GATGATGACT	TTCTTACAAG	GTTTCGCTCA	CTCCAGTAAT	700
	GTTGGAATGA	GTCTACTTGA	ACAAAAATG	GGAGATGCTA	CTTGTTGGA	750
	TTATCTAAAA	CGCTTTAAAT	TTGGGGTTCC	AACTCGCTTT	GGCTTGACAG	800
35	ATGAATACGC	TGGTCAACTT	CCAGCTGATA	ATATTGTTAG	TATTGCTCAA	850
	AGCTCATTTG	GGCAAGGAAT	TTCAGTGACA	CAAACACAAA	TGCTTCGTGC	900
	CTTTACAGCT	ATTGCTAATG	ATGGAGTTAT	GCTGGAGCCA	AAATTTATAA	950
	GTGCTATTTA	TGATACTAAC	AATCAGTCTG	TACGTAAGTC	ACAAAAAGAA	1000
	ATAGTAGGAA	ATCCTGTTTC	CAAAGAGGCA	GCAAGCACAA	CTCGAAATCA	1050
40	CATGATCTTA	GTTGGGACGG	ACCCTCTATA	TGGAACATATG	TATAATCACT	1100
	ACACAGGAAA	GCCAATTATA	ACAGTTCCTG	GACAAAATGT	AGCAGTTAAA	1150
	TCCGGTACGG	CTCAAATCGC	TGATGAGAAA	AATGGAGGAT	ACTTGGTTGG	1200
	TTCTACCAAT	TATATTTTCT	CAGTTGTGAC	TATGAATCCT	GCTGAAAATC	1250
	CTGATTTTAT	CTTGTATGTA	ACGGTTCAAC	AGCCTGAGCA	TTATTCAGGT	1300
45	ATCCAGTTGG	GAGAATTTGC	CACCCCAATC	TTGGAGCGGG	CTTCAGCTAT	1350
	GAAAGAATCT	CTCAATCTTC	AATCTCCAGC	CAAAAATTTA	GATAAAGTTA	1400
	CGACAGAATC	TTCTTATGCA	ATGCCTAGCA	TCAAGGATAT	TTCACCTGGT	1450
	GAGTTGGCGG	AAGCCTTACG	CCGAAATATT	GTGCAACCAA	TCGTTGTAGG	1500
	TACTGGAACA	AAGATTAAAG	AGACTTCTGT	AGAAGAAGGG	ACCAATCTTG	1550
50	CACCAAACCA	ACAAGTTCTC	CTTTTATCGG	ATAAGGTAGA	AGAAATTCCA	1600
	GACATGTATG	GCTGGAAAAA	AGAGACTGCC	GAGACCTTTG	CTAAATGGTT	1650
	GGATATTGAA	CTGGAATTTG	AAGGTTCAAG	TTCCGTTGTT	CAGAAG	1696

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2) INFORMATION FOR SEQ ID NO: 1042

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1689 bases
 (B) TYPE: Nucleic acid

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(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

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(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*
(B) STRAIN: StrR-09

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1042

	AAAAAAGAGT	TGGAAACTGC	AGAGGTCAAG	GGGATTGATT	TTACAACCAG	50
	TCCCAATCGT	AGTTACCCAA	ACGGACAATT	TGCTTCTAGT	TTTATCGGAC	100
	TAGCTCAGCT	CCATGAAAAT	GAAGATGGCA	GCAAGAGCTT	GCTGGGAACC	150
15	TCTGGAATGG	AGAGTTCCTT	GAACAGTATT	CTTGCAGGGA	CAGACGGCAT	200
	TATTACCTAT	GAAAAGGATC	GTCTGGGAAA	TATTGTCCCC	GGAACGGAAC	250
	AAGTTTCCCA	ACAAACTGTA	GATGGCAAGG	ATGTTTATAC	GACTATTTCC	300
	AGCACCTTC	AGTCCTTCAT	GGAAACTCAG	ATGGATGCCT	TTCTAGAAAA	350
	AGTAAAAGGT	AAGTATATGA	CCGCGACCTT	GGTCAGTGCA	AAGACCGGTG	400
20	AAATCCTCGC	TACCACCCAA	CGACCTACCT	TTAATGCAGA	TACTAAAGAA	450
	GGAATCACTG	AGGACTTTGT	TTGGCGTGAT	ATTCTTTATC	AAAGTAACTA	500
	TGAACCAGGA	TCAGCCATGA	AGGTTATGAC	GTTAGCTTCT	TCTATTGATA	550
	ATAATACCTT	CCCAAGTGGA	GAATACTTCA	ATAGCAGTGA	ATTCAAAATA	600
	GCGGATGCGA	CGACTCGAGA	TTGGGATGTT	AATGATGGTT	TGACTACTGG	650
25	TGGGATGATG	ACTTTCTTAC	AAGGTTTCGC	TCACTCCAGT	AATGTTGGAA	700
	TGAGTCTACT	TGAACAAAAA	ATGGGAGATG	CTACTTG GTT	GGATTATCTA	750
	AAACGCTTTA	AATTTGGGGT	TCCAACTCGC	TTTGGCTTGA	CAGATGAATA	800
	CGCTGGTCAA	CTTCCAGCTG	ATAATATTGT	TAGTATTGCT	CAAAGCTCAT	850
	TTGGGCAAGG	AATTTTCAGT	ACACAAACAC	AAATGCTTCG	TGCCTTTACA	900
30	GCTATTGCTA	ATGATGGAGT	TATGCTGGAG	CCAAAATTTA	TAAGTGCTAT	950
	TTATGATACT	AACAATCAGT	CTGTACGTAA	GTCACAAAAA	GAAATAGTAG	1000
	GAAATCCTGT	TTCCAAAGAG	GCAGCAAGCA	CAACTCGAAA	TCACATGATC	1050
	TTAGTTGGGA	CGGACCCTCT	ATATGGA ACT	ATGTATAATC	ACTACACAGG	1100
	AAAGCCAATT	ATAACAGTTC	CTGGACAAAA	TGTAGCAGTT	AAATCCGGTA	1150
35	CGGCTCAAAT	CGCTGATGAG	AAAAATGGAG	GATACTTGGT	TGGTTCTACC	1200
	AATTATATTT	TCTCAGTTGT	GACTATGAAT	CCTGCTGAAA	ATCCTGATTT	1250
	TATCTTGTAT	GTAACGGTTC	AACAGCCTGA	GCATTATTCA	GGTATCCAGT	1300
	TGGGAGAATT	TGCCACCCCA	ATCTTGGAGC	GGGCTTCAGC	TATGAAAGAC	1350
	TCTCTCAATC	TTCAAACAAC	AGCTAAAGCT	TTGGAGCAAG	TAAGTCAACA	1400
40	AAGTCCTTAT	CCTATGCCTA	GTGTCAAGGA	TATTTACCTT	GGTGATTTAG	1450
	CAGAAGAATT	GCGTCGCAAT	CTTGTAACAC	CCATCGTTGT	GGGAACAGGA	1500
	ACGAAGATTA	AAAACAGTTC	TGCTGAAGAA	GGGAAGAATC	TTGCCCCGAA	1550
	TCAGCAAGTC	CTTATCTTAT	CTGATAAAGT	AGAGGAAGTT	CCAGATATGT	1600
	ATGGTTGGAC	AAAGGAGACT	GCTGAGACCC	TTGCTAAGTG	GCTCAATATA	1650
45	GAAC TTGAAT	TTCAAGGTTC	GGGTTCTACT	GTGCAGAAG		1689

2) INFORMATION FOR SEQ ID NO: 1043

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(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1690 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

55

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

60

(B) STRAIN: StrR-10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1043

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5  CAAAAAAGAG TTGGAAACTG CAGAGGTCAA GGGGATTGAT TTTACAACCA      50
   GTCCTAATCG TAGTTACCCA AACGGACAAT TTGCTTCTAG TTTTATCGGT      100
   CTAGCTCAAC TCCATGAAAA TGAAGATGGA AGCAAGAGTT TGCTGGGAAC      150
   TTCTGGAATG GAGAGTTCCT TGAACAGTAT TCTTGCAGGG AAAGACGGTA      200
   TTATTACTTA TGAAAAGGAT CGTCTGGGTA ATATTGTCCC TGGAACAGAA      250
10  CAAGTTTCCC AACAAACGGT AGATGGCAAG GATGTTTATA CAACATTGTC      300
   TAGTCCGCTC CAATCTTTCA TGGAAACTCA GATGGATGCC TTTCTAGAAA      350
   AAGTAAAGG TAAGTATATG ACCGCGACCT TGGTCAGTGC AAAGACCGGT      400
   GAAATCCTCG CTACCACCCA ACGACCTACC TTTAATGCAG ATACTAAAGA      450
   AGGAATCACT GAGGACTTTG TTTGGCGTGA TATTCTTTAT CAAAGTAACT      500
15  ATGAACCAGG ATCAGCCATG AAGGTTATGA CGTTAGCTTC TTCTATTGAT      550
   AATAATACCT TCCCAAGTGG AGAATACTTC AATAGCAGTG AATTCAAAT      600
   AGCGGATGCG ACGACTCGAG ATTGGGATGT TAATGATGGT TTGACTACTG      650
   GTGGGATGAT GACTTTCTTA CAAGGTTTCG CTCACTCCAG TAATGTTGGA      700
   ATGAGTCTAC TTGAACAAAA AATGGGAGAT GCTACTTGGT TGGATTATCT      750
20  AAAACGCTTT AAATTTGGGG TTCCAACCTCG CTTTGGCTTG ACAGATGAAT      800
   ACGCTGGTCA ACTTCCAGCT GATAATATTG TTAGTATTGC TCAAAGCTCA      850
   TTTGGGCAAG GAATTTCACT GACACAAACA CAAATGCTTC GTGCCTTTAC      900
   AGCTATTGCT AATGATGGAG TTATGCTGGA GCCAAAATTT ATAAGTGCTA      950
   TTTATGATAC TAACAATCAG TCTGTACGTA AGTCACAAAA AGAAATAGTA     1000
25  GGAAATCCTG TTTCCAAAGA GGCAGCAAGC ACAACTCGAA ATCACATGAT     1050
   CTTAGTTGGG ACGGACCCTC TATATGGAAC TATGTATAAT CACTACACAG     1100
   GAAAGCCAAT TATAACAGTT CCTGGACAAA ATGTAGCAGT TAAATCCGGT     1150
   ACGGCTCAAA TCGCTGATGA GAAAAATGGA GGATACTTGG TTGGTTCTAC     1200
   CAATTATATT TTCTCAGTTG TGACTATGAA TCCTGCTGAA AATCCTGATT     1250
30  TTATCTTGTA TGTAACGGTT CAACAGCCTG AGCATTATTC AGGTATCCAG     1300
   TTGGGAGAAT TTGCCACCCC AATCTTGAGG CGGGCTTCAG CTATGAAAGA     1350
   ATCTCTCAAT CTTCAATCTC CAGCCAAAAA TTTAGATAAA GTTACGACAG     1400
   AATCTTCTTA TGCAATGCCT AGCATCAAGG ATATTTTACC TGGTGAGTTG     1450
   GCGGAAGCCT TACGCCGAAA TATTGTGCAA CCAATCGTTG TAGGTACTGG     1500
35  AACAAAGATT AAAGAGACTT CTGTAGAAGA AGGGACCAAT CTTGCACCAA     1550
   ACCAACAAGT TCTCCTTTTA TCGGATAAGG TAGAAGAAAT TCCAGACATG     1600
   TATGGCTGGA AAAAAGAGAC TGCCGAGACC TTTGCTAAAT GGTGATATAT     1650
   TGAAGTGAAG TTTGAAGGTT CAGGTTCCGT TGTTCAGAAG     1690

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2) INFORMATION FOR SEQ ID NO: 1044

(i) SEQUENCE CHARACTERISTICS:

- 45 (A) LENGTH: 1668 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

50 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
 (B) STRAIN: StrR-11

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1044

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AGTTGGAAAC TGCAGAGGTC AAGGGGATTG ATTTTACAAC CAGTCCTAAT      50
CGTAGTTACC CAAACGGACA ATTTGCTTCT AGTTTATATCG GACTAGCTCA      100
60  GCTCCATGAA AATGAAGATG GCAGCAAGAG CTTGCTGGGA ACCTCTGGGA      150

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	TGGAGAGTTC	TTTAAATAGA	ATTCTTGCAG	GGACAGACGG	CATTATTACC	200
	TATGAAAAGG	ATCGTCTGGG	AAATATTGTC	CCCGGAACGG	AACAAGTTTC	250
	CCAACAAACG	GTAGATGGCA	AGGATGTTTA	TACGACTATT	TCCAGCACCC	300
	TTCAGTCCTT	CATGGAGACC	CAGATGAATG	CCTTTCAAGA	AAAAGTAAAA	350
5	GGCAAGTATA	TGACGGCTAC	CTTGGTCACT	GCTAAAACAG	GGGAAATTCT	400
	TGCAACAACG	CAACGGCCGA	CCTTCGATGC	TGATACTAAG	GAAGGACTTA	450
	CCAAGGACTT	TGTTTGGCGT	GATATCCTCT	ATCAAAGTAA	CTATGAGCCA	500
	GGGTCAACCA	TGAAGGTCAT	GACGCTTGCT	GCTGCTATTG	ATAATAACAC	550
	TTTCCCAGGA	GGAGAAGTTT	TCAATAGTAG	TGAATTAAAA	ATAGCGGATG	600
10	CGACAATTCG	AGATTGGGAT	GTTAATGATG	GTTTGACGAC	TGGTGGGATG	650
	ATGACTTTCT	TACAAGGTTT	CGCTCACTCC	AGTAATGTTG	GAATGAGTCT	700
	ACTTGAACAA	AAAATGGGAG	ATGCTACTTG	GTTGGATTAT	CTAAACCGCT	750
	TTAAGTTTGG	GGTGCCGACG	CGTTTTGGTC	TGACTGATGA	GTATTTCAGGT	800
	CAATTGCCTG	CAGATAATAT	TGTTAATATT	GCCATGAGTG	CATTTGGTCA	850
15	GGGGATTTCA	GTGACCCAGA	CGCAAATGAT	TCGTGCCTTT	ACAGCTATTG	900
	CTAATGATGG	TGTTATGCTG	GAGCCTAAAT	TTATTAGTGC	CATTTATGAT	950
	CCAAATGATC	AAACTGCTCG	GAAATCTCAA	AAAGAAATTG	TGGGAAATCC	1000
	TGTTTCTAAA	GATGCAGCTA	GTCTAAGTCG	GACTAACATG	ATTTTGGTAG	1050
	GGACGGATCC	GGTTTATGGA	ACCATGTATA	ACCACAGCAC	AGGTAAGCCA	1100
20	ACTGTAACCTG	TTCCTGGGCA	AAATGTAGCC	CTCAAGTCTG	GTACGGCTCA	1150
	GATTGCTGAC	GAGAAAAATG	GTGGTTATCT	AGTCGGGTTA	ACCAACTATA	1200
	TTTTCTCGGC	TGTATCGATG	AATCCGGCTG	AAAATCCTGA	TTTTATCTTG	1250
	TATGTAACGG	TACAGCAACC	TGAACATTAT	TCAGGTATCC	AGTTGGGAGA	1300
	ATTTGCCACC	CCAATCTTGG	AGCGGGCTTC	AGCTATGAAA	GAATCTCTCA	1350
25	ATCTTCAATC	TCCAGCCAAG	AATTTAGATA	AAGTTACGAC	AGAATCTTCT	1400
	TATGCAATGC	CTAGCATCAA	GGATATTTCA	CCTGGTGAGT	TGGCGGAAGC	1450
	CTTACGCCGA	AATATTGTGC	AACCAATCGT	TGTAGGTACT	GGAACAAAGA	1500
	TTAAAGAGAC	TTCTGTAGAA	GAAGGGACCA	ATCTTGCACC	AAACCAACAA	1550
	GTTCTCCTTT	TATCGGATAA	GGTAGAAGAA	ATTCCAGACA	TGTATGGCTG	1600
30	GAAAAAAGAG	ACTGCTGAAA	CCTTTGCTAA	ATGGTTGGAT	ATTGAGCTGG	1650
	AATTTGAAGG	GTCAGGTT				1668

35 2) INFORMATION FOR SEQ ID NO: 1045

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1680 bases
- (B) TYPE: Nucleic acid
- 40 (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

- 45 (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Streptococcus pneumoniae*
- (B) STRAIN: StrR-12

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1045

50	TTGGAAACTG	CAGAGGTCAA	GGGGATTGAT	TTTACAACCA	GTCCCAATCG	50
	TAGTTACCCA	AATGGACAAT	TTGCTTCTAG	TTTTATCGGT	CTAGCTCAGC	100
	TCCATGAAAA	TGAAGATGGA	AGCAAGAGTT	TGCTGGGAAC	CTCTGGAATG	150
	GAGAGTTTCT	TGAACAGTAT	TCTTGCAGGG	ACAGACGGCA	TTATTACCTA	200
55	TGAAAAGGAT	CGTCTGGGCA	ATATTGTACC	CGGAACAGAA	CAAGTTTCCC	250
	AACAAACGGT	GGATGGCAAG	GATGTTTACA	CAACCATTTT	CAGCCCCCTC	300
	CAGTCCTTCA	TGGAAACTCA	GATGGATGCC	TTTCTAGAAA	AAGTAAAAGG	350
	TAAGTATATG	ACCGCGACCT	TGGTCAGTGC	AAAGACCGGT	GAAATCCTCG	400
	CTACCACCCA	ACGACCTACC	TTTAATGCAG	ATACTAAAGA	AGGAATCACT	450
60	GAGGACTTTG	TTTGGCGTGA	TATTCTTTAT	CAAAGTAACT	ATGAACCAGG	500

	ATCAGCCATG	AAGGTTATGA	CGTTAGCTTC	TTCTATTGAT	AATAATACCT	550
	TCCCAAGTGG	AGAATACTTC	AATAGCAGTG	AATTCAAAAT	AGCGGATGCG	600
	ACGACTCGAG	ATTGGGATGT	TAATGATGGT	TTGACTACTG	GTGGGATGAT	650
	GACTTTCTTA	CAAGGTTTCG	CTCACTCCAG	TAATGTTGGA	ATGAGTCTAC	700
5	TTGAACAAAA	AATGGGAGAT	GCTACTTGGT	TGGATTATCT	AAAACGCTTT	750
	AAATTTGGGG	TTCCAACCTG	CTTTGGCTTG	ACAGATGAAT	ACGCTGGTCA	800
	ACTTCCAGCT	GATAATATTG	TTAGTATTGC	TCAAAGCTCA	TTTGGGCAAG	850
	GAATTTGAGT	GACACAAACA	CAAATGCTTC	GTGCCTTTAC	AGCTATTGCT	900
	AATGATGGAG	TTATGCTGGA	GCCAAAATTT	ATAAGTGCTA	TTTATGATAC	950
10	TAACAATCAG	TCTGTACGTA	AGTCACAAAA	AGAAATAGTA	GGAAATCCTG	1000
	TTTCCAAAGA	GGCAGCAAGC	ACAACCTCGAA	ATCAGATGAT	CTTAGTTGGG	1050
	ACGGACCCCTC	TATATGGAAC	TATGTATAAT	CACTACACAG	GAAAGCCAAT	1100
	TATAACAGTT	CCTGGACAAA	ATGTAGCAGT	TAAATCCGGT	GCGGCTCAAA	1150
	TCGCTGATGA	GAAAAATGGA	GGATACTTGG	TTGGTTCTAC	CAATTATATT	1200
15	TTCTCAGTTG	TGACTATGAA	TCCTGCTGAA	AATCCTGATT	TTATCTTGTA	1250
	TGTAACGGTT	CAACAGCCTG	AGCATTATTC	AGGTATCCAG	TTGGGAGAAT	1300
	TTGCCACCCC	AATCTTGAG	CGGGCTTCAG	CTATGAAAGA	ATCTCTCAAT	1350
	CTTCAATCTC	CAGCCAAAAA	TTTAGATAAA	GTTACGACAG	AATCTTCTTA	1400
	TGCAATGCCT	AGCATCAAGG	ATATTTACCC	TGGTGAGTTG	GCGGAAGCCT	1450
20	TACGCCGAAA	TATTGTGCAA	CCAATCGTTG	TAGGTACTGG	AACAAAGATT	1500
	AAAGAGACTT	CTGTAGAAGA	AGGGACCAAT	CTTGCACCAA	ACCAACAAGT	1550
	TCTCCTTTTA	TCGGATAAGG	TAGAAGAAAT	TCCAGACATG	TATGGCTGGA	1600
	AAAAAGAGAC	TGCCGAGACC	TTTGCTAAAT	GGTTGGATAT	TGAACTGGAA	1650
	TTTGAAGGTT	CAGGTTCCGT	TGTTCAGAAG			1680
25						

2) INFORMATION FOR SEQ ID NO: 1046

- 30 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1689 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
- 35 (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus pneumoniae*
 40 (B) STRAIN: StrR-13
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1046

	AAAAAAGAGT	TGGAAACTGC	AGAGGTCAAG	GGGATTGATT	TTACAACCAG	50
45	TCCTAATCGT	AGTTACCCAA	ACGGACAATT	TGCTTCTAGT	TTTATCGGTC	100
	TAGCTCAACT	CCATGAAAAT	GAAGATGGAA	GCAAGAGTTT	GCTGGGAACT	150
	TCTGGAATGG	AGAGTTCCTT	GAACAGTATT	CTTGCAGGGA	AAGACGGTAT	200
	TATTACTTAT	GAAAAGGATC	GTCTGGGTAA	TATTGTCCCT	GGAACAGAAC	250
	AAGTTTCCCA	ACAAACGGTA	GATGGCAAGG	ATGTTTATAC	AACATTGTCT	300
50	AGTCCGCTCC	AATCTTTCAT	GGAAACTCAG	ATGGATGCCT	TTCTAGAAAA	350
	AGTAAAAGGT	AAGTATATGA	CCGCGACCTT	GGTCAGTGCA	AAGACCGGTG	400
	AAATCCTCGC	TACCACCCAA	CGACCTACCT	TTAATGCAGA	TACTAAAGAA	450
	GGAATCACTG	AGGACTTTGT	TTGGCGTGAT	ATTCTTTATC	AAAGTAACTA	500
	TGAACCAGGA	TCAGCCATGA	AGGTTATGAC	GTTAGCTTCT	TCTATTGATA	550
55	ATAATACCTT	CCCAAGTGGA	GAATACTTCA	ATAGCAGTGA	ATTCAAAATA	600
	GCGGATGCGA	CGACTCGAGA	TTGGGATGTT	AATGATGGTT	TGACTACTGG	650
	TGGGATGATG	ACTTTCTTAC	AAGGTTTCGC	TCACTCCAGT	AATGTTGGAA	700
	TGAGTCTACT	TGAACAAAAA	ATGGGAGATG	CTACTTGTTT	GGATTATCTA	750
	AAACGCTTTA	AATTTGGGGT	TCCAACCTCG	TTTGGCTTGA	CAGATGAATA	800
60	CGCTGGTCAA	CTTCCAGCTG	ATAATATTGT	TAGTATTGCT	CAAAGCTCAT	850

	TTGGGCAAGG	AATTTTCAGTG	ACACAAACAC	AAATGCTTCG	TGCCTTTACA	900
	GCTATTGCTA	ATGATGGAGT	TATGCTGGAG	CCAAAATTTA	TAAGTGCTAT	950
	TTATGATACT	AACAATCAGT	CTGTACGTAA	GTCACAAAAA	GAAATAGTAG	1000
	GAAATCCTGT	TTCCAAAGAG	GCAGCAAGCA	CAACTCGAAA	TCACATGATC	1050
5	TTAGTTGGGA	CGGACCCTCT	ATATGGAAC	ATGTATAATC	ACTACACAGG	1100
	AAAGCCAATT	ATAACAGTTC	CTGGACAAAA	TGTAGCAGTT	AAATCCGGTA	1150
	CGGCTCAAAT	CGCTGATGAG	AAAAATGGAG	GATACTTGGT	TGTTTCTACC	1200
	AATTATATTT	TCTCAGTTGT	GACTATGAAT	CCTGCTGAAA	ATCCTGATTT	1250
	TATCTTGAT	GTAACGGTTC	AACAGCCTGA	GCATTATTCA	GGTATCCAGT	1300
10	TGGGAGAATT	TGCCACCCCA	ATCTTGGAGC	GGGCTTCAGC	TATGAAAGAA	1350
	TCTCTCAATC	TTCAATCTCC	AGCCAAAAAT	TTAGATAAAG	TTACGACAGA	1400
	ATCTTCTTAT	GCAATGCCTA	GCATCAAGGA	TATTTACCT	GGTGAGTTGG	1450
	CGGAAGCCTT	ACGCCGAAAT	ATTGTGCAAC	CAATCGTTGT	AGGTACTGGA	1500
	ACAAAGATTA	AAGAGACTTC	TGTAGAAGAA	GGGACCAATC	TTGCACCAAA	1550
15	CCAACAAGTT	CTCCTTTTAT	CGGATAAGGT	AGAAGAAATT	CCAGACATGT	1600
	ATGGCTGGAA	AAAAGAGACT	GCCGAGACCT	TTGCTAAATG	GTTGGATATT	1650
	GAACTGGAAT	TTGAAGGTTC	AGGTTCGGTT	GTTCAGAAG		1689

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2) INFORMATION FOR SEQ ID NO: 1047

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1690 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

30

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
 (B) STRAIN: StrR-14

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1047

	CAAAAAAGAA	TTGGAAGCTG	CAGAGGTCAA	GGGGATTGAT	TTTACAACCA	50
	GTCCCAACCG	TAGTTACCCA	AACGGACAAT	TTGCTTCTAG	TTTTATCGGA	100
	CTAGCTCAGC	TCCATGAAAA	TGAAGATGGC	AGCAAGAGCT	TGCTGGGAAC	150
40	TTCTGGAATG	GAGAGTTCCT	TGAACAGTAT	TCTTGCAGGG	ACAGACGGCA	200
	TTATTACCTA	TGAAAAGGAT	CGTCTGGGTA	ATATTGTACC	CGGAACAGAA	250
	CAAGTTTCCC	AACAAACGGT	AGATGGCAAG	GATGTTTACA	CAACCATTTT	300
	CAGCCCCCTC	CAGTCCTTTA	TGGAAACCCA	GATGGATGCT	TTTCAAGAGA	350
	AGGTAAAGG	AAAGTACACG	ACAGCGACTT	TGGTCAGTGC	TAAAACAGGG	400
45	GAAATTCTGG	CAACAACGCA	ACGACCGACC	TTTGATGCAG	ATACAAAAGA	450
	AGGCATTACA	GAGGACTTTG	TTTGGCGTGA	TATCCTTTAC	CAAAGTAACT	500
	ATGAGCCAGG	TTCCCCTATG	AAAGTGATGA	TGTTGGCTGC	TGCTATTGAT	550
	AATAATACCT	TTCCAGGGGG	AGAAGTCTTC	AATAGTAGTG	AGTTAAAAAT	600
	TGCAGATGTC	ACGATTCGAG	ATTGGGACGT	CAATGAAGGA	TTGACTGGTG	650
50	GCAGAATGAT	GACCTTTTCT	CAAGGGTTTC	CTCACTCAAG	TAACGTTGGG	700
	ATGACGCTTC	TTGAGCAAAA	GATGGGAGAT	GCTACATGGC	TTGATTATCT	750
	AAATCGCTTT	AAATTTGGTG	TTCCGACTCG	TTTTGGCTTG	ACGGATGAAT	800
	ATGCAGGCCA	ACTTCCAGCT	GACAATATCG	TAAATATTGC	TCAGAGTTCA	850
	TTTGGACAAG	GGATTTTCAGC	GACCCAGACG	CAAATGATTTC	GTGCCTTCAC	900
55	GGCTATTGCC	AACGATGGAG	TCATGTTAGA	ACCTAAATTT	ATCAGTGCCA	950
	TTTATGATCC	AAATGATCAA	ACTGCTCGGA	AATCACAAAA	AGAAGTTGTG	1000
	GGAAATCCTG	TGTCTAAAGA	TGCAGCGAGC	TTGACGCGAA	CGCATATGGT	1050
	TTTAGTCGGT	ACCGATCCAG	TATATGGAAC	TATGTATAAT	CATAAGACAG	1100
	GGAAACCAAC	TGTAAGTGT	CCTGGGCAAA	ATGTAGCCCT	CAAGTCTGGT	1150
60	ACGGCTCAGA	TTGCCGATGA	GAAAAATGGA	GGTTACTTAG	TTGGTACGAC	1200

	CAATTACATT	TTTTCGGCTG	TATCGATGAA	CCCTGCTGAA	AATCCTGATT	1250
	TTATTCTCTA	TGTGACGGTT	CAACAGCCTG	AGCATTATTC	AGGTATTCAG	1300
	TTGGGGGAAT	TTGCCAATCC	TATCTTGGAA	AGGGCAGTGG	CTATGAAAGA	1350
	TTCCCTTAAC	CTCCAATCTA	CCGCTAAAAC	GTTAAATCAG	GTAACCAATC	1400
5	AAAGCGCTTA	TGCCATGCCT	AGCATCAAGG	ACATTTACC	TGGCGATTTG	1450
	GCGGAAGCCT	TACGTCGCAA	TATTGTGCAA	CCAATCGTTG	TAGGAACAGG	1500
	AACAAAATT	AAAGAATCAT	CTGTAGAAGA	AGGGACGGAT	CTTGACCTA	1550
	ACCAGCAAGT	TCTTCTCTTA	TCTGATAAAG	CAGAGGAAGT	TCCAGATATG	1600
	TATGGTTGGA	CAAAAGAGAC	TGCTGAGACC	TTTGCTAAGT	GGCTCAATAT	1650
10	AGAACTTGAA	TTTGAAGGTT	CGGGCTCTAC	TGTGCAGAAG		1690

2) INFORMATION FOR SEQ ID NO: 1048

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(i) SEQUENCE CHARACTERISTICS:

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- (A) LENGTH: 1682 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

25

- (A) ORGANISM: *Streptococcus pneumoniae*
- (B) STRAIN: StrR-15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1048

30	AAAAGAGTTG	GAAACTGCAG	AGGTCAAGGG	GATTGATTTT	ACAACCAGTC	50
	CCAATCGTAG	TTACCCAAAC	GGACAATTG	CTTCTAGCTT	TATTGGCTTA	100
	GCCCAACTTC	ATGAAAATGA	GGATGGTAGT	AAGAGTTTGT	TAGGGACTTC	150
	TGGTTTGGAG	AGTTCTTTAA	ATACCATTCT	TGCTGGGACA	GACGGTATTA	200
	TTACCTATGA	AAAAGACCGT	GTAGGAAATA	TCGTACCAGG	TACAGAACTG	250
35	GTATCGCAAC	AAACTGTGGA	TGGCAAGGAT	GTTTATACAA	CATTGTCTAG	300
	TCCGCTACAA	TCTTTCATGG	AAACTCAGAT	GGATGCCTTT	CTAGAAAAAG	350
	TAAAAGGTAA	GTATATGACC	GCGACCTTGG	TCAGTGCAAA	GACCGGTGAA	400
	ATCCTCGTAA	CCACCCAACG	ACCTACCTTT	AATGCAGATA	CTAAAGAAGG	450
	AATCACTGAG	GACTTTGTTT	GGCGTGATAT	TCTTTATCAA	AGTAACTATG	500
40	AACCAGGATC	AGCCATGAAG	GTTATGACGT	TAGCTTCTTC	TATTGATAAT	550
	AATACCTTCC	CAAGTGGAGA	ATACTTCAAT	AGCAGTGAAT	TCAAAATAGC	600
	GGATGCGACG	ACTCGAGATT	GGGATGTAA	TGAAGGTTTG	ACTACTGGTG	650
	GGATGATGAC	TTTCTTACAA	GGTTTCGCTC	ACTCCAGTAA	TGTTGGAATG	700
	AGTCTACTTG	AACAAAAAAT	GGGAGATGCT	ACTTGGTG	ATTATCTAAA	750
45	ACGCTTTAAA	TTTGGGGTTC	CAACTCGCTT	TGGCTTGACA	GATGAATACG	800
	CTGGTCAACT	TCCAGCTGAT	AATATTGTTA	GTATTGCTCA	AAGCTCATTT	850
	GGGCAAGGAA	TTTCAGTGAC	ACAAACACAA	ATGCTTCGTG	CCTTTACAGC	900
	TATTGCTAAT	GATGGAGTTA	TGCTGGAGCC	AAAATTTATA	AGTGCTATTT	950
	ATGATACTAA	CAATCAGTCT	GTACGTAAGT	CACAAAAAGA	AATAGTAGGA	1000
50	AATCCTGTTT	CCAAAGAGGC	AGCAAGCACA	ACTCGAAATC	ACATGATCTT	1050
	AGTTGGGACG	GACCCTCTAT	ATGGAACAT	GTATAATCAC	TACACAGGAA	1100
	AGCCAATTAT	AACAGTTCCT	GGACAAAATG	TAGCAGTTAA	ATCCGGTACG	1150
	GCTCAAATCG	CTGATGAGAA	AAATGGAGGA	TACTTGGTTG	GTTCTACCAA	1200
	TTATATTTTC	TCAGTTGTGA	CTATGAATCC	TGCTGAAAAT	CCTGATTTTA	1250
55	TCTTGTATGT	AACGGTTCAA	CAGCCTGAGC	ATTATTCAGG	TATCCAGTTG	1300
	GGAGAATTTG	CCACCCCAAT	CTTGGAGCGG	GCTTCAGCTA	TGAAAGAATC	1350
	TCTCAATCTT	CAATCTCCAG	CCAAAAATTT	AGATAAAGTT	ACGACAGAAT	1400
	CTTCTTATGC	AATGCCTAGC	ATCAAGGATA	TTTCACCTGG	TGAGTTGGCG	1450
	GAAGCCTTAC	GCCGAAATAT	TGTGCAACCA	ATCGTTGTAG	GTACTGGAAC	1500
60	AAAGATTAAA	GAGACTTCTG	TAGAAGAAGG	GACCAATCTT	GCACCAAACC	1550

AACAAGTTCT	CCTTTTATCG	GATAAGGTAG	AAGAAATTCC	AGACATGTAT	1600
GGCTGGAAAA	AAGAGACTGC	TGAAACCTTT	GCTAAATGGT	TGGATATTGA	1650
GTTGGAATTT	GAAGGTTTCA	GTTCCGTCGT	TC		1682

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2) INFORMATION FOR SEQ ID NO: 1049

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 1241 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

15 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus faecium*
 (B) STRAIN: R690

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1049

GCAGCGTTGC	GTGATACCGT	TGAAAAAACC	ATTAAAAACT	GTTTGGATTT	50
TGAAAGGAGA	CAGGAGCATG	AATAGAATAA	AAGTTGCAAT	ACTGTTTGGG	100
25 GGTGCTCAG	AGGAGCATGA	CGTATCGGTA	AAATCTGCAA	TAGAGATAGC	150
CGCTAACATT	AATAAAGAAA	AATACGAGCC	GTTATACATT	GGAATTACGA	200
AATCTGGTGT	ATGGAAAATG	TGCGAAAAAC	CTTGCGCGGA	ATGGGAAAAC	250
GACAATTGCT	ATTCAGCTGT	ACTCTCGCCG	GATAAAAAAA	TGCACGGATT	300
ACTTGTTAAA	AAGAACCATG	AATATGAAAT	CAACCATGTT	GATGTAGCAT	350
30 TTTTCACTTT	GCATGGCAAG	TCAGGTGAAG	ATGGATCCAT	ACAAGGTCTG	400
TTTGAATTGT	CCGGTATCCC	TTTTGTAGGC	TGCGATATTC	AAAGCTCAGC	450
AATTTGTATG	GACAAATCGT	TGACATACAT	CGTTGCGAAA	AATGCTGGGA	500
TAGCTACTCC	CGCCTTTTGG	GTTATTAATA	AAGATGATAG	GCCGGTGGCA	550
GCTACGTTTA	CCTATCCTGT	TTTTGTAAAG	CCGGCGCGTT	CAGGCTCATC	600
35 CTTCCGTGTG	AAAAAAGTCA	ATAGCGCGGA	CGAATTGGAC	TACGCAATTG	650
AATCGGCAAG	ACAATATGAC	AGCAAAATCT	TAATTGAGCA	GGCTGTTTCG	700
GGCTGTGAGG	TCGGTTGTGC	GGTATTGGGA	AACAGTGCCG	CGTTAGCTGT	750
TGGCGAGGTG	GACCAAATCA	GGCTGCAGTA	CGGAATCTTT	CGTATTCATC	800
AGGAAGTCGA	GCCGGAAAAA	GGCTCTGAAA	ACGCAGTTAT	AACCGTTCCC	850
40 GCAGACCTTT	CAGCAGAGGA	GCGAGGACGG	ATACAGGAAA	CGGCAAAAAA	900
AATATATAAA	GCGCTCGGCT	GTAGAGGTCT	AGCCCGTGTG	GATATGTTTT	950
TACAAGATAA	CGGCCGCATT	GTAATGAACG	AAGTCAATAC	TCTGCCCGGT	1000
TTCACGTCAT	ACAGTCGTTA	TCCCCGTATG	ATGGCCGCTG	CAGGTATTGC	1050
ACTTCCCGAA	CTGATTGACC	GCTTGATCGT	ATTAGCGTTA	AAGGGGTGAT	1100
45 AAGCATGGAA	ATAGGATTTA	CTTTTTTAGA	TGAAATAGTA	CACGGTGTTC	1150
GTTGGGACGC	TAAATATGCC	ACTTGGGATA	ATTCACCGG	AAAACCGGTT	1200
GACGGTTATG	AAGTAAATCG	CATTGTAGGG	ACATACGAAT	T	1241

50

2) INFORMATION FOR SEQ ID NO: 1050

(i) SEQUENCE CHARACTERISTICS:

- 55 (A) LENGTH: 1249 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

60

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Enterococcus gallinarum*

(B) STRAIN: R691

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1050

	TCACACCGCA	TACGGCCTAT	TATACCGAGC	AAGCGTTGCG	TGATACCGTT	50
	GAAAAAACCA	TTAAAACTG	TTTGGATTTT	GAAAGGAGAC	AGGAGCATGA	100
	ATAGAATAAA	AGTTGCAATA	CTGTTTGGGG	GTTGCTCAGA	GGAGCATGAC	150
10	GTATCGGTAA	AATCTGCAAT	AGAGATAGCC	GCTAACATTA	ATAAAGAAAA	200
	ATACGAGCCG	TTATACATTG	GAATTACGAA	ATCTGGTGTA	TGGAAAATGT	250
	GCGAAAAACC	TTGCGCGGAA	TGGGAAAACG	ACAATTGCTA	TTCAGCTGTA	300
	CTCTCGCCCG	ATAAAAAAAT	GCACGGATTA	CTTGTTAAAA	AGAACCATGA	350
	ATATGAAATC	AACCATGTTG	ATGTAGCATT	TTCAGCTTTG	CATGGCAAGT	400
15	CAGGTGAAGA	TGGATCCATA	CAAGGTCTGT	TTGAATTGTC	CGGTATCCCT	450
	TTTGTAGGCT	GCGATATTCA	AAGCTCAGCA	ATTTGTATGG	ACAAATCGTT	500
	GACATACATC	GTTGCGAAAA	ATGCTGGGAT	AGCTACTCCC	GCCTTTTGGG	550
	TTATTAATAA	AGATGATAGG	CCGGTGGCAG	CTACGTTTAC	CTATCCTGTT	600
	TTTGTTAAGC	CGGCGCGTTC	AGGCTCATCC	TTCGGTGTGA	AAAAAGTCAA	650
20	TAGCGCGGAC	GAATTGGACT	ACGCAATTGA	ATCGGCAAGA	CAATATGACA	700
	GCAAAATCTT	AATTGAGCAG	GCTGTTTCGG	GCTGTGAGGT	CGGTTGTGCG	750
	GTATTGGGAA	ACAGTGCCGC	GTTAGCTGTT	GGCGAGGTGG	ACCAAATCAG	800
	GCTGCAGTAC	GGAATCTTTC	GTATTCATCA	GGAAGTCGAG	CCGGAAAAAG	850
	GCTCTGAAAA	CGCAGTTATA	ACCGTTCCCG	CAGACCTTTC	AGCAGAGGAG	900
25	CGAGGACGGA	TACAGGAAAC	GGCAAAAAAA	ATATATAAAG	CGCTCGGCTG	950
	TAGAGGTCTA	GCCCCGTGTG	ATATGTTTTT	ACAAGATAAC	GGCCGCATTG	1000
	TACTGAACGA	AGTCAATACT	CTGCCCCGTT	TCACGTCATA	CAGTCGTTAT	1050
	CCCCGTATGA	TGGCCGCTGC	AGGTATTGCA	CTTCCCGAAC	TGATTGACCG	1100
	CTTGATCGTA	TTAGCGTTAA	AGGGGTGATA	AGCATGGAAA	TAGGATTTAC	1150
30	TTTTTTTAGAT	GAAATAGTAC	ACGGTGTTCG	TTGGGACGCT	AAATATGCCA	1200
	CTTGGGATAA	TTTCACCGGA	AAACCGGTTG	ACGGTTATGA	AGTAAATCG	1249

35 2) INFORMATION FOR SEQ ID NO: 1051

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1272 bases

(B) TYPE: Nucleic acid

40 (C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

45 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Enterococcus faecium*

(B) STRAIN: R481

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1051

50	TATACCGAGC	AAGCGTTGCG	TGATACCGTT	GAAAAAACCA	TTAAAACTG	50
	TTTGGATTTT	GAAAGGAGAC	AGGAGCATGA	ATAGAATAAA	AGTTGCAATA	100
	CTGTTTGGGG	GTTGCTCAGA	GGAGCATGAC	GTATCGGTAA	AATCTGCAAT	150
	AGAGATAGCC	GCTAACATTA	ATAAAGAAAA	ATACGAGCCG	TTATACATTG	200
55	GAATTACGAA	ATCTGGTGTA	TGGAAAATGT	GCGAAAAACC	TTGCGCGGAA	250
	TGGGAAAACG	ACAATTGCTA	TTCAGCTGTA	CTCTCGCCCG	ATAAAAAAAT	300
	GCACGGATTA	CTTGTTAAAA	AGAACCATGA	ATATGAAATC	AACCATGTTG	350
	ATGTAGCATT	TTCAGCTTTG	CATGGCAAGT	CAGGTGAAGA	TGGATCCATA	400
	CAAGGTCTGT	TTGAATTGTC	CGGTATCCCT	TTTGTAGGCT	GCGATATTCA	450
60	AAGCTCAGCA	ATTTGTATGG	ACAAATCGTT	GACATACATC	GTTGCGAAAA	500

	ATGCTGGGAT	AGCTACTCCC	GCCTTTTGGG	TTATTAATAA	AGATGATAGG	550
	CCGGTGGCAG	CTACGTTTAC	CTATCCTGTT	TTTGTTAAGC	CGGCGCGTTC	600
	AGGCTCATCC	TTCGGTGTGA	AAAAAGTCAA	TAGCGCGGAC	GAATTGGACT	650
	ACGCAATTGA	ATCGGCAAGA	CAATATGACA	GCAAAATCTT	AATTGAGCAG	700
5	GCTGTTTCGG	GCTGTGAGGT	CGGTTGTGCG	GTATTGGGAA	ACAGTGCCGC	750
	GTTAGTTGTT	GGCGAGGTGG	ACCAAATCAG	GCTGCAGTAC	GGAATCTTTC	800
	GTATTCATCA	GGAAGTCGAG	CCGGAAAAAG	GCTCTGAAAA	CGCAGTTATA	850
	ACCGTTCCCG	CAGACCTTTC	AGCAGAGGAG	CGAGGACGGA	TACAGGAAAC	900
	GGCAAAAAAA	ATATATAAAG	CGCTCGGCTG	TAGAGGTCTA	GCCCGTGTGG	950
10	ATATGTTTTT	ACAAGATAAC	GGCCGCATTG	TACTGAACGA	AGTCAATACT	1000
	CTGCCCGGTT	TCACGTCATA	CAGTCGTTAT	CCCCGTATGA	TGGCCGCTGC	1050
	AGGTATTGCA	CTTCCCGAAC	TGATTGACCG	CTTGATCGTA	TTAGCGTTAA	1100
	AGGGGTGATA	AGCATGGAAA	TAGGATTTAC	TTTTTTAGAT	GAAATAGTAC	1150
	ACGGTGTTTCG	TTGGGACGCT	AAATATGCCA	CTTGGGATAA	TTTCACCGGA	1200
15	AAACCGGTTG	ACGGTTATGA	AGTAAATCGC	ATTGTAGGGA	CATACGAATT	1250
	GGCTTGAATC	GCTTTTTGAA	GG			1272

20 2) INFORMATION FOR SEQ ID NO: 1052

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1237 bases
 (B) TYPE: Nucleic acid
 25 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

30 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus faecium*
 (B) STRAIN: R492

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1052

35	TCCCCCGGCA	TACGGCCTAT	TATACCGAGC	AAGCGTTGCG	TGATACCGTT	50
	GAAAAAACCA	TTAAAAACTG	TTTGGAATTT	GAAAGGAGAC	AGGAGCATGA	100
	ATAGAATAAA	AGTTGCAATA	CTGTTTGGGG	GTTGCTCAGA	GGAGCATGAC	150
	GTATCGGTAA	AATCTGCAAT	AGAGATAGCC	GCTAACATTA	ATAAAGAAAA	200
40	ATACGAGCCG	TTATACATTG	GAATTACGAA	ATCTGGTGTA	TGGAAAATGT	250
	GCGAAAAACC	TTGCGCGGAA	TGGGAAAACG	ACAATTGCTA	TTCAGCTGTA	300
	CTCTCGCCGG	ATAAAAAAAT	GCACGGATTA	CTTGTTAAAA	AGAACCATGA	350
	ATATGAAATC	AACCATGTTG	ATGTAGCATT	TTCAGCTTTG	CATGGCAAGT	400
	CAGGTGAAGA	TGGATCCATA	CAAGGTCTGT	TTGAATTGTC	CGGTATCCCT	450
45	TTTGTAGGCT	GCGATATTCA	AAGCTCAGCA	ATTTGTATGG	ACAAATCGTT	500
	GACATACATC	GTTGCGAAAA	ATGCTGGGAT	AGCTACTCCC	GCCTTTTGGG	550
	TTATTAATAA	AGATGATAGG	CCGGTGGCAG	CTACGTTTAC	CTATCCTGTT	600
	TTTGTTAAGC	CGGCGCGTTC	AGGCTCATCC	TTCGGTGTGA	AAAAAGTCAA	650
	TAGCGCGGAC	GAATTGGACT	ACGCAATTGA	ATCGGCAAGA	CAATATGACA	700
50	GCAAAATCTT	AATTGAGCAG	GCTGTTTCGG	GCTGTGAGGT	CGGTGTGTGCG	750
	GTATTGGGAA	ACAGTGCCGC	GTTAGCTGTT	GGCGAGGTGG	ACCAAATCAG	800
	GCTGCAGTAC	GGAATCTTTC	GTATTCATCA	GGAAGTCGAG	CCGGAAAAAG	850
	GCTCTGAAAA	CGCAGTTATA	ACCGTTCCCG	CAGACCTTTC	AGCAGAGGAG	900
	CGAGGACGGA	TACAGGAAAC	GGCAAAAAAA	ATATATAAAG	CGCTCGGCTG	950
55	TAGAGGTCTA	GCCCGTGTGG	ATATGTTTTT	ACAAGATAAC	GGCCGCATTG	1000
	TACTGAACGA	AGTCAATACT	CTGCCCGGTT	TCACGTCATA	CAGTCGTTAT	1050
	CCCCGTATGA	TGGCCGCTGC	AGGTATTGCA	CTTCCCGAAC	TGATTGACCG	1100
	CTTGATCGTA	TTAGCGTTAA	AGGGGTGATA	AGCATGGAAA	TAGGATTTAC	1150
	TTTTTTAGAT	GAAATAGTAC	ACGGTGTTTCG	TTGGGACGCT	AAATATGCCA	1200
60	CTTGGGATAA	TTTCACCGGA	AAACCGGTTG	ACGGTTA		1237

2) INFORMATION FOR SEQ ID NO: 1053

- 5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1263 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 10 (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
 15 (A) ORGANISM: *Enterococcus faecium*
 (B) STRAIN: R581
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1053

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20 CATACGGCCT ATTATACCGA GCAAGCGTTG CGTGATACCG TTGAAAAAAC      50
   CATTAAAAAC TGTTTGGATT TTGAAAGGAG ACAGGAGCAT GAATAGAATA      100
   AAAGTTGCAA TACTGTTTGG GGGTTGCTCA GAGGAGCATG ACGTATCGGT      150
   AAAATCTGCA ATAGAGATAG CCGCTAACAT TAATAAAGAA AAATACGAGC      200
   CGTTATACAT TGAATTACG AAATCTGGTG TATGAAAAAT GTGCGAAAAA      250
25 CCTTGCGCGG AATGGGAAAA CGACAATTGC TATTCAGCTG TACTCTCGCC      300
   GGATAAAAAA ATGCACGGAT TACTTGTTAA AAAGAACCAT GAATATGAAA      350
   TCAACCATGT TGATGTAGCA TTTTCAGCTT TGCATGGCAA GTCAGGTGAA      400
   GATGGATCCA TACAAGGTCT GTTTGAATTG TCCGGTATCC CTTTTGTAGG      450
   CTGCGATATT CAAAGCTCAG CAATTTGTAT GGACAAATCG TTGACATACA      500
30 TCGTTGCGAA AAATGCTGGG ATAGCTACTC CCGCCTTTTG GGTTATTAAT      550
   AAAGATGATA GGCCGGTGGC AGCTACGTTT ACCTATCCTG TTTTGTAA      600
   GCCGGCGCGT TCAGGCTCAT CCTTCGGTGT GAAAAAAGTC AATAGCGCGG      650
   ACGAATTGGA CTACGCAATT GAATCGGCAA GACAATATGA CAGCAAAATC      700
   TTAATTGAGC AGGCTGTTTC GGGCTGTGAG GTCGGTTGTG CGGTATTGGG      750
35 AAACAGTGCC GCGTTAGCTG TTGGCGAGGT GGACCAAATC AGGCTGCAGT      800
   ACGGAATCTT TCGTATTCAT CAGGAAGTCG AGCCGAAAAA AGGCTCTGAA      850
   AACGCAGTTA TAACCGTTCC CGCAGACCTT TCAGCAGAGG AGCGAGGACG      900
   GATACAGGAA ACGGCAAAAA AAATATATAA AGCGCTCGGC TGTAGAGGTC      950
   TAGCCCGTGT GGATATGTTT TTACAAGATA ACGGCCGCAT TGTACTGAAC      1000
40 GAAGTCAATA CTCTGCCCGG TTTCACGTCA TACAGTCGTT ATCCCCGTAT      1050
   GATGGCCGCT GCAGGTATTG CACTTCCCGA ACTGATTGAC CGCTTGATCG      1100
   TATTAGCGTT AAAGGGGTGA TAAGCATGGA AATAGGATTT ACTTTTTTAG      1150
   ATGAAATAGT ACACGGTGTG CGTTGGGACG CTAAATATGC CACTTGGGAT      1200
   AATTTACCGG GAAAACCGGT TGACGGGTAT GAAAGTAAAT CGCATTGTAG      1250
45 GGACATTCGA ATT                                           1263
  
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2) INFORMATION FOR SEQ ID NO: 1054

- 50 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1232 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 55 (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
 60 (A) ORGANISM: *Enterococcus faecalis*

(B) STRAIN: R610

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1054

5	CGGCCTATTA	TNCCGAGCAA	GCGTTGCGTG	ATACCGTTGA	AAAAACCATT	50
	AAAAACTGTT	TGGATTTTGA	AAGGAGACAG	GAGCATGAAT	AGAATAAAAAG	100
	TTGCAATACT	GTTTGGGGGT	TGCTCAGAGG	AGCATGACGT	ATCGGTAAAA	150
	TCTGCAATAG	AGATAGCCGC	TAACATTAAT	AAAGAAAAAT	ACGAGCCGTT	200
	ATTACATTGGA	ATTACGAAAT	CTGGTGTATG	GAAAATGTGC	GAAAAACCTT	250
10	GCGCGGAATG	GGAAAACGAC	AATTGCTATT	CAGCTGTACT	CTCGCCGGAT	300
	AAAAAAATGC	ACGGATTACT	TGTTAAAAAG	AACCATGAAT	ATGAAATCAA	350
	CCATGTTGAT	GTAGCATTTT	CAGCTTTGCA	TGGCAAGTCA	GGTGAAGATG	400
	GATCCATACA	AGGTCTGTTT	GAATTGTCCG	GTATCCCTTT	TGTAGGCTGC	450
	GATATTCAAA	GCTCAGCAAT	TTGTATGGAC	AAATCGTTGA	CATACATCGT	500
15	TGCGAAAAAT	GCTGGGATAG	CTACTCCCGC	CTTTTGGGTT	ATTAATAAAG	550
	ATGATAGGCC	GGTGGCAGCT	ACGTTTACCT	ATCCTGTTTT	TGTTAAGCCG	600
	GCGCGTTCAG	GCTCATCCTT	CGGTGTGAAA	AAAGTCAATA	GCGCGGACGA	650
	ATTGGACTAC	GCAATTGAAT	CGGCAAGACA	ATATGACAGC	AAAATCTTAA	700
	TTGAGCAGGC	TGTTTCGGGC	TGTGAGGTCG	GTTGTGCGGT	ATTGGGAAAC	750
20	AGTGCCGCGT	TAGTTGTTGG	CGAGGTGGAC	CAAATCAGGC	TGCAGTACGG	800
	AATCTTTTCG	ATTCATCAGG	AAGTCGAGCC	GGAAAAAGGC	TCTGAAAACG	850
	CAGTTATAAC	CGTTCCTGCA	GACCTTTCAG	CAGAGGAGCG	AGGACGGATA	900
	CAGGAAACGG	CAAAAAAAT	ATATAAAGCG	CTCGGCTGTA	GAGGTCTAGC	950
	CCGTGTGGAT	ATGTTTTTAC	AAGATAACGG	CCGCATTGTA	CTGAACGAAG	1000
25	TCAATACTCT	GCCCGGTTTC	ACGTCATACA	GTCGTTATCC	CCGTATGATG	1050
	GCCGCTGCAG	GTATTGCACT	TCCCGAACTG	ATTGACCGCT	TGATCGTATT	1100
	AGCGTTAAAG	GGGTGATAAG	CATGGAAATA	GGATTTACTT	TTTTAGATGA	1150
	AATAGTACAC	GGTGTTTCGT	GGGACGCTAA	ATATGCCACT	TGGGATAATT	1200
30	TCACCGGAAA	ACCGGTTGAC	GGTTATAAGT	AA		1232

2) INFORMATION FOR SEQ ID NO: 1055

- 35 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1218 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Double
 - (D) TOPOLOGY: Linear
- 40 (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Enterococcus gallinarum*
 - 45 (B) STRAIN: R684

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1055

50	TACCGAGCAA	GCGTTGCGTG	ATACCGTTGA	AAAAACCATT	AAAAACTGTT	50
	TGGATTTTGA	AAGGAGACAG	GAGCATGAAT	AGAATAAAAAG	TTGCAATACT	100
	GTTTGGGGGT	TGCTCAGAGG	AGCATGACGT	ATCGGTAAAA	TCTGCAATAG	150
	AGATAGCCGC	TAACATTAAT	AAAGAAAAAT	ACGAGCCGTT	ATACATTGGA	200
	ATTACGAAAT	CTGGTGTATG	GAAAATGTGC	GAAAAACCTT	GCGCGGAATG	250
	GGAAAACGAC	AATTGCTATT	CAGCTGTACT	CTCGCCGGAT	AAAAAAATGC	300
55	ACGGATTACT	TGTTAAAAAG	AACCATGAAT	ATGAAATCAA	CCATGTTGAT	350
	GTAGCATTTT	CAGCTTTGCA	TGGCAAGTCA	GGTGAAGATG	GATCCATACA	400
	AGGTCTGTTT	GAATTGTCCG	GTATCCCTTT	TGTAGGCTGC	GATATTCAAA	450
	GCTCAGCAAT	TTGTATGGAC	AAATCGTTGA	CATACATCGT	TGCGAAAAAT	500
	GCTGGGATAG	CTACTCCCGC	CTTTTGGGTT	ATTAATAAAG	ATGATAGGCC	550
60	GGTGGCAGCT	ACGTTTACCT	ATCCTGTTTT	TGTTAAGCCG	GCGCGTTCAG	600

	GCTCATCCTT	CGGTGTGAAA	AAAGTCAATA	GCGCGGACGA	ATTGGACTAC	650
	GCAATTGAAT	CGGCAAGACA	ATATGACAGC	AAAATCTTAA	TTGAGCAGGC	700
	TGTTTCGGGC	TGTGAGGTCG	GTTGTGCGGT	ATTGGGAAAC	AGTGCCGCGT	750
	TAGCTGTTGG	CGAGGTGGAC	CAAATCAGGC	TGCAGTACGG	AATCTTTCGT	800
5	ATTCATCAGG	AAGTCGAGCC	GGAAAAAGGC	TCTGAAAACG	CAGTTATAAC	850
	CGTTCCCGCA	GACCTTTCAG	CAGAGGAGCG	AGGACGGATA	CAGGAAACGG	900
	CAAAAAAAT	ATATAAAGCG	CTCGGCTGTA	GAGGTCTAGC	CCGTGTGGAT	950
	ATGTTTTTAC	AAGATAACGG	CCGCATTGTA	CTGAACGAAG	TCAATACTCT	1000
	GCCCCGTTTC	ACGTCATACA	GTCGTTATCC	CCGTATGATG	GCCGCTGCAG	1050
10	GTATTGCACT	TCCCGAACTG	ATTGACCGCT	TGATCGTATT	AGCGTTAAAG	1100
	GGGTGATAAG	CATGGAAATA	GGATTTACTT	TTTGTAGATGA	AATAGTACAC	1150
	GGTGTTCGTT	GGGACGCTAA	ATATGCCACT	TGGGATAATT	TCACCGGAAA	1200
	ACCGGTTGAC	GGTTAGAA				1218

15

2) INFORMATION FOR SEQ ID NO: 1056

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 1265 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

25 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus faecium*
 (B) STRAIN: R688

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1056

	AATCACACCG	CATACGGCCT	ATTATACCGA	GCAAGCGTTG	CGTGATACCG	50
	TTGAAAAAAC	CATTAAAAAC	TGTTTGGATT	TTGAAAGGAG	ACAGGAGCAT	100
35	GAATAGAATA	AAAGTTGCAA	TACTGTTTGG	GGGTTGCTCA	GAGGAGCATG	150
	ACGTATCGGT	AAAATCTGCA	ATAGAGATAG	CCGCTAACAT	TAATAAAGAA	200
	AAATACGAGC	CGTTATACAT	TGGAATTACG	AAATCTGGTG	TATGGAAAAT	250
	GTGCGAAAAA	CCTTGCGCGG	AATGGGAAAA	CGACAATTGC	TATTCAGCTG	300
	TACTCTCGCC	GGATAAAAAA	ATGCACGGAT	TACTTGTTAA	AAAGAACCAT	350
40	GAATATGAAA	TCAACCATGT	TGATGTAGCA	TTTTTCAGCTT	TGCATGGCAA	400
	GTCAGGTGAA	GATGGATCCA	TACAAGGTCT	GTTTGAATTG	TCCGGTATCC	450
	CTTTTGTAGG	CTGCGATATT	CAAAGCTCAG	CAATTTGTAT	GGACAAATCG	500
	TTGACATACA	TCGTTGCGAA	AAATGCTGGG	ATAGCTACTC	CCGCCTTTTG	550
	GGTTATTAAT	AAAGATGATA	GGCCGGTGCC	AGCTACGTTT	ACCTATCCTG	600
45	TTTTTGTAA	GCCGGCGCGT	TCAGGCTCAT	CCTTCGGTGT	GAAAAAAGTC	650
	AATAGCGCGG	ACGAATTGGA	CTACGCAATT	GAATCGGCAA	GACAATATGA	700
	CAGCAAAATC	TTAATTGAGC	AGGCTGTTTC	GGGCTGTGAG	GTCGGTTGTG	750
	CGGTATTGGG	AAACAGTGCC	GCGTTAGCTG	TTGGCGAGGT	GGACCAAATC	800
	AGGCTGCAGT	ACGGAATCTT	TCGTATTCAT	CAGGAAGTCG	AGCCGGAAAA	850
50	AGGCTCTGAA	AACGCAGTTA	TAACCGTTCC	CGCAGACCTT	TCAGCAGAGG	900
	AGCGAGGACG	GATACAGGAA	ACGGCAAAAA	AAATATATAA	AGCGCTCGGC	950
	TGTAGAGGTC	TAGCCCGTGT	GGATATGTTT	TTACAAGATA	ACGGCCGCAT	1000
	TGTACTGAAC	GAAGTCAATA	CTCTGCCCCG	TTTCACGTCA	TACAGTCGTT	1050
	ATCCCCGTAT	GATGGCCGCT	GCAGGTATTG	CACTTCCCGA	ACTGATTGAC	1100
55	CGCTTGATCG	TATTAGCGTT	AAAGGGGTGA	TAAGCATGGA	AATAGGATTT	1150
	ACTTTTTTAG	ATGAAATAGT	ACACGGTGTT	CGTTGGGACG	CTAAATATGC	1200
	CACTTGGGAT	AATTTACCCG	GAAAACCGGT	TGACGGTTAT	GAAGTAAATC	1250
	GCATTGTAGG	GACAT				1265

60

2) INFORMATION FOR SEQ ID NO: 1057

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 1269 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

10 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus flavescens*
 (B) STRAIN: R689

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1057

	TCACACCGCA	TACGGCCTAT	TATACCGAGC	AAGCGTTGCG	TGATACCGTT	50
	GAAAAAACCA	TTAAAAACTG	TTTGGATTTT	GAAAGGAGAC	AGGAGCATGA	100
20	ATAGAATAAA	AGTTGCAATA	CTGTTTGGGG	GTTGCTCAGA	GGAGCATGAC	150
	GTATCGGTAA	AATCTGCAAT	AGAGATAGCC	GCTAACATTA	ATAAAGAAAA	200
	ATACGAGCCG	TTATACATTG	GAATTACGAA	ATCTGGTGTA	TGGAAAATGT	250
	GCGAAAAACC	TTGCGCGGAA	TGGGAAAACG	ACAATTGCTA	TTCAGCTGTA	300
	CTCTCGCCGG	ATAAAAAAAT	GCACGGATTA	CTTGTTAAAA	AGAACCATGA	350
25	ATATGAAATC	AACCATGTTG	ATGTAGCATT	TTCAGCTTTG	CATGGCAAGT	400
	CAGGTGAAGA	TGGATCCATA	CAAGGTCTGT	TTGAATTGTC	CGGTATCCCT	450
	TTTGTAGGCT	GCGATATTCA	AAGCTCAGCA	ATTTGTATGG	ACAAATCGTT	500
	GACATACATC	GTTGCGAAAA	ATGCTGGGAT	AGCTACTCCC	GCCTTTTGGG	550
	TTATTAATAA	AGATGATAGG	CCGGTGGCAG	CTACGTTTAC	CTATCCTGTT	600
30	TTTGTTAAGC	CGGCGCGTTC	AGGCTCATCC	TTCGGTGTGA	AAAAAGTCAA	650
	TAGCGCGGAC	GAATTGGACT	ACGCAATTGA	ATCGGCAAGA	CAATATGACA	700
	GCAAAATCTT	AATTGAGCAG	GCTGTTTCGG	GCTGTGAGGT	CGGTTGTGCG	750
	GTATTGGGAA	ACAGTGCCGC	GTTAGCTGTT	GGCGAGGTGG	ACCAAATCAG	800
	GCTGCAGTAC	GGAATCTTTC	GTATTCATCA	GGAAGTCGAG	CCGGA AAAAG	850
35	GCTCTGAAAA	CGCAGTTATA	ACCGTTCCCG	CAGACCTTTC	AGCAGAGGAG	900
	CGAGGACCGA	TACAGGAAAC	GGCAAAAAAA	ATATATAAAG	CGCTCGGCTG	950
	TAGAGTCTA	GCCCGTGTGG	ATATGTTTTT	ACAAGATAAC	GGCCGCATTG	1000
	TACTGAACGA	AGTCAATACT	CTGCCCCGTT	TCACGTCATA	CAGTCGTTAT	1050
	CCCCGTATGA	TGGCCGCTGC	AGGTATTGCA	CTTCCCGAAC	TGATTGACCG	1100
40	CTTGATCGTA	TTAGCGTTAA	AGGGGTGATA	AGCATGGAAA	TAGGATTTAC	1150
	TTTTTTAGAT	GAAATAGTAC	ACGGTGTTTC	TTGGGACGCT	AAATATGCCA	1200
	CTTGGGATAA	TTTCACCGGA	AAACCGGTTG	ACGGTTATGA	AGTAAATCGC	1250
	ATTGTAGGGA	CATACGAAT				1269

45

2) INFORMATION FOR SEQ ID NO: 1058

(i) SEQUENCE CHARACTERISTICS:

- 50 (A) LENGTH: 1169 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

55 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus gallinarum*
 (B) STRAIN: R420

60

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1058

	CAAATTTTCT	TTTCTTTTCC	TAGGTACACT	GAATGTAACC	TTAAAAGAAA	50
	AAAGGAAAGG	AAGAAAATGA	TGAAAAAAT	TGCCGTTTTA	TTTGGAGGGA	100
5	ATTCTCCAGA	ATACTCAGTG	TCACTAACCT	CAGCAGCAAG	TGTGATCCAA	150
	GCTATTAACC	CGCTGAAATA	TGAAGTAATG	ACCATTGGCA	TCGCACCAAC	200
	AATGGATTGG	TATTGGTATC	AAGGAAACCT	CGCGAATGTT	CGCAATGATA	250
	CTTGGCTAGA	AGATCACAAA	AACTGTCACC	AGCTGACTTT	TTCTAGCCAA	300
	GGATTTATAT	TAGGAGAAAA	ACGAATCGTC	CCTGATGTCC	TCTTTCCAGT	350
10	CTTGCATGGG	AAGTATGGCG	AGGATGGCTG	TATCCAAGGA	CTGCTTGAAC	400
	TAATGAACCT	GCCTTATGTT	GGTTGCCATG	TCGCTGCCTC	CGCATTATGT	450
	ATGAACAAAT	GGCTCTTGCA	TCAACTTGCT	GATACCATGG	GAATCGCTAG	500
	TGCTCCCACT	TTGCTTTTAT	CCCGCTATGA	AAACGATCCT	GCCACAATCG	550
	ATCGTTTTAT	TCAAGACCAT	GGATTCCCGA	TCTTTATCAA	GCCGAATGAA	600
15	GCCGGTTCTT	CAAAAGGGAT	CACAAAAGTA	ACTGACAAAA	CAGCGCTCCA	650
	ATCTGCATTA	ACGACTGCTT	TTGCTTACGG	TTCTACTGTG	TTGATCCAAA	700
	AGGCGATAGC	GGGTATTGAA	ATTGGCTGCG	GCATCTTAGG	AAATGAGCAA	750
	TTGACGATTG	GTGCTTGTGA	TGCGATTCTT	CTTGTGACG	GTTTTTTTGA	800
	TTTTGAAGAG	AAATACCAAT	TAATCAGCGC	CACGATCACT	GTCCCAGCAC	850
20	CATTGCCTCT	CGCGCTTGAA	TCACAGATCA	AGGAGCAGGC	ACAGCTGCTT	900
	TATCGAAACT	TGGGATTGAC	GGGTCTGGCT	CGAATCGATT	TTTTTCGTCAC	950
	CAATCAAGGA	GCGATTTATT	TAAACGAAAT	CAACACCATG	CCGGGATTTA	1000
	CTGGGCACTC	CCGCTACCCA	GCTATGATGG	CGGAAGTCGG	GTTATCCTAC	1050
	GAAATATTAG	TAGAGCAATT	GATTGCACTG	GCAGAGGAGG	ACAAACGATG	1100
25	AACACATTAC	AATTGATCAA	TAAAAACCAT	CCATTGAAAA	AAAATCAAGA	1150
	GCCCCCGCAC	TTAGTGCTA				1169

30 2) INFORMATION FOR SEQ ID NO: 1059

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1166 bases
 (B) TYPE: Nucleic acid
 35 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

40 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus gallinarum*
 (B) STRAIN: R631

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1059

45	CAAATTTTCT	TTTCTTTTCC	TAGGTACACT	GAATGTAACC	TTAAAAGAAA	50
	AAAGGAAAGG	AAGAAAATGA	TGAAAAAAT	TGCCGTTTTA	TTTGGAGGGA	100
	ATTCTCCAGA	ATACTCAGTG	TCACTAGCCT	CAGCAGCAAG	TGTGATCCAA	150
	GCTATTGACC	CGCTGAAATA	TGAAGTAATG	ACCATTGGCA	TCGCACCAAC	200
50	AATGGATTGG	TATTGGTATC	AAGGAAACCT	CGCGAATGTT	CGCAATGATA	250
	CTTGGCTAGA	AGATCACAAA	AACTGTCACC	AGCTGACTTT	TTCTAGCCAA	300
	GGATTTATAT	TAGGAGAAAA	ACGAATCGTC	CCTGATGTCC	TCTTTCCAGT	350
	CTTGCATGGG	AAGTATGGCG	AGGATGGCTG	TATCCAAGGA	CTGCTTGAAC	400
	TAATGAACCT	GCCTTATGTT	GGTTGCCATG	TCGCTGCCTC	CGCATTATGT	450
55	ATGAACAAAT	GGCTCTTGCA	TCAACTTGCT	GATACCATGG	GAATCGCTAG	500
	TGCTCCCACT	TTGCTTTTAT	CCCGCTATGA	AAACGATCCT	GCCACAATCG	550
	ATCGTTTTAT	TCAAGACCAT	GGATTCCCGA	TCTTTATCAA	GCCGAATGAA	600
	GCCGGTTCTT	CAAAAGGGAT	CACAAAAGTA	ACTGACAAAA	CAGCGCTCCA	650
	ATCTGCATTA	ACGACTGCTT	TTGCTTACGG	TTCTACTGTG	TTGATCCAAA	700
60	AGGCGATAGC	GGGTATTGAA	ATTGGCTGCG	GCATCTTAGG	AAATGAGCAA	750

	TTGACGATTG	GTGCTTGTGA	TGCGATTTCT	CTTGTCGACG	GTTTTTTTGA	800
	TTTTGAAGAG	AAATACCAAT	TAATCAGCGC	CACGATCACT	GTCCCAGCAC	850
	CATTGCCTCT	CGCGCTTGAA	TCACAGATCA	AGGAGCAGGC	ACAGCTGCTT	900
	TATCGAAACT	TGGGATTGAC	GGGTCTGGCT	CGAATCGATT	TTTTCGTCAC	950
5	CAATCAAGGA	GCGATTTATT	TAAACGAAAT	CAACACCATG	CCGGGATTTA	1000
	CTGGGCACTC	CCGCTACCCA	GCTATGATGG	CGGAAGTCGG	GTTATCCTAC	1050
	GAAATATTAG	TAGAGCAATT	GATTGCACTG	GCAGAGGAGG	ACAAACGATG	1100
	AACACATTAC	AATTGATCAA	TAAAAACCAT	CCATTGAAAA	AAAATCAAGA	1150
	GCCCCCGCAC	TTAGTG				1166

2) INFORMATION FOR SEQ ID NO: 1060

- 15 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1028 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Double
 - (D) TOPOLOGY: Linear
- 20 (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Enterococcus casseliflavus*
 - 25 (B) STRAIN: ATCC 25788

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1060

	AACATGAAAA	AAATCGCCTT	ATTTTTGGAG	GCAATTCACC	GGAATACACC	50
30	GTTTCTTTAG	CTTCAGCAAC	TAGCGCAATC	GAAGCACTCC	AATCATCTCC	100
	CTATGACTAC	GACCTCTCTT	TGATCGGGAT	CGCCCCAGAT	GCTATGGATT	150
	GGTACTTGTA	TACAGGAGAA	CTGGAAAACA	TCCGACAAGA	CACGTGGTTG	200
	TTGGATACGA	AACATAAACA	GAAAATACAG	CCGCTATTTC	AAGGAAACGG	250
	CTTTTGGCTA	AGTGAAGAGC	AGCAAACGTT	GGTACCTGAT	GTTTTATTTC	300
35	CCATTATGCA	TGGCAAATAC	GGGGAAGATG	GCAGTATCCA	AGGATTGTTT	350
	GAATTGATGA	AGCTGCCTTA	TGTAGGCTGC	GGGGTGGCAG	GTTCTGCCTT	400
	ATGTATGAAC	AAATGGCTGC	TGCATCAAGC	TGCAGCAGCC	ATTGGCGTAC	450
	AAAGTGCTCC	TACGATTCTC	TTGACAAATC	AAGCCAACCA	GCAAGAACAA	500
	ATCGAAGCTT	TTATCCAGAC	CCATGGCTTC	CCAGTTTTCT	TTAAGCCTAA	550
40	TGAAGCGGGC	TCCTCAAAAG	GGATCACTAA	AGTCACCTGC	GTTGAAGAAA	600
	TCGCTTCTGC	CTTAAAAGAA	GCCTTTACTT	ATTGTTCCGC	AGTGCTCCTA	650
	CAAAAAAATA	TTGCCGGTGT	TGAGATCGGT	TGCGGTATTT	TGGGCAACGA	700
	CTCTTTGACT	GTCGGTGCTT	GTGACGCCAT	TTCATTAGTA	GACGGCTTTT	750
	TCGATTTTGA	AGAAAAGTAC	CAGCTGATCA	GCGCCAAAAT	CACCGTCCCT	800
45	GCGCCATTGC	CTGAAACGAT	TGAAACCAAG	GTCAAAGAAC	AAGCTCAGCT	850
	GCTCTATCGT	AGTCTTGCTC	TTAAAGGTCT	TGCTCGCATC	GACTTTTTTG	900
	TCACGGAGCG	AGGAGAACTA	TACTTGAATG	AAATCAATAC	TATGCCGGGC	950
	TTTACGAGTC	ACTCCCGCTA	TCCTGCCATG	ATGGCAGCGG	TCGGCTTATC	1000
	CTATCAAGAA	CTACTACAAA	AACTGCTT			1028

2) INFORMATION FOR SEQ ID NO: 1061

- 55 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1030 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Double
 - 60 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus casseliflavus*
 5 (B) STRAIN: R689

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1061

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10 AATATGAAAA AAATCGCCTT ATTTTGGAG GCAATTCACC GGAGTACGCC      50
   GTTCTTTTAG CCTCAGCAAC TAGCGCAATC GAAGCACTCC AATCATCTCC      100
   CGATGACTAT GACCTCTCTT TGATCGGGAT CGCCCCAGAT GCTATGGATT      150
   GGTATTTGTA TACAGGAGAA CTGGAAAACA TCCGACAAGA CACGTGGTTG      200
   TTGGATACGA AACATAAACA GAAAATCCAG CCGCTTTTGT AAGGAAACGG      250
   CTTTTGGCTA AGTGAAGAGC AACAAACGTT GGTTCCTGAT GTTTTATTTT      300
15 CCATTATGCA TGGCAAATAC GGGGAAGATG GCAGTATCCA AGGATTGTTT      350
   GAATTGATGA AACTACCTTA TGTAGGCTGC GGGGTGGCAG CCTCTGCCTT      400
   ATGTATGAAC AAATGGCTGC TGCATCAAGC AGCAGAAGCG ATTGGCGTAC      450
   AAAGTGCTCC TACGATTCTC TTGACAAATC AAGCCAACCA GCAAGATCAA      500
   ATCGAAGCTT TTATCCAGAC CCATGGCTTT CCGGTTTTTT TTAAGCCTAA      550
20 TGAAGCGGGC TCCTCAAAAG GGATCACTAA AGTCACCTGC GTTGAAGAAA      600
   TCGCTTCTGC CTTAAAAGAA GCCTTTACTT ATTGTTCAGC AGTGCTCCTA      650
   CAAAAAATA TTGCCGGTGT TGAGATCGGT TGCGGTATTT TGGGCAACGA      700
   CTCTTTGACT GTCGGTGCTT GTGACGCTAT TTCATTAGTA GACGGCTTTT      750
   TCGATTTTGA AGAAAAGTAC CAGCTGATCA GCGCCAAGAT CACCGTTCCT      800
25 GCACCATTGC CTGAAACGAT TGAAACCAAG GTCAAAGAAC AAGCTCAGCT      850
   GCTCTATCGT AGTCTTTGTC TTAAAGGTCT TGCTCGCATC GACTTTTTTG      900
   TCACGGATCA AGGAGAACTA TACTTGAATG AAATCAATAC TATGCCGGGC      950
   TTTACGAGTC ACTCCCGCTA TCCTGCCATG ATGGCAGCGA TCGGCTTATC     1000
   CTATCAAGAA CTACTACAAA AACTGCTTGT     1030
30

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2) INFORMATION FOR SEQ ID NO: 1062

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1031 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus casseliflavus*
 45 (B) STRAIN: R754

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1062

```

50 AAACATGAAA AAAATCGCCA TTATTTTGG AGGCAATTCA CCGGAATACA      50
   CCGTTTCTTT AGCTTCAGCA ACTAGCGCAA TCGAAGCACT CCAATCATCT      100
   CCCTATGACT ACGACCTCTC TTTGATCGGG ATCGCCCCAG ATGCTATGGA      150
   TTGGTACTTG TATACAGGAG AACTGGAAAA CATCCGACAA GACACGTGGT      200
   TGTTGGATAC GAAACATAAA CAGAAAATAC AGCCGCTATT CGAAGGAAAC      250
   GGCTTTTGGC TAAGTGAAGA GCAGCAAACG TTGGTACCTG ATGTTTTATT      300
55 TCCCATTATG CATGGCAAAT ACGGGGAAGA TGGCAGTATC CAAGGATTGT      350
   TTGAATTGAT GAAGCTGCCT TATGTAGGCT GCGGGGTGGC AGGTTCTGCC      400
   TTATGTATGA ACAAATGGCT GCTGCATCAA GCTGCAGCAG CCATTGGCGT      450
   ACAAAGTGCT CCTACGATTC TCTTGACAAA TCAAGCCAAC CAGCAAGAAC      500
   AAATCGAAGC TTTTATCCAG ACCCATGGCT TCCCAGTTTT CTTTAAGCCT      550
60 AATGAAGCGG GCTCCTCAAA AGGGATCACT AAAGTCACCT GCGTTGAAGA      600

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	AATCGCTTCT	GCCTTAAAAG	AAGCCTTTAC	TTATTGTTCC	GCAGTGCTCC	650
	TACAAAAAAA	TATTGCCGGT	GTTGAGATCG	GTTGCCGTAT	TTTGGGCAAC	700
	GACTCTTTGA	CTGTCGGTGC	TTGTGACGCC	ATTTTCATTAG	TAGACGGCTT	750
	TTTCGATTTT	GAAGAAAAGT	ACCAGCTGAT	CAGCGCCAAA	ATCACCGTCC	800
5	CTGCGCCATT	GCCTGAAACG	ATTGAAACCA	AGGTCAAAGA	ACAAGCTCAG	850
	CTGCTCTATC	GTAGTCTTGG	TCTTAAAGGT	CTTGCTCGCA	TCGACTTTTT	900
	TGTCACGGAG	CGAGGAGAAC	TATACTTGAA	TGAAATCAAT	ACTATGCCGG	950
	GCTTTACGAG	TCACTCCCGC	TATCCTGCCA	TGATGGCAGC	GGTCGGCTTA	1000
10	TCCTATCAAG	AACTACTACA	AAAAGTGTCT	G		1031

2) INFORMATION FOR SEQ ID NO: 1063

- 15 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1030 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Double
 - (D) TOPOLOGY: Linear
- 20 (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Enterococcus casseliflavus*
 - 25 (B) STRAIN: R775

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1063

	AACATGAAAA	AAATCGCCAT	TATTTTTTGA	GGCAATTCAC	CGGAATACAC	50
30	CGTTTCTTTA	GCTTCAGCAA	CTAGCGCAAT	CGAAGCACTC	CAATCATCTC	100
	CCTATGACTA	CGACCTCTCT	TTGATCGGGA	TCGCCCCAGA	TGCTATGGAT	150
	TGGTACTTGT	ATACAGGAGA	ACTGGAAAAC	ATCCGACAAG	ACACGTGGTT	200
	GTTGGATACG	AAACATAAAC	AGAAAATACA	GCCGCTATTT	GAAGGAAACG	250
	GCTTTTGGCT	AAGTGAAGAG	CAGCAAACGT	TAGTACCTGA	TATTTTATTT	300
35	CCCATTATGC	ATGGCAAATA	CGGGGAAGAT	GGCAGTATCC	AAGGATTGTT	350
	TGAATTGATG	AAACTACCTT	ATGTAGGTTG	CGGGGTGGCA	GGTTCTGCCT	400
	TATGTATGAA	CAAATGGCTG	CTGCATCAAG	CTGCAGCAGC	CATTGGCGTA	450
	CAAAGTGCTC	CTACGATTCT	CTTGACAAAT	CAAGCCAACC	AGCAAGAACA	500
	AATCGAAGCT	TTTATCCAGA	CCCATGGCTT	CCCAGTTTTT	TTTAAGCCTA	550
40	ATGAAGCGGG	CTCTTCAAAA	GGGATCACTA	AAGTCACCTG	CGTTGAAGAA	600
	ATCGCTTCTG	CCTTAAAAAA	AGCCTTTACT	TATTGTTCCG	CAGTGCTCCT	650
	ACAAAAAAT	ATTGCCGGTG	TTGAGATCGG	TTGCCGTATT	TTGGGCAACG	700
	ACTCTTTGAC	TGTCGGTGCT	TGTGACGCCA	TTTCATTAGT	AGACGGCTTT	750
	TTCGATTTTG	AAGAAAAGTA	CCAGCTGATC	AGCGCCAAAA	TCACCGTCCC	800
45	TGCGCCATTG	CCTGAAACGA	TTGAAACCAA	GGTCAAAGAA	CAAGCTCAGC	850
	TGCTCTATCG	TAGTCTTGGT	CTTAAAGGTC	TTGCTCGCAT	CGACTTTTTT	900
	GTCACGGATC	AAGGAGAACT	ATACTTGAAT	GAAATCAATA	CTATGCCGGG	950
	CTTTACGAGT	CACTCCCGTT	ATCCTGCCAT	GATGGCAGCG	GTCGGCTTAT	1000
50	CCTATCAAGA	ACTACTACAA	AAACTGCTTG			1030

2) INFORMATION FOR SEQ ID NO: 1064

- 55 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1032 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Double
 - 60 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Enterococcus flavescens*

5 (B) STRAIN: ATCC 49996

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1064

	AAACATGAAA	AAAATCGCCA	TTATTTTGG	AGGCAATTCA	CCGGAATACA	50
10	CCGTTTCTTT	AGCTTCAGCA	ACTAGCGCAA	TCAAGCACT	CCAATCATCT	100
	CCCTATGACT	ACGACCTCTC	TTTGATCGGG	ATCGCCCCAG	ATGCTATGGA	150
	TTGGTACTTG	TATACAGGAG	AACTGGAAAA	CATCCGACAA	GACACGTGGT	200
	TGTTGGATAC	GAAACAGAAA	CAGAAAATAC	AGCCGCTATT	CGAAGGAAAC	250
	GGCTTTTGGT	TAAGTGAAGA	GCAGCAAACG	TTGGTACCTG	ATGTTTATT	300
15	TCCCATTATG	CATGGCAAAT	ACGGGGAAGA	TGGCAGTATC	CAAGGATTGT	350
	TTGAATTGAT	GAAGCTACCT	TATGTAGGCT	GCGGGGTGGC	AGGTTCTGCC	400
	TTATGTATGA	ACAAATGGTT	GCTGCATCAA	GCTGCAGCAG	CCATTGGCGT	450
	ACAAAGTGCT	CCTACGATTC	TCTTGACAAA	TCACGCCAAC	CAGCAAGAAC	500
	AAATCGAAGC	TTTTATCCAG	ACCCATGGCT	TTCCAGTTTT	CTTTAAGCCT	550
20	AATGAAGCGG	GTTCTCAAA	AGGGATCACT	AAAGTCACCT	GCGTTGAAGA	600
	AATCGCTTCT	GCCTTAAAAG	AAGCCTTTAC	TTATTGTTCC	GCAGTGCTCC	650
	TACAAAAAAA	TATTGCCGGT	GTTGAGATCG	GTTGCGGTAT	TTTGGGCAAC	700
	GACTCTTTGA	CTGTCGGTGC	TTGTGACGCC	ATTTCATTAG	TAGACGGCTT	750
	TTTCGATTTT	GAAGAAAAGT	ACCAGCTGAT	CAGCGCCAAA	ATCACCGTCC	800
25	CTGCGCCATT	GCCTGAAACG	ATTGAAACTA	AGGTCAAAGA	ACAAGCTCAG	850
	CTGCTCTATC	GTAGTCTTGG	ACTTAAAGGT	CTTGCTCGCA	TCGACTTTTT	900
	TGTCACGGAT	CAAGGAGAAC	TATACTTGAA	TGAAATCAAT	ACTATGCCGG	950
	GCTTTACGAG	TCACTCCCGC	TATCCTGCCA	TGATGGCAGC	GGTCGGGTTA	1000
30	TCCTATCAAG	AACTACTACA	AAAATACTT	GT		1032

2) INFORMATION FOR SEQ ID NO: 1065

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1034 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

40

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Enterococcus flavescens*

45 (B) STRAIN: R758

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1065

	AAAAACATGA	AAAAAATCGC	CATTATTTTT	GGAGGCAATT	CACCGGAATA	50
50	CACCGTTTCT	TTAGCTTCAG	CAACTAGCGC	AATCGAAGCA	CTCCAATCAT	100
	CTCCCTATGA	CTACGACCTC	TCTTTGATCG	GGATCGCCCC	AGATGCTATG	150
	GATTGGTACT	TGTATACAGG	AGAAGTGGAA	AACATCCGAC	AAGACACGTG	200
	GTTGTTGGAT	ACGAAACATA	AACAGAAAAT	ACAGCCGCTA	TTCGAAGGAA	250
	ACGGCTTTTG	GCTAAGTGAA	GAGCAGCAAA	CGTTGGTACC	TGATGTTTTA	300
55	TTTCCCATTA	TGCATGGCAA	ATACGGGGAA	GATGGCAGTA	TCCAAGGATT	350
	GTTTGAATTG	ATGAAGCTGC	CTTATGTAGG	CTGCGGGGTG	GCAAGTTCTG	400
	CCTTATGTAT	GAACAAATGG	CTGCTGCATC	AAGCTGCAGC	AGCCATTGGC	450
	GTACAAAGTG	CTCCTACGAT	TCTCTTGACA	AATCAAGCCA	ACCAGCAAGA	500
	ACAAATCGAA	GCTTTTATCC	AGACCCATGG	CTTTCCAGTT	TTCTTTAAGC	550
60	CTAATGAAGC	GGGCTCCTCA	AAAGGGATCA	CTAAAGTCAC	CTGCGTTGAA	600

GAAATCGCTT CTGCCTTAAA AGAAGCCTTT ACTTATTGTT CCGCAGTGCT 650
 CCTACAAAAA AATATTGCCG GTGTTGAGAT CGGTTGCGGT ATTTTGGGCA 700
 ACGACTCTTT GACTGTCCGT GCTTGTGACG CCATTTTCATT AGTAGACGGC 750
 TTTTTCGATT TTGAAGAAAA GTACCAGCTG ATCAGCGCCA AAATCACCGT 800
 5 CCCTGCGCCA TTGCCTGAAA CGATTGAAAC CAAGGTCAAA GAACAAGCTC 850
 AGCTGCTCTA TCGTAGTCTT GGTCTTAAAG GTCTTGCTCG CATCGACTTT 900
 TTTGTCACGG ATCAAGGAGA ACTATACTTG AATGAAATCA ATACTATGCC 950
 GGGCTTTACG AGTCACTCCC GCTATCCTGC CATGATGGCA GCGGTCGGCT 1000
 TATCCTATCA AGAACTACTA CAAAAACTGC TTGT 1034
 10

2) INFORMATION FOR SEQ ID NO: 1066

- 15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1012 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
 20
 (ii) MOLECULE TYPE: Genomic DNA
 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Enterococcus flavescens*
 25 (B) STRAIN: R760

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1066

CATGAAAAAA ATCGCCATTA TTTTGGAGG CAATTCACCG GAATACACCG 50
 30 TTTCTTTAGC CTCAGCAACT AGCGCAATCG AAGCACTCCA ATCATCTCCC 100
 TATGATTACG ACCTCTCTTT GATCGGGATC GCCCCAGATG CTATGGATTG 150
 GTAATTGTAT ACAGGAGAAC TGGAAAACAT CCGACAAGAC ACGTGGTTGT 200
 TGGATACGAA ACATACACAG AAAATCCAGC CACTTTTGA AGGAAACGGC 250
 TTTTGGATAA GTGAAGCGCA GCAAACGTTG GTACCTGATG TTTTATTTCC 300
 35 CATTATGCAT GGTAAATACG GGGAAAGATGG CAGTATCCAA GGATTGTTTG 350
 AATTGATGAA GCTGCCTTAT GTAGGCTGTG GGGTGGCAGC CTCTGCCTTA 400
 TGTATGAACA AATGGTTATT GCATCAAGCA GCAGCAGCGA TTGGCGTACA 450
 AAGCGTCCTT ACGATTCTCT TGACAAATCA AGCCAACCAG CAAAGACAAA 500
 TCGAAGCCTT TATCCAGACC CATGGCTTTC CAGTTTTCTT TAAGCCTAAT 550
 40 GAAGCGGGCT CCTCAAAAGG GATCACAAAA GTAACCTGTG TTGAAGAAAT 600
 CGCTCCTGCC TTGAAGGAAG CCTTCGCTTA TTGTTCGCA GTGCTCTTAC 650
 AAAAAAATAT CGCTGGCGTT GAGATTGGTT GCGGTATCTT AGGCAACGAC 700
 TCTTTGACTG TCGGTGCTTG TGACGCTATT TCATTAGTAG ACGGCTTTTT 750
 CGATTTTGAA GAAAAGTACC AGTTGATCAG CGCCAAAATC ACCGTTCTCTG 800
 45 CGCCATTGCC TGAAACGATT GAAACCAAAG TCAAAGAACA AGCTCAGCTG 850
 CTCTATCACA GTCTTGGTCT TAAAGGACTT GCTCGCATCG ACTTTTTTGT 900
 CACGGATCAA GGAGAACTAT ACTTGAATGA AATCAATACT ATGCCGGGCT 950
 TTACGAGTCA CTCCCGCTAT CCTGCCATGA TGGCAGCGGT CGGCTTATCC 1000
 TATCAAGAAT TA 1012
 50

2) INFORMATION FOR SEQ ID NO: 1067

- 55 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 721 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
 60

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 5 (A) ORGANISM: *Enterococcus faecium*
(B) STRAIN: R481

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1067

```
10 CTTACGCTTT ATCGATTAGA CACGGGNAGC TTGTCCAATG GGRAGCCGAT 50
   TTGATTTTAT GGATGAACGC TCTCATCATG CGGCAAATGG AATATCATGC 100
   AATGAAGCGC AAAATCGCAG ACGTTTGCGC TCCATCATGG AAAACAGTGG 150
   GTTTGAAGCA TATAGCCTCG AATGGTGGCA CTATGTATTA AGAGACGAAC 200
   CATACCCCAA TAGCTATTTT GATTTCCCCG TTAAATAAAC TTTTAACCGT 250
   TGCACGGACA AACTATATAA GCTAACTCTT TCGGCAGGAA ACCCGACGTA 300
   15 TGTAAGTGGT TCTTAGGGAA TTTATATATA GTAGATAGTA TTGAAGATGT 350
   AAGGCAGAGC GATATTGCGG TCATTATCTG CGTGCCTGCT GCAGAGATAG 400
   CCTGATAATA AGACTGATCG CATAGAGGGG TGGTATTTCA CACCGCCCAT 450
   TGTCAACAGG CAGTTCAGCC TCGTTAAATT CAGCATGGGT ATCACTTATG 500
   AAAATTCATC TACATTGGTG ATAATAGTAA ATCCAGTAGG GCGAAATAAT 550
   20 TGAAGTGAAT TTACGGGGCA AAACGGCACA ATCTCAAACG AGATTGTGCC 600
   GTTTAAGGGG AAGATTCTAG AAATATTTCA TACTTCCAAC TATATAGTTA 650
   AGGAGGAGAC TGAAAATGAA GAAGTTGTTT TTTTATTGTT TATTGTTATT 700
   CTTAATATAC TTAGGTTATT G 721
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25

2) INFORMATION FOR SEQ ID NO: 1068

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 668 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

35 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 40 (A) ORGANISM: *Enterococcus faecium*
(B) STRAIN: R492

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1068

```
45 ATTTTTAAGG ATGAACGCTC TTCATCATGC GGCAAATGGA ATATCATGCA 50
   ATGAAGCGCA AAATCGCAGA CGTTTGCGCT CCATCATGGA AAACAGTGGG 100
   TTTGAAGCAT ATAGCCTCGA ATGGTGGCAC TATGTATTAA GAGACGAACC 150
   ATACCCCAAT AGCTATTTTG ATTTCCCCGT TAAATAAACT TTTAACCGTT 200
   GCACGGACAA ACTATATAAG CTAACCTCTT CCGCAGGAAA CCCGACGTAT 250
   GTAAGTGGTT CTTAGGGAAT TTATATATAG TAGATAGTAT TGAAGATGTA 300
   AGGCAGAGCG ATATTGCGGT CATTATCTGC GTGCGCTGCG GCAAGATAGC 350
   50 CTGATAATAA GACTGATCGC ATAGAGGGGT GGTATTTTCA ACCGCCCAT 400
   GTCAACAGGC AGTTCAGCCT CGTTAAATTC AGCATGGGTA TCACTTATGA 450
   AAATTCATCT ACATTGGTGA TAATAGTAAA TCCAGTAGGG CGAAATAATT 500
   GACTGTAATT TACGGGGCAA AACGGCACAA TCTCAAACGA GATTGTGCCG 550
   TTTAAGGGGA AGATTCTAG AATATTTTCA ACTTCCAAC TATATAGTTA 600
   55 GGAGGAGACT GAAAATGAAG AAGTTGTTT TTTTATTGTT ATTGTTATTC 650
   TTAATATACT TAGGTTAT 668
```

60 2) INFORMATION FOR SEQ ID NO: 1069

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 760 bases
 (B) TYPE: Nucleic acid
 5 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

- 10 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Enterococcus faecium*
 (B) STRAIN: R581

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1069

```

15 CGGCAAGTGC CATTGATCTT ACGCTTTATC GATTAGACAC GGGTRAGCTT      50
   GTACCAATGG GAAGCCGATT TGATTTTATG GATGAACGCT CTCATCATGC      100
   GGCAAATGGA ATATCATGCA ATGAAGCGCA AAATCGCAGA CGTTTGCGCT      150
   CCATCATGGA AAACAGTGGG TTTGAAGCAT ATAGCCTCGA ATGGTGGCAC      200
20 TATGTATTAA GAGACGAACC ATACCCCAAT AGCTATTTTG ATTTCCCCGT      250
   TAAATAAACT TTAAACCGTT GCACGGACAA ACTATATAAG CTAACTCTTT      300
   CGGCAGGAAA CCCGACGTAT GTAACGGTGT CTTAGGGAAT TTATATATAG      350
   TAGATAGTAT TGAAGATGTA AGGCAGAGCG ATATTGCGGT CATTATCTGC      400
   GTGCGCTGCG GCAAGATAGC CTGATAATAA GACTGATCGC ATAGAGGGGT      450
25 GGTATTTTAC ACCGCCCATT GTCAACAGGC AGTTCAGCCT CGTTAAATTC      500
   AGCATGGGTA TCACTTATGA AAATTCATCT ACATTGGTGA TAATAGTAAA      550
   TCCAGTAGGG CGAAATAATT GACTGTAATT TACGGGGCAA AACGGCACAA      600
   TCTCAAACGA GATTGTGCCG TTAAAGGGGA AGATTCTAGA AATATTTTCAT      650
   ACTTCCAACT ATATAGTTAA GGAGGAGACT GAAAATGAAG AAGTTGTTTT      700
30 TTTTATTGTT ATTGTTATTC TTAATATACT TAGGTTATGA CTACGTTAAT      750
   GAAANCCTGA                                     760

```

35 2) INFORMATION FOR SEQ ID NO: 1070

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 801 bases
 (B) TYPE: Nucleic acid
 40 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

- 45 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Enterococcus faecalis*
 (B) STRAIN: R610

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1070

```

50 AAAAGGAATA CGGGGCTTTC AAAAATCCAA GCCATAACCC GCGGGCAAGT      50
   GCCATTTGAT TCTTACGCTT TAATCGATTA GACACGGGTA AGCTTGATACC      100
   AATGGGGAAC CGATTTGATT TTAATGNATG AACGCTCTTC ATCATGCGGC      150
   AAATGGAATA TCATGCAATG AAGCGCAAAA TCGCAGACGT TTGCGCTCCA      200
55 TCATGGAAAA CAGTGGGTTT GAAGCATATA GCCTCGAATG GTGGCACTAT      250
   GTATTAAGAG ACGAACCATA CCCCAATAGC TATTTTGATT TCCCCGTAA      300
   ATAACTTTT AACCGTTGCA CGGACAAACT ATATAAGCTA ACTCTTTCGG      350
   CAGGAAACCC GACGTATGTA ACTGGTTCCT AGGGAATTTA TATATAGTAG      400
   ATAGTATTGA AGATGTAAGG CAGAGCGATA TTGCGGTCAT TATCTGCGTG      450
60 CGCTGCGGCA AGATAGCCTG ATAATAAGAC TGATCGCATA GAGGGGTGGT      500

```

ATTTACACACC GCCCATTGTC AACAGGCAGT TCAGCCTCGT TAAATTCAGC 550
 ATGGGTATCA CTTATGAAAA TTCATCTACA TTGGTGATAA TAGTAAATCC 600
 AGTAGGGCGA AATAATTGAC TGTAATTTAC GGGGCAAAAC GGCACAATCT 650
 CAAACGAGAT TGTGCCGTTT AAGGGGAAGA TTCTAGAAAT ATTTCACTACT 700
 5 TCCAACATA TAGTTAAGGA GGAGACTGAA AATGAAGAAG TTGTTTTTTT 750
 TTATTGTTAT TGTTATTCTT AATATACTTA GGTTATGACT ACGTTAATGA 800
 A 801

10

2) INFORMATION FOR -SEQ ID NO: 1071

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 711 bases
 15 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

20

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus gallinarum*
 (B) STRAIN: R684

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1071

TTGTACCAAT GGGGAGCCGA TTTGATTTTA TGGATGAACG CTCTCATCAT 50
 GCGGCAAATG GAATATCATG CAATGAAGCG CAAAATCGCA GACGTTTGCG 100
 CTCCATCATG GAAAACAGTG GGTTTGAAGC ATATAGCCTC GAATGGTGGC 150
 30 ACTATGTATT AAGAGACGAA CCATACCCCA ATAGCTATTT TGATTTCCCC 200
 GTTAAATAAA CTTTTAACCG TTGCACGGAC AAACATATA AGCTAACTCT 250
 TTCGGCAGGA AACCCGACGT ATGTAAGTGG TTCTTAGGGA ATTTATATAT 300
 AGTAGATAGT ATTGAAGATG TAAGGCAGAG CGATATTGCG GTCATTATCT 350
 GCGTGCGCTG CGGCAAGATA GCCTGATAAT AAGACTGATC GCATAGAGGG 400
 35 GTGGTATTTT ACACCGCCCA TTGTCAACAG GCAGTTCAGC CTCGTTAAAT 450
 TCAGCATGGG TATCACTTAT GAAAATTCAT CTACATTGGT GATAATAGTA 500
 AATCCAGTAG GCGGAAATAA TTGACTGTAA TTTACGGGGC AAAACGGCAC 550
 AATCTCAAAC GAGATTGTGC CGTTTAAGGG GAAGATTCTA GAAATATTTT 600
 ATACTTCCAA CTATATAGTT AAGGAGGAGA CTGAAAATGA AGAAGTTGTT 650
 40 TTTTTTATTG TTATTGTTAT TCTTAATATA CTTAGGTTAT GACTACGTTA 700
 ATGAAGCACT G 711

45 2) INFORMATION FOR SEQ ID NO: 1072

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 751 bases
 (B) TYPE: Nucleic acid
 50 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

55 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus faecium*
 (B) STRAIN: R688

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1072

60

	GCCATTGATC	TTACGCTTTA	TCGATTAGAC	ACGGGTNAGC	TTGTACCAAT	50
	GGGGAGCCGA	TTTGATTTTA	TGGATGAACG	CTCTCATCAT	GCGGCAAATG	100
	GAATATCATG	CAATGAAGCG	CAAAATCGCA	GACGTTTGCG	CTCCATCATG	150
	GAAAACAGTG	GGTTTGAAGC	ATATAGCCTC	GAATGGTGGC	ACTATGTATT	200
5	AAGAGACGAA	CCATACCCCA	ATAGCTATTT	TGATTTCCCC	GTTAAATAAA	250
	CTTTTAACCG	TTGCACGGAC	AAACTATATA	AGCTAACTCT	TTCGGCAGGA	300
	AACCCGACGT	ATGTAAGTGG	TTCTTAGGGA	ATTTATATAT	AGTAGATAGT	350
	ATTGAAGATG	TAAGGCAGAG	CGATATTGCG	GTCATTATCT	GCGTGCGCTG	400
	CGGCAAGATA	GCCTGATAAT	AAGACTGATC	GCATAGAGGG	GTGGTATTTC	450
10	ACACCGCCCA	TTGTCAACAG	GCAGTTCAGC	CTCGTTAAAT	TCAGCATGGG	500
	TATCACTTAT	GAAAATTCAT	CTACATTGGT	GATAATAGTA	AATCCAGTAG	550
	GGCGAAATAA	TTGACTGTAA	TTTACGGGGC	AAAACGGCAC	AATCTCAAAC	600
	GAGATTGTGC	CGTTTAAGGG	GAAGATTCTA	GAAATATTTT	ATACTTCCAA	650
	CTATATAGTT	AAGGAGGAGA	CTGAAAATGA	AGAAGTTGTT	TTTTTTATTG	700
15	TTATTGTTAT	TCTTAATATA	CTTAGGTTAT	GACTACGTTA	ATGAAGCACT	750
	G					751

20 2) INFORMATION FOR SEQ ID NO: 1073

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 685 bases
 (B) TYPE: Nucleic acid
 25 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

30 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus flavescens*
 (B) STRAIN: R689

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1073

35	ATTTGATTTT	ATGGATGAAC	GCTCTCATCA	TGCGGCAAAT	GGAATATCAT	50
	GCAATGAAGC	GCAAAATCGC	AGACGTTTGC	GCTCCATCAT	GGAAAACAGT	100
	GGGTTTGAAG	CATATAGCCT	CGAATGGTGG	CACTATGTAT	TAAGAGACGA	150
	ACCATACCCC	AATAGCTATT	TTGATTTCCC	CGTTAAATAA	ACTTTTAACC	200
40	GTTGCACGGA	CAAACTATAT	AAGCTAATC	TTTCGGCAGG	AAACCCGACG	250
	TATGTAAGTG	GTTCCTTAGG	AATTTATATA	TAGTAGATAG	TATTGAAGAT	300
	GTAAGGCAGA	GCGATATTGC	GGTCATTATC	TGCGTGCGCT	GCGGCAAGAT	350
	AGCCTGATAA	TAAGACTGAT	CGCATAGAGG	GGTGGTATTT	CACACCGCCC	400
	ATTGTCAACA	GGCAGTTCAG	CCTCGTTAAA	TTCAGCATGG	GTATCACTTA	450
45	TGAAAATTCA	TCTACATTGG	TGATAATAGT	AAATCCAGTA	GGGCGAAATA	500
	ATTGACTGTA	ATTTACGGGG	CAAAACGGCA	CAATCTCAAA	CGAGATTGTG	550
	CCGTTTAAGG	GGAAGATTCT	AGAAATATTT	CATACTTCCA	ACTATATAGT	600
	TAAGGAGGAG	ACTGAAAATG	AAGAAGTTGT	TTTTTTTATT	GTTATTGTTA	650
50	TTCTTAATAT	ACTTAGGTTA	TGACTACGTT	AATGA		685

2) INFORMATION FOR SEQ ID NO: 1074

55 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 732 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 60 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 5 (A) ORGANISM: *Enterococcus faecium*
(B) STRAIN: R690

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1074

```

10 ATCGATTAGA CACGGGTGAG CTTGTACCAA TGGGGAGCCG ATTTGATTTT      50
   ATGGATGAAC GCTCTCATCA TCGGCGAAAT GGAATATCAT GCAATGAAGC      100
   GCAAAATCGC AGACGTTTGC GCTCCATCAT GGAAAACAGT GGGTTTGAAG      150
   CATATAGCCT CGAATGGTGG CACTATGTAT TAAGAGACGA ACCATACCCC      200
   AATAGCTATT TTGATTTCCC CGTTAAATAA ACTTTTAACC GTTGCACGGA      250
   CAAACTATAT AAGCTAACTC TTTCGGCAGG AAACCCGACG TATGTAAGTG      300
15 GTTCTTAGGG AATTTATATA TAGTAGATAG TATTGAAGAT GTAAGGCAGA      350
   GCGATATTGC GGTCATTATC TCGGTGCGCT GCGGCAAGAT AGCCTGATAA      400
   TAAGACTGAT CGCATAGAGG GGTGGTATTT CACACCGCCC ATTGTCAACA      450
   GGCAGTTCAG CCTCGTTAAA TTCAGCATGG GTATCACTTA TGAAAATTCA      500
   TCTACATTGG TGATAATAGT AAATCCAGTA GGGCGAAATA ATTGACTGTA      550
20 ATTTACGGGG CAAAACGGCA CAATCTCAAA CGAGATTGTG CCGTTTAAGG      600
   GGAAGATTCT AGAAATATTT CATACTTCCA ACTATATAGT TAAGGAGGAG      650
   ACTGAAAATG AAGAAGTTGT TTTTTTTATT GTTATTGTTA TTCTTAATAT      700
   ACTTAGGTTA TGAAGTACGTT AATGAAGCAC TG                          732

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25

2) INFORMATION FOR SEQ ID NO: 1075

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 670 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

35 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 40 (A) ORGANISM: *Enterococcus gallinarum*
(B) STRAIN: R691

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1075

```

45 TCTCATCATG CGGCAAATGG AATATCATGC AATGAAGCGC AAAATCGCAG      50
   ACGTTTGCGC TCCATCATGG AAAACAGTGG GTTTGAAGCA TATAGCCTCG      100
   AATGGTGGCA CTATGTATTA AGAGACGAAC CATACCCCAA TAGCTATTTT      150
   GATTTCCCCG TTAAATAAAC TTTTAACCGT TGCACGGACA AACTATATAA      200
   GCTAACTCTT TCGGCAGGAA ACCCGACGTA TGTAAGTGGT TCTTAGGGAA      250
   TTTATATATA GTAGATAGTA TTGAAGATGT AAGGCAGAGC GATATTGCGG      300
   TCATTATCTG CGTGCCTGCT GCAAGATAG CCTGATAATA AGACTGATCG      350
50 CATAGAGGGG TGGTATTTCA CACCGCCCAT TGTCAACAGG CAGTTCAGCC      400
   TCGTTAAATT CAGCATGGGT ATCACTTATG AAAATTCATC TACATTGGTG      450
   ATAATAGTAA ATCCAGTAGG GCGAAATAAT TGAAGTGAAT TTACGGGGCA      500
   AAACGGCACA ATCTCAAACG AGATTGTGCC GTTTAAGGGG AAGATTCTAG      550
   AAATATTTCA TACTTCCAAC TATATAGTTA AGGAGGAGAC TGAAAATGAA      600
55 GAAGTTGTTT TTTTATTGT TATTGTTATT CTTAATATAC TTAGGTTATG      650
   ACTACGTAA TGAAGCACTG                          670

```

60 2) INFORMATION FOR SEQ ID NO: 1076

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 948 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Escherichia coli*
 (B) STRAIN: DG131/3 serotype OX3:H8
 (C) ACCESSION NUMBER: Z36901
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1076

	ATGAAAATAA	TAATTTTTAG	AGTGCTAACT	TTTTTCTTTG	TTATCTTTTC	50
	TGTTAATGTG	GTTGCGAAGG	AATTTACCTT	AGATTTCTCG	ACAGCAAAGA	100
	CGTATGTAGA	TTCGCTGAAT	GTCATTCGCT	CTGCAATAGG	TACTCCATTA	150
20	CAGACTATTT	CATCAGGAGG	TACGTCCTTA	CTGATGATTG	ATAGTGGCAC	200
	AGGGGATAAT	TTGTTTGCAG	TTGATGTCAG	AGGGATAGAT	CCAGAGGAAG	250
	GGCGGTTTAA	TAATCTACGG	CTTATTGTTG	AACGAAATAA	TTTATATGTG	300
	ACAGGATTTG	TTAACAGGAC	AAATAATGTT	TTTTATCGCT	TTGCTGATTT	350
	TTCACATGTT	ACCTTTCCTG	GTACAACTGC	GGTTACATTG	TCTGGTGACA	400
25	GTAGCTATAC	CACGTTACAG	CGTGTTGCGG	GGATCAGTCG	TACGGGGATG	450
	CAGATAAATC	GCCATTCGTT	GACTACTTCT	TATCTGGATT	TAATGTCGCA	500
	TAGCGGAACC	TCACTGACGC	AGTCTGTGGC	AAGAGCGATG	TTACGGTTTG	550
	TTACTGTGAC	AGCTGAAGCT	TTACGTTTTT	GGCAAATTCA	GAGGGGATTT	600
	CGTACAACAC	TTGATGATCT	CAGTGGGCGT	TCTTATGTAA	TGACTGCTGA	650
30	AGATGTTGAT	CTTACGTTGA	ACTGGGGAAG	GTTGAGTAGT	GTCCTGCCTG	700
	ACTATCATGG	ACAAGACTCT	GTTTCGTGTT	GAAGAATTTT	TTTTGGAAGT	750
	GTTAATGCAA	TTCTGGGTAG	CGTGGCATT	ATACTGAATT	GTCATCATCA	800
	TGCATCGCGA	GTTGCCAGAA	TTGTACCTAA	TGAGTTTCCT	TCTATGTGCC	850
	CGGTAGATGG	AAGAGTGCGT	GGGATTACGC	ACAATAAAAT	ATTGTGGGAC	900
35	TCATCCACTC	TGGGGGCAAT	TTTGATACGC	AGGGCTATTA	GCAGTTGA	948

2) INFORMATION FOR SEQ ID NO: 1077

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1259 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Escherichia coli*
 (B) STRAIN: 94C serotype O48:H21
 (C) ACCESSION NUMBER: extracted from Z37725

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1077

55	CACCTGTATA	TGAAGTGTAT	ATTATTTAAA	TGGGTACTGT	GCCTGTTACT	50
	GGGTTTTTCT	TCGGTATCCT	ATTCCCGGGA	GTTTACGATA	GACTTTTCGA	100
	CCCAACAAAG	TTATGTCTCT	TCGTTAAATA	GTATACGGAC	AGAGATATCG	150
	ACCCCTCTTG	AACATATATC	TCAGGGGACC	ACATCGGTGT	CTGTTATTAA	200
60	CCACACCCCA	CCGGGCAGTT	ATTTTGCTGT	GGATATACGA	GGGCTTGATG	250

	TCTATCAGGC	GCGTTTTGAC	CATCTTCGGC	TGATTATTGA	GCAAAAATAAT	300
	TTATATGTGG	CCGGGTTCGT	TAATACGGCA	ACAAATACTT	TCTACCGTTT	350
	TTCAGATTTT	ACACATATAT	CAGTGCCCCG	TGTGACAACG	GTTTCCATGA	400
	CAACGGACAG	CAGTTATACC	ACTCTGCAAC	GTGTGCGAGC	GCTGGAACGT	450
5	TCCGGAATGC	AAATCAGTCG	TCACTCACTG	GTTTCATCAT	ATCTGGCGTT	500
	AATGGAGTTC	AGTGGTAATA	CAATGACCAG	AGATGCATCC	AGAGCAGTTC	550
	TGCGTTTTGT	CACTGTCACA	GCAGAAGCCT	TACGCTTCAG	GCAGATACAG	600
	AGAGAATTTT	GTCAGGCACT	GTCTGAAACT	GCTCCTGTGT	ATACCATGAC	650
	GCCGGGAGAC	GTGGACCTCA	CTCTGAACTG	GGGGCGAATC	AGCAATGTGC	700
10	TTCCGGAGTA	TCGGGGAGAG	GATGGTGTCA	GAGTGGGGAG	AATATCCTTT	750
	AATAATATAT	CAGCGATACT	GGGTACTGTG	GCCGTTATAC	TGAATTGCCA	800
	TCATCAGGGG	GCGCGTTCTG	TTCGCGCCGT	GAATGAAGAG	AGTCAACCAG	850
	AATGTCAGAT	AACTGGCGAC	AGGCCCGTTA	TAAAAATAAA	CAATACATTA	900
	TGGGAAAGTA	ATACAGCTGC	AGCGTTTCTG	AACAGAAAGT	CACAGTTTTT	950
15	ATATACAACG	GGTAAATAAA	GGAGTTAAGT	ATGAAGAAGA	TGTTTATGGC	1000
	GGTTTTATTT	GCATTAGTTT	CTGTTAATGC	AATGGCGGCG	GATTGTGCTA	1050
	AAGGTAAAAT	TGAGTTTTCC	AAGTATAATG	AGGATGACAC	ATTTACAGTG	1100
	AAGGTTGACG	GGAAAGAATA	CTGGACCACT	CGCTGGAATC	TGCAACCGTT	1150
	ACTGCAAAGT	GCTCAGCTGA	CAGGAATGAC	TGTCACAATC	AAATCCAGTA	1200
20	CCTGTGAATC	AGGCTCCGGA	TTTGCTGAAG	TGCAGTTTAA	TAATGACTGA	1250
	GGCATAACC					1259

25 2) INFORMATION FOR SEQ ID NO: 1078

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
 (B) TYPE: Nucleic acid
 30 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1078

AGTTCTGCGT TTTGTCACTG TC

22

40

2) INFORMATION FOR SEQ ID NO: 1079

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 bases
 45 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1079

CGGAAGCACA TTGCTGATT

19

55

2) INFORMATION FOR SEQ ID NO: 1080

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 bases
 60

(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

5 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1080

10 TATAGCTACT GTCACCAGAC AATGT

25

2) INFORMATION FOR SEQ ID NO: 1081

15 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1081

25 ATGTCAGAGG GATAGATCCA

20

2) INFORMATION FOR SEQ ID NO: 1082

30

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1082

40

TTGARCRAAA TAATTTATAT GTG

23

45 2) INFORMATION FOR SEQ ID NO: 1083

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: DNA

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1083

TGATGATGRC AATTCAGTAT

20

60

2) INFORMATION FOR SEQ ID NO: 1084

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 39 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1084

CCACGCCGCT TTGCTGATTT TTCACATGTT ACCGCGTGG

39

15

2) INFORMATION FOR SEQ ID NO: 1085

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 34 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1085

CCACGCCACT GTCTGAAACT GCTCCTGTGC GTGG

34

30

2) INFORMATION FOR SEQ ID NO: 1086

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

40

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1086

45 CTACTCCCGC CTTTGGGTT

20

2) INFORMATION FOR SEQ ID NO: 1087

50

(i) SEQUENCE CHARACTERISTICS:

- 55 (A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1087

60

5 2) INFORMATION FOR SEQ ID NO: 1088

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- 10 (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1088

TGCCGTTTCC TGTATCCGTC

20

20

2) INFORMATION FOR SEQ ID NO: 1089

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- 25 (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1089

ATCCACACGG GCTAGACCTC

20

35

2) INFORMATION FOR SEQ ID NO: 1090

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 21 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1090

AATAGCGCGG ACGAATTGGA C

21

50

2) INFORMATION FOR SEQ ID NO: 1091

(i) SEQUENCE CHARACTERISTICS:

- 55 (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

60

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1091

5 AACGCGGCAC TGTTTCCCAA

20

2) INFORMATION FOR SEQ ID NO: 1092

10

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

15 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1092

20

TCGGCAAGAC AATATGACAG C

21

25 2) INFORMATION FOR SEQ ID NO: 1093

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 381 bases

(B) TYPE: Nucleic acid

30 (C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

35 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Staphylococcus saprophyticus*

(B) STRAIN: CSsa-165

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1093

40

TAACGGGCGT	CTCGATAGAA	AAACACGTGA	AAATCCCAAT	GATTATAAAC	50
AATCAATATA	CGATTTTGCT	GAAGCTGTAA	CAAAAGGTAT	TAAGGAACAA	100
ACAAATAAAA	ATTAATAGGC	AACTTAACCA	GAATCGTTAA	AACTATATGA	150
CGATTCTGGT	TTTTTAAATT	CAAAAAGTTT	TCTAAAAAAT	TTACCTGCTT	200
45 TTTTAAAGTA	TAGGTATAAA	ATACAATTGA	TTAAAATAGT	AAAGGAAATG	250
AATCATGAAA	CAATTAACCTA	AGCCTTTTATA	CTTTTACCTA	TTACTTTTTA	300
TTACAACAAC	ACTGATTGGC	GCGTTACTAT	TATATTTGCC	AATCACAGGT	350
AAACATCCTA	TTGATTTTGT	GGACGCCCGT	T		381

50

2) INFORMATION FOR SEQ ID NO: 1094

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

60 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1094

GGTAAAACAG GTACTTCTAA CTA

23

5

2) INFORMATION FOR SEQ ID NO: 1095

10 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

15

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1095

20 CGATAGAAGC AGCAGGACAA

20

2) INFORMATION FOR SEQ ID NO: 1096

25

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 bases

(B) TYPE: Nucleic acid

30 (C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1096

CTGATGGATG CGGAAGATAC

20

40

2) INFORMATION FOR SEQ ID NO: 1097

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 26 bases

45 (B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1097

TCYTCAAAAG GGATCACWAA AGTMAC

26

55

2) INFORMATION FOR SEQ ID NO: 1098

(i) SEQUENCE CHARACTERISTICS:

60 (A) LENGTH: 23 bases

- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

5 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1098

10 TCTTCAAAT CGAAAAGCC GTC 23

2) INFORMATION FOR SEQ ID NO: 1099

- 15 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 23 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

20 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1099

25 TCAAAAGGGA TCACWAAAGT MAC 23

2) INFORMATION FOR SEQ ID NO: 1100

- 30 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 26 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

35 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1100

40 GTAAAKCCCG GCATRGTRTT GATTTC 26

2) INFORMATION FOR SEQ ID NO: 1101

- 45 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 23 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - 50 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1101

55 GACGGYTTTT TYGATTTTGA AGA 23

60 2) INFORMATION FOR SEQ ID NO: 1102

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 bases
(B) TYPE: Nucleic acid
5 (C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1102

AAAAARTCGA TKCGAGCMAG ACC

23

15

2) INFORMATION FOR SEQ ID NO: 1103

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 bases
20 (B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1103

ATCCCGCTAT GAAAACGATC

20

30

2) INFORMATION FOR SEQ ID NO: 1104

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 bases
35 (B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

40 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1104

GGATCAACAC AGTAGAACCG

20

45

2) INFORMATION FOR SEQ ID NO: 1105

- 50 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
55 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1105

50 CTCCTACGAT TCTCTTGAYA AATCA

25

2) INFORMATION FOR SEQ ID NO: 1106

5

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

10

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1106

15

CAACCGATCT CAACACCGGC AAT

23

20 2) INFORMATION FOR SEQ ID NO: 1107

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

25

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1107

30

CTCATTTGAC TTCCTCCTTT GCT

23

35 2) INFORMATION FOR SEQ ID NO: 1108

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

40

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1108

45

GTAAGAATCG GAAAAGCGGA AGG

23

50

2) INFORMATION FOR SEQ ID NO: 1109

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

55

(ii) MOLECULE TYPE: DNA

60

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1109

ACATCGTGAT CGCTAAAAGG AGC

23

5

2) INFORMATION FOR SEQ ID NO: 1110

10 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

15

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1110

20 ACGAGAAAGA CAACAGGAAG ACC

23

2) INFORMATION FOR SEQ ID NO: 1111

25

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 25 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

30

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1111

35

CTTTTCCGG CTCGWYTTCC TGATG

25

40 2) INFORMATION FOR SEQ ID NO: 1112

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 bases

(B) TYPE: Nucleic acid

15

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1112

GGCTGYGATA TTCAAAGCTC

20

55

2) INFORMATION FOR SEQ ID NO: 1113

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 bases

50

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1113

ACCGACCTCA CAGCCCGAAA

20

10

2) INFORMATION FOR SEQ ID NO: 1114

(i) SEQUENCE CHARACTERISTICS:

15

(A) LENGTH: 21 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1114

TCWGAGCCTT TTTCCGGCTC G

21

25

2) INFORMATION FOR SEQ ID NO: 1115

(i) SEQUENCE CHARACTERISTICS:

30

(A) LENGTH: 26 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1115

40

TTTCGGGCTG TGAGGTCGGB TGHGCG

26

2) INFORMATION FOR SEQ ID NO: 1116

45

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 27 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1116

55

TTTCGGGCTG TGAGGTCGGB TGHGCGG

27

60 2) INFORMATION FOR SEQ ID NO: 1117

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 801 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Enterococcus faecium*
 (B) STRAIN: 94
 (C) ACCESSION NUMBER: U94526
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1117

```

AAATTCGATC CGCACTACAT CGGAATTACA AAAAACGGTG TATGGAAGCT      50
ATGCAAGAAG CCATGTACGG AATGGGAAGC CGACAGTCTC CCCGCCATAC      100
TCTCCCCGGA TAGGAAAACG CATGGGCTGC TTGTCATGAA AGAAAGCGAA      150
TACGAAACAC GCGGTATTGA TGTGGCTTTC CCGGTTTTGC ATGGCAAATG      200
CGGGGAGGAT GGTGCGATAC AGGGGCTGTT TGTATTGTCT GGTATCCCCT      250
ATGTGGGCTG TGATATTCAA AGCTCCGCAG CTTGCATGGA CAAATCACTG      300
GCCTACATTC TTACAAAAAA TGCGGGCATC GCCGTTCCCG AATTTCAAAT      350
GATTGATAAA GGTGACAAGC CGGAGGCGGG TGCCTTACC TACCCTGTCT      400
TTGTGAAGCC GGCACGGTCA GGTTCGTCCT TTGGCGTAAC CAAAGTAAAC      450
GGTACGGAAG AACTTAACGC TGCATAGAA GCGGCAGGAC AATATGATGG      500
AAAAATCTTA ATTGAGCAAG CGATTTCTGGG CTGTGAGGTC GGGTGTGCGG      550
TCATGGGGAA CGAGGATGAT TTGATTGTCG GCGAAGTGGA TCAAATCCGG      600
CTGAGCCACG GTATCTTCCG CATCCATCAG GAAAACGAGC CGGAAAAAGG      650
CTCAGAAAAT GCGATGATTA CAGTTCCCGC AGACATTCCG GTCGAGGAAC      700
GAAATCGGGT GCAGGAAACG GCAAAGAAAG TATATCGGGT GCTTGGATGC      750
AGAGGGCTTG CCCGTGTTGA TCTTTTTTTT CAGGAGGATG GCGGCATCGT      800
T

```

35

2) INFORMATION FOR SEQ ID NO: 1118

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 24 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: DNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1118

```

TTTTCWGAGC CTTTTTCCGG CTCG

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50

24

2) INFORMATION FOR SEQ ID NO: 1119

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 25 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1119

5 TTTCGGGCTG TGAGGTCGGB TGHGC 25

2) INFORMATION FOR SEQ ID NO: 1120

10

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

15 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1120

20

TTTCGGGCTG TGAGGTCGGB TGHG 24

25 2) INFORMATION FOR SEQ ID NO: 1121

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 bases

(B) TYPE: Nucleic acid

30 (C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1121

TGTTTGWATT GTCYGGYATC CC 22

40

2) INFORMATION FOR SEQ ID NO: 1122

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 18 bases

45 (B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1122

TGGTGCATTG CTACGTGG 18

55

2) INFORMATION FOR SEQ ID NO: 1123

(i) SEQUENCE CHARACTERISTICS:

60 (A) LENGTH: 22 bases

- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

5 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1123

TTTCGGGCTG TGAGGTCGGB TG

22

10

2) INFORMATION FOR SEQ ID NO: 1124

15 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1124

25 GATTTGRTCC ACYTCGCCRA CA

22

2) INFORMATION FOR SEQ ID NO: 1125

30

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1125

40

ACTCACAAC TGGATGGATG

20

45 2) INFORMATION FOR SEQ ID NO: 1126

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: DNA

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1126

TTATGGTTGT GCTGGTTGAG G

21

60

2) INFORMATION FOR SEQ ID NO: 1127

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1127

KCAAAYGCCA TTTCAAGTAA

20

15

2) INFORMATION FOR SEQ ID NO: 1128

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

25 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1128

GACGACYTTA TKGATATACA

20

30

2) INFORMATION FOR SEQ ID NO: 1129

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 23 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

40

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1129

45 ATGATGACHG AMATGATGAA AAC

23

2) INFORMATION FOR SEQ ID NO: 1130

50

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
55 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1130

60

5 2) INFORMATION FOR SEQ ID NO: 1131

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
- (B) TYPE: Nucleic acid
- 10 (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1131

CATCTGGAGC TACRTARCCA GT

22

20

2) INFORMATION FOR SEQ ID NO: 1132

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- 25 (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1132

AGTGAAAARA TGGCTGCTGC

20

35

2) INFORMATION FOR SEQ ID NO: 1133

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

45 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1133

CATCAAGAAC ACTGGCTAYG TAG

23

50

2) INFORMATION FOR SEQ ID NO: 1134

(i) SEQUENCE CHARACTERISTICS:

- 55 (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- 60 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1134

5 CTAGATAGAG CTAAACCTT CCT 23

2) INFORMATION FOR SEQ ID NO: 1135

10

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

15 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1135

20

CATTATGCAA ACGCCATTTT AAG 23

25 2) INFORMATION FOR SEQ ID NO: 1136

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 bases

(B) TYPE: Nucleic acid

30 (C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1136

ACTTGTCCAC GTTSGATRTC T 21

40

2) INFORMATION FOR SEQ ID NO: 1137

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 bases

45 (B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1137

AATTAATGGC TGCWGTTGAY GAA 23

55

2) INFORMATION FOR SEQ ID NO: 1138

(i) SEQUENCE CHARACTERISTICS:

60 (A) LENGTH: 1032 bases

(B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

5 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Enterococcus gallinarum*
 (C) ACCESSION NUMBER: M75132

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1138

	ATGAAAAAAA	TTGCCGTTTT	ATTTGGAGGG	AATTCTCCAG	AATACTCAGT	50
	GTCACTAACC	TCAGCAGCAA	GTGTGATCCA	AGCTATTGAC	CCGCTGAAAT	100
15	ATGAAGTAAT	GACCATTGGC	ATCGCACCAA	CAATGGATTG	GTATTGGTAT	150
	CAAGGAAACC	TCGCGAATGT	TCGCAATGAT	ACTTGGCTAG	AAGATCACAA	200
	AAACTGTCAC	CAGCTGACTT	TTTCTAGCCA	AGGATTTATA	TTAGGAGAAA	250
	AACGAATCGT	CCCTGATGTC	CTCTTTCCAG	TCTTGCATGG	GAAGTATGGC	300
	GAGGATGGCT	GTATCCAAGG	ACTGCTTGAA	CTAATGAACC	TGCCTTATGT	350
20	TG GTTGCCAT	GTCGCTGCCT	CCGCATTATG	TATGAACAAA	TGGCTCTTGC	400
	ATCAACTTGC	TGATACCATG	GGAATCGCTA	GTGCTCCAC	TTTGCTTTTA	450
	TCCCGCTATG	AAAACGATCC	TGCCACAATC	GATCGTTTTA	TTCAAGACCA	500
	TGGATTCCCG	ATCTTTATCA	AGCCGAATGA	AGCCGGTTCT	TCAAAAGGGA	550
	TCACAAAAGT	AACTGACAAA	ACAGCGCTCC	AATCTGCATT	AACGACTGCT	600
25	TTTGCTTACG	GTTCTACTGT	GTTGATCCAA	AAGGCGATAG	CGGGTATTGA	650
	AATTGGCTGC	GGCATCTTAG	GAAATGAGCA	ATTGACGATT	GGTGCTTGTG	700
	ATGCGATTTT	TCTTGTCGAC	GGTTTTTTTG	ATTTTGAAGA	GAAATACCAA	750
	TTAATCAGCG	CCACGATCAC	TGTCCCAGCA	CCATTGCCTC	TCGCGCTTGA	800
	ATCACAGATC	AAGGAGCAGG	CACAGCTGCT	TTATCGAAAC	TTGGGATTGA	850
30	CGGGTCTGGC	TCGAATCGAT	TTTTTTCGTCA	CCAATCAAGG	AGCGATTTAT	900
	TTAAACGAAA	TCAACACCAT	GCCGGGATTT	ACTGGGCACT	CCCGCTACCC	950
	AGCTATGATG	GCGGAAGTCG	GGTTATCCTA	CGAAATATTA	GTAGAGCAAT	1000
	TGATTGCACT	GGCAGAGGAG	GACAAACGAT	GA		1032

35

2) INFORMATION FOR SEQ ID NO: 1139

(i) SEQUENCE CHARACTERISTICS:

40 (A) LENGTH: 1768 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

45 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Enterococcus faecium*
 (B) STRAIN: BM4147
 50 (C) ACCESSION NUMBER: X56895

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1139

	GATATCGTTA	CGCTTCATGT	GCCGCTCAAT	ACGGATACGC	ACTATATTAT	50
55	CAGCCACGAA	CAAATACAGA	GAATGAAGCA	AGGAGCATTT	CTTATCAATA	100
	CTGGGCGCGG	TCCACTTGTA	GATACCTATG	AGTTGGTTAA	AGCATTAGAA	150
	AACGGGAAAC	TGGGCGGTGC	CGCATTGGAT	GTATTGGAAG	GAGAGGAAGA	200
	GTTTTTCTAC	TCTGATTGCA	CCCAAAAACC	AATTGATAAT	CAATTTTAC	250
	TTAAACTTCA	AAGAATGCCT	AACGTGATAA	TCACACCGCA	TACGGCCTAT	300
60	TATACCGAGC	AAGCGTTGCG	TGATACCGTT	GAAAAAACCA	TTAAAACTG	350

	TTTGGATTTT	GAAAGGAGAC	AGGAGCATGA	ATAGAATAAA	AGTTGCAATA	400
	CTGTTTGGGG	GTTGCTCAGA	GGAGCATGAC	GTATCGGTAA	AATCTGCAAT	450
	AGAGATAGCC	GCTAACATTA	ATAAAGAAAA	ATACGAGCCG	TTATACATTG	500
	GAATTACGAA	ATCTGGTGTA	TGGAAAATGT	GCGAAAAACC	TTGCGCGGAA	550
5	TGGGAAAACG	ACAATTGCTA	TTCAGCTGTA	CTCTCGCCGG	ATAAAAAAAT	600
	GCACGGATTA	CTTGTTAAAA	AGAACCATGA	ATATGAAATC	AACCATGTTG	650
	ATGTAGCATT	TTCAGCTTTG	CATGGCAAGT	CAGGTGAAGA	TGGATCCATA	700
	CAAGGTCTGT	TTGAATTGTC	CGGTATCCCT	TTTGTAGGCT	GCGATATTCA	750
	AAGCTCAGCA	ATTTGTATGG	ACAAATCGTT	GACATACATC	GTTGCGAAAA	800
10	ATGCTGGGAT	AGCTACTCCC	GCCTTTTGGG	TTATTAATAA	AGATGATAGG	850
	CCGGTGGCAG	CTACGTTTAC	CTATCCTGTT	TTTGTTAAGC	CGGCGCGTTC	900
	AGGCTCATCC	TTCGGTGTGA	AAAAAGTCAA	TAGCGCGGAC	GAATTGGACT	950
	ACGCAATTGA	ATCGGCAAGA	CAATATGACA	GCAAAATCTT	AATTGAGCAG	1000
	GCTGTTTTCG	GCTGTGAGGT	CGGTTGTGCG	GTATTGGGAA	ACAGTGCCGC	1050
15	GTTAGTTGTT	GGCGAGGTGG	ACCAAATCAG	GCTGCAGTAC	GGAATCTTTC	1100
	GTATTCATCA	GGAAGTCGAG	CCGGA AAAAG	GCTCTGAAAA	CGCAGTTATA	1150
	ACCGTTCCCG	CAGACCTTTC	AGCAGAGGAG	CGAGGACGGA	TACAGGAAAC	1200
	GGCAAAAAAA	ATATATAAAG	CGCTCGGCTG	TAGAGGTCTA	GCCCCGTGTG	1250
	ATATGTTTTT	ACAAGATAAC	GGCCGCATTG	TACTGAACGA	AGTCAATACT	1300
20	CTGCCCCGTT	TCACGTCATA	CAGTCGTTAT	CCCCGTATGA	TGGCCGCTGC	1350
	AGGTATTGCA	CTTCCCGAAC	TGATTGACCG	CTTGATCGTA	TTAGCGTTAA	1400
	AGGGGTGATA	AGCATGGAAA	TAGGATTTAC	TTTTTTTAGAT	GAAATAGTAC	1450
	ACGGTGTTTC	TTGGGACGCT	AAATATGCCA	CTTGGGATAA	TTTCACCGGA	1500
	AAACCGGTTG	ACGGTTATGA	AGTAAATCGC	ATTGTAGGGA	CATACGAGTT	1550
25	GGCTGAATCG	CTTTTGAAGG	CAAAAGA AACT	GGCTGCTACC	CAAGGGTACG	1600
	GATTGCTTCT	ATGGGACGGT	TACCGTCTTA	AGCGTGCTGT	AAACTGTTTT	1650
	ATGCAATGGG	CTGCACAGCC	GGAAAATAAC	CTGACAAAGG	AAAGTTATTA	1700
	TCCCAATATT	GACCGAACTG	AGATGATTTT	AAAAGGATAC	GTGGCTTCAA	1750
	AATCAAGCCA	TAGCCGCG				1768
30						

2) INFORMATION FOR SEQ ID NO: 1140

35 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1086 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

40

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus casseliflavus*
 (C) ACCESSION NUMBER: L29638

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1140

	GTAAGAATCG	GAAAAGCGGA	AGGAAGAAAA	ACATGAAAAA	AATCGCCATT	50
50	ATTTTTGGAG	GCAATTCACC	GGAATACACC	GTTTCTTTAG	CTTCAGCAAC	100
	TAGCGCAATC	GAAGCACTCC	AATCATCTCC	CTATGACTAC	GACCTCTCTT	150
	TGATCGGGAT	CGCCCCAGAT	GCTATGGATT	GGTACTTGTA	TACAGGAGAA	200
	CTGGAAAACA	TCCGACAAGA	CACGTGGTTG	TTGGATACGA	AACATAAACA	250
	GAAAATACAG	CCGCTATTCG	AAGGAAACGG	CTTTTGGCTA	AGTGAAGAGC	300
55	AGCAAACGTT	GGTACCTGAT	GTTTTATTTC	CCATTATGCA	TGGCAAATAC	350
	GGGGAAGATG	GCAGTATCCA	AGGATTGTTT	GAATTGATGA	AGCTGCCTTA	400
	TGTAGGCTGC	GGGGTGGCAG	GTTCTGCCTT	ATGTATGAAC	AAATGGCTGC	450
	TGCATCAAGC	TGCAGCAGCC	ATTGGCGTAC	AAAGTGCTCC	TACGATTCTC	500
	TTGACAAATC	AAGCCAACCA	GCAAGAACAA	ATCGAAGCTT	TTATCCAGAC	550
60	CCATGGCTTC	CCAGTTTTCT	TTAAGCCTAA	TGAAGCGGGC	TCCTCAA AAG	600

	GGATCACTAA	AGTCACCTGC	GTTGAAGAAA	TCGCTTCTGC	CTTAAAAGAA	650
	GCCTTTACTT	ATTGTTCCGC	AGTGCTCCTA	CAAAAAAATA	TTGCCGGTGT	700
	TGAGATCGGT	TGCGGTATTT	TGGGCAACGA	CTCTTTGACT	GTCGGTGCTT	750
	GTGACGCCAT	TTCATTAGTA	GACGGCTTTT	TCGATTTTGA	AGAAAAGTAC	800
5	CAGCTGATCA	GCGCCAAAAT	CACCGTCCCT	GCGCCATTGC	CTGAAACGAT	850
	TGAAACCAAG	GTCAAAGAAC	AAGCTCAGCT	GCTCTATCGT	AGTCTTGCTC	900
	TTAAAGGTCT	TGCTCGCATC	GACTTTTTTG	TCACGGAGCG	AGGAGAACTA	950
	TACTTGAATG	AAATCAATAC	TATGCCGGGC	TTTACGAGTC	ACTCCCGCTA	1000
	TCCTGCCATG	ATGGCAGCGG	TCGGCTTATC	CTATCAAGAA	CTACTACAAA	1050
10	AACTGCTTGT	CTTAGCAAAG	GAGGAAGTCA	AATGAG		1086

2) INFORMATION FOR SEQ ID NO: 1141

15 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3946 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus faecium*
 25 (B) STRAIN: BM4147
 (C) ACCESSION NUMBER: extracted from M97297

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1141

30	ATGAATAACA	TCGGCATTAC	TGTTTATGGA	TGTGAGCAGG	ATGAGGCAGA	50
	TGCATTCCAT	GCTCTTTCGC	CTCGCTTTGG	CGTTATGGCA	ACGATAATTA	100
	ACGCCAACGT	GTCGGAATCC	AACGCCAAAT	CCGCGCCTTT	CAATCAATGT	150
	ATCAGTGTGG	GACATAAAATC	AGAGATTTCC	GCCTCTATTC	TTCTTGCGCT	200
	GAAGAGAGCC	GGTGTGAAAT	ATATTTCTAC	CCGAAGCATC	GGCTGCAATC	250
35	ATATAGATAC	AACTGCTGCT	AAGAGAATGG	GCATCACTGT	CGACAATGTG	300
	GCGTACTCGC	CGGATAGCGT	TGCCGATTAT	ACTATGATGC	TAATTCTTAT	350
	GGCAGTACGC	AACGTAAAAT	CGATTGTGCG	CTCTGTGGAA	AAACATGATT	400
	TCAGGTTGGA	CAGCGACCGT	GGCAAGGTAC	TCAGCGACAT	GACAGTTGGT	450
	GTGGTGGGAA	CGGGCCAGAT	AGGCAAAGCG	GTTATTGAGC	GGCTGCGAGG	500
40	ATTTGGATGT	AAAGTGTTGG	CTTATAGTCG	CAGCCGAAGT	ATAGAGGTAA	550
	ACTATGTACC	GTTTGATGAG	TTGCTGCAAA	ATAGCGATAT	CGTTACGCTT	600
	CATGTGCCGC	TCAATACGGA	TACGCACTAT	ATTATCAGCC	ACGAACAAAT	650
	ACAGAGAATG	AAGCAAGGAG	CATTTCTTAT	CAATACTGGG	CGCGGTCCAC	700
	TTGTAGATAC	CTATGAGTTG	GTTAAAGCAT	TAGAAAACGG	GAAACTGGGC	750
45	GGTGCCGCAT	TGGATGTATT	GGAAGGAGAG	GAAGAGTTTT	TCTACTCTGA	800
	TTGCACCCAA	AAACCAATTG	ATAATCAATT	TTTACTTAAA	CTTCAAAGAA	850
	TGCCTAACGT	GATAATCACA	CCGCATACGG	CCTATTATAC	CGAGCAAGCG	900
	TTGCGTGATA	CCGTTGAAAA	AACCATTAAA	AACTGTTTGG	ATTTTGAAAG	950
	GAGACAGGAG	CATGAATAGA	ATAAAAGTTG	CAATACTGTT	TGGGGGTTGC	1000
50	TCAGAGGAGC	ATGACGTATC	GGTAAAATCT	GCAATAGAGA	TAGCCGCTAA	1050
	CATTAATAAA	GAAAAATACG	AGCCGTTATA	CATTGGAATT	ACGAAATCTG	1100
	GTGTATGGAA	AATGTGCGAA	AAACCTTGCG	CGGAATGGGA	AAACGACAAT	1150
	TGCTATTGAG	CTGTACTCTC	GCCGGATAAA	AAAATGCACG	GATTACTTGT	1200
	TAAAAAGAAC	CATGAATATG	AAATCAACCA	TGTTGATGTA	GCATTTTCAG	1250
55	CTTTGCATGG	CAAGTCAGGT	GAAGATGGAT	CCATACAAGG	TCTGTTTGAA	1300
	TTGTCCGGTA	TCCCTTTTGT	AGGCTGCGAT	ATTCAAAGCT	CAGCAATTTG	1350
	TATGGACAAA	TCGTTGACAT	ACATCGTTGC	GAAAAATGCT	GGGATAGCTA	1400
	CTCCCGCCTT	TTGGGTTATT	AATAAAGATG	ATAGGCCGGT	GGCAGCTACG	1450
	TTTACCTATC	CTGTTTTTGT	TAAGCCGGCG	CGTTCAGGCT	CATCCTTCGG	1500
60	TGTGAAAAAA	GTCAATAGCG	CGGACGAATT	GGACTACGCA	ATTGAATCGG	1550

	CAAGACAATA	TGACAGCAAA	ATCTTAATTG	AGCAGGCTGT	TTCGGGCTGT	1600
	GAGGTCGGTT	GTGCGGTATT	GGGAAACAGT	GCCGCGTTAG	TTGTTGGCGA	1650
	GGTGGACCAA	ATCAGGCTGC	AGTACGGAAT	CTTTCGTATT	CATCAGGAAG	1700
	TCGAGCCGGA	AAAAGGCTCT	GAAAACGCAG	TTATAACCGT	TCCCGCAGAC	1750
5	CTTTCAGCAG	AGGAGCGAGG	ACGGATACAG	GAAACGGCAA	AAAAAATATA	1800
	TAAAGCGCTC	GGCTGTAGAG	GTCTAGCCCG	TGTGGATATG	TTTTTACAAG	1850
	ATAACGGCCG	CATTGTACTG	AACGAAGTCA	ATACTCTGCC	CGGTTTCACG	1900
	TCATACAGTC	GTTATCCCCG	TATGATGGCC	GCTGCAGGTA	TTGCACTTCC	1950
	CGAACTGATT	GACCGCTTGA	TCGTATTAGC	GTTAAAGGGG	TGATAAGCAT	2000
10	GGAAATAGGA	TTTACTTTTT	TAGATGAAAT	AGTACACGGT	GTTTCGTTGGG	2050
	ACGCTAAATA	TGCCACTTGG	GATAATTTCA	CCGGAAAACC	GGTTGACGGT	2100
	TATGAAGTAA	ATCGCATTGT	AGGGACATAC	GAGTTGGCTG	AATCGCTTTT	2150
	GAAGGCAAAA	GAACCTGGCTG	CTACCCAAGG	GTACGGATTG	CTTCTATGGG	2200
	ACGGTTACCG	TCCTAAGCGT	CTGTGAAACT	GTTTTATGCA	ATGGGCTGCA	2250
15	CAGCCGGAAA	ATAACCTGAC	AAAGGAAAGT	TATTATCCCA	ATATTGACCG	2300
	AACTGAGATG	ATTTCAAAAG	GATACGTGGC	TTCAAAATCA	AGCCATAGCC	2350
	GCGGCAGTGC	CATTGATCTT	ACGCTTTATC	GATTAGACAC	GGGTGAGCTT	2400
	GTACCAATGG	GGAGCCGATT	TGATTTTATG	GATGAACGCT	CTCATCATGC	2450
	GGCAAATGGA	ATATCATGCA	ATGAAGCGCA	AAATCGCAGA	CGTTTGCGCT	2500
20	CCATCATGGA	AAACAGTGGG	TTTGAAGCAT	ATAGCCTCGA	ATGGTGGCAC	2550
	TATGTATTAA	GAGACGAACC	ATACCCCAAT	AGCTATTTTG	ATTTCCCCGT	2600
	TAAATAAACT	TTTAACCGTT	GCACGGACAA	ACTATATAAG	CTAACTCTTT	2650
	CGGCAGGAAA	CCCGACGTAT	GTAACCTGGT	CTTAGGGAAT	TTATATATAG	2700
	TAGATAGTAT	TGAAGATGTA	AGGCAGAGCG	ATATTGCGGT	CATTATCTGC	2750
25	GTGCGCTGCG	GCAAGATAGC	CTGATAATAA	GACTGATCGC	ATAGAGGGGT	2800
	GGTATTTTAC	ACCGCCCAT	GTCAACAGGC	AGTTCAGCCT	CGTTAAATTC	2850
	AGCATGGGTA	TCACTTATGA	AAATTCATCT	ACATTGGTGA	TAATAGTAAA	2900
	TCCAGTAGGG	CGAAATAATT	GACTGTAATT	TACGGGGCAA	AACGGCACAA	2950
	TCTCAAACGA	GATTGTGCCG	TTTAAGGGGA	AGATTCTAGA	AATATTTTCAT	3000
30	ACTTCCAAC	ATATAGTTAA	GGAGGAGACT	GAAAATGAAG	AAGTTGTTTT	3050
	TTTTATTGTT	ATTGTTATTC	TTAATATACT	TAGGTTATGA	CTACGTTAAT	3100
	GAAGCACTGT	TTTCTCAGGA	AAAAGTCGAA	TTTCAAAATT	ATGATCAAAA	3150
	TCCCAAAGAA	CATTTAGAAA	ATAGTGGGAC	TTCTGAAAAT	ACCCAAGAGA	3200
	AAACAATTAC	AGAAGAACAG	GTTTATCAAG	GAAATCTGCT	ATTAATCAAT	3250
35	AGTAAATATC	CTGTTTCGCCA	AGAAAGTGTG	AAGTCAGATA	TCGTGAATTT	3300
	ATCTAAACAT	GACGAATTAA	TAAATGGATA	CGGGTTGCTT	GATAGTAATA	3350
	TTTATATGTC	AAAAGAAATA	GCACAAAAT	TTTCAGAGAT	GGTCAATGAT	3400
	GCTGTAAAGG	GTGGCGTTAG	TCATTTTATT	ATTAATAGTG	GCTATCGAGA	3450
	CTTTGATGAG	CAAAGTGTGC	TTTACCAAGA	AATGGGGGCT	GAGTATGCCT	3500
40	TACCAGCAGG	TTATAGTGAG	CATAATTCAG	GTTTATCACT	AGATGTAGGA	3550
	TCAAGCTTGA	CGAAAATGGA	ACGAGCCCCCT	GAAGGAAAGT	GGATAGAAGA	3600
	AAATGCTTGG	AAATACGGGT	TCATTTTACG	TTATCCAGAG	GACAAAACAG	3650
	AGTTAACAGG	AATTCAATAT	GAACCATGGC	ATATTCGCTA	TGTTGGTTTA	3700
	CCACATAGTG	CGATTATGAA	AGAAAAGAAT	TTCGTTCTCG	AGGAATATAT	3750
45	GGATTACCTA	AAAGAAGAAA	AAACCATTTC	TGTTAGTGTA	AATGGGGGAA	3800
	AATATGAGAT	CTTTTATTAT	CCTGTTACTA	AAAATACCAC	CATTCATGTG	3850
	CCGACTAATC	TTCGTTATGA	GATATCAGGA	AACAATATAG	ACGGTGTAAT	3900
	TGTGACAGTG	TTTCCCGGAT	CAACACATAC	TAATTCAAGG	AGGTAA	3946

50

2) INFORMATION FOR SEQ ID NO: 1142

(i) SEQUENCE CHARACTERISTICS:

- 55 (A) LENGTH: 25 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

60 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1142

GATCCTCTAA ATGATTCTCA GGTGG

25

5

2) INFORMATION FOR SEQ ID NO: 1143

10 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 25 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

15

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1143

20 CAATTAGCTT AGCAATAGGT GTTGG

25

2) INFORMATION FOR SEQ ID NO: 1144

25

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

30

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1144

35

TGTYTTCCAA GGTTTCAGCTC

20

40 2) INFORMATION FOR SEQ ID NO: 1145

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 bases

(B) TYPE: Nucleic acid

45

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1145

AACATATTKG GTTGATAGGT

20

55

2) INFORMATION FOR SEQ ID NO: 1146

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 bases

60

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1146

GGGATTACCT ATGCCAATAT GAT

23

10

2) INFORMATION FOR SEQ ID NO: 1147

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 24 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

20 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1147

AGCTGTGTTA GCVCGAACAT CTTG

24

25

2) INFORMATION FOR SEQ ID NO: 1148

(i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1148

40 GACTTTGTTT GCGTGATAT

20

2) INFORMATION FOR SEQ ID NO: 1149

45

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
50 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1149

55

TCCYACWATT TCTTTTGWG

20

60 2) INFORMATION FOR SEQ ID NO: 1150

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
5 (C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1150

TGATAATCAC ACCGCATACG

20

15

2) INFORMATION FOR SEQ ID NO: 1151

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 bases
20 (B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1151

TGCTGTCATA TTGTCTTGCC

20

30

2) INFORMATION FOR SEQ ID NO: 1152

- (i) SEQUENCE CHARACTERISTICS:
35 (A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

40 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1152

ATAAAGATGA TAGGCCGGTG

20

45

2) INFORMATION FOR SEQ ID NO: 1153

- 50 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
55 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1153

60 CTCGTATGTC CCTACAATGC

20

2) INFORMATION FOR SEQ ID NO: 1154

5

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

10

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1154

15

GTTTGAAGCA TATAGCCTCG

20

20 2) INFORMATION FOR SEQ ID NO: 1155

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

25

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1155

30

CAGTGCTTCA TTAACGTAGT C

21

35 2) INFORMATION FOR SEQ ID NO: 1156

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

40

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1156

45

GTTGAAATGC ATCACGAACA ATT

23

50

2) INFORMATION FOR SEQ ID NO: 1157

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

55

(ii) MOLECULE TYPE: DNA

60

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1157

AAGAACGTTT CAGTTAAGGA AAT

23

5

2) INFORMATION FOR SEQ ID NO: 1158

10 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 19 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

15

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1158

20 AAGAGGTAAT GTCTGTGGT

19

2) INFORMATION FOR SEQ ID NO: 1159

25

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 18 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

30

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1159

35

TGAAGGTTTG CCAGGTGA

18

40 2) INFORMATION FOR SEQ ID NO: 1160

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

45

(ii) MOLECULE TYPE: DNA

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1160

CGTTTCTGTT AAAGAAATTA GAAG

24

55

2) INFORMATION FOR SEQ ID NO: 1161

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 18 bases

(B) TYPE: Nucleic acid

60

(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1161

TCCAGGTGAT AACGTTGG

18

10

2) INFORMATION FOR SEQ ID NO: 1162

(i) SEQUENCE CHARACTERISTICS:

15

(A) LENGTH: 18 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1162

CAAGTCCGTG GAAATGCA

18

25

2) INFORMATION FOR SEQ ID NO: 1163

(i) SEQUENCE CHARACTERISTICS:

30

(A) LENGTH: 21 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1163

40 GTTGGTTTCA ACGTTAAGAA C

21

45

2) INFORMATION FOR SEQ ID NO: 1164

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 18 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1164

55

GGTTTCAACG TCAAGAAC

18

60 2) INFORMATION FOR SEQ ID NO: 1165

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1165

GGTTTCAACG TGAAGAAC

18

15

2) INFORMATION FOR SEQ ID NO: 1166

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1166

ACGTTAAGAA TGTTTCTGTC AA

22

30

2) INFORMATION FOR SEQ ID NO: 1167

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 14 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1167

GTTGGTTTCA ACGT

14

45

2) INFORMATION FOR SEQ ID NO: 1168

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

55

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1168

GAACAATTGG TTGAAGGTGT

20

2) INFORMATION FOR SEQ ID NO: 1169

5

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2160 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

10

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
(B) STRAIN: SP-665
(C) ACCESSION NUMBER: AF139883

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1169

20

ATGAACAAAC	CAACGATTCT	GCGCCTAATC	AAGTATCTGA	GCATTAGCTT	50	
CTTAAGCTTG	GTTATCGCAG	CCATTGTCTT	AGGCGGAGGA	GTTTTTTTCT	100	
ACTACGTTAG	CAAGGCTCCT	AGCCTATCCG	AGAGTAAACT	AGTTGCAACA	150	
ACTTCTAGTA	AAATCTACGA	CAATAAAAAT	CAACTCATTG	CTGACTTGGG	200	
25	TTCTGAACGC	CGCGTCAATG	CCCAAGCTAA	TGATATTCCC	250	
TTAAGGCAAT	CGTTTCTATC	GAAGACCATC	GCTTCTTCGA	CCACAGGGGG	300	
ATTGATTCCA	TCCGTATCCT	GGGAGCTTTC	TTGCGCAATC	TGCAAAGTAA	350	
TTCCCTCCAA	GGTGGATCAA	CTCTCACCCA	ACAGTTGATT	AAGTTGACTT	400	
ACTTTTCAAC	CTCGACTTCC	GACCAGACTA	TTTCTCGTAA	GGCTCAGGAA	450	
30	GCTTGGTTAG	CGATTCAAGT	AGAACAAAAA	GCAACCAAAC	AGGAAATCTT	500
GACCTACTAT	ATAAATAAGG	TCTACATGTC	TAATGGCAAC	TATGGAATGC	550	
AGACAGCAGC	TCAAAACTAC	TATGGTAAAG	ACCTCAATAA	TTTAAGTTTA	600	
CCTCAGTTAG	CCTTGCTGGC	TGGAATGCCT	CAGGCACCAA	ACCAATATGA	650	
CCCCTATTCA	CATCCAGAAG	CAGCCCAAGA	CCGCCGAAAC	TTGGTCTTAT	700	
35	CTGAAATGAA	AAATCAAGGT	TACATCTCTG	CTGAACAGTA	TGAGAAAGCA	750
GTCAATACAC	CAATTACTGA	TGGACTACAA	AGTCTCAAAT	CAGCAAGTAA	800	
TTACCCCTGCT	TACATGGATA	ATTACCTCAA	GGAGGTCATC	AATCAAGTAG	850	
AACAAGAAAC	TGGCTATAAC	CTTCTAACTA	CTGGGATGGA	TGTTTACACA	900	
AATGTAGACC	AAGAAGCTCA	AAAACATCTG	TGGGATATCT	ACAACCTCCGA	950	
40	TCAATACGTC	TCTTACCCTG	ACGATGATTT	GCAAGTCGCA	TCTACGGTCTG	1000
TAGATGTTTC	AAATGGTAAA	GTCATCGCCC	AACCTGGAGC	TCGTCACCAA	1050	
GCAAGTAAAC	TTTCATTTGG	TACCAACCAA	GCTGTGGAAA	CCAATCGTGA	1100	
CTGGGGTTCT	GCTATGAAAC	CAATCACCGA	TTATGCACCT	GCCATAGAAT	1150	
ACGGTGTTTA	TGATTCCACT	GCAACTATGG	TTAATGATAT	TCCTTATAAC	1200	
45	TATCCGGGAA	CAAGCACACC	TGTCTACAAC	TGGGATAGAG	CATATTTCGG	1250
TAATATTACT	CTGCAATATG	CTCTTCAACA	ATCACGAAAT	GTCACAGCCG	1300	
TTGAGACTTT	GAATAAGGTC	GGTCTAGATA	GAGCTAAAAC	CTTCCTTAAT	1350	
GGTCTTGCTA	TCGACTATCC	AAGCATGCAT	TATGCAAACG	CCATTTCAAG	1400	
TAATACAACA	GAATCTAATA	AACAATACGG	AGCAAGTAGT	GAAAAAATGG	1450	
50	CTGCTGCTTA	TGCTGCCTTT	GCAAATGGTG	GCACTTACTA	TAAACCAATG	1500
TATATCCATA	AAGTCGTCTT	CAGTGATGGA	AGTAAAAAAG	AGTTCTCTAA	1550	
TGTCGGAACT	CGTGCCATGA	AGGAAACGAC	AGCCTATATG	ATGACCGACA	1600	
TGATGAAAAC	AGTCTTGACT	TATGGAAC TG	GGCGTGGAGC	CTATCTTCCT	1650	
TGGCTTCCTC	AAGCTGGTAA	AACAGGAACC	TCTAACTATA	CAGATGAGGA	1700	
55	AGTTGAAAAC	CACATCAAGA	ACACTGGCTA	TGTAGCTCCA	GATGAAATGT	1750
TTGTTGGTTA	TACTCGTAAG	TATTCTATGG	CTGTATGGAC	AGGTTATTCG	1800	
AATCGTTTAA	CTCCTATCGT	TGGAGATGGT	TTCCTAGTTG	CAGCTAAAGT	1850	
TTATCGCTCA	ATGATAACGT	ATCTATCAGA	AGATACTCAT	CCAGAAGACT	1900	
GGACGATGCC	AGACGGACTT	TTCAGAAACG	GGGAATTGTG	ATTCAAAAAT	1950	
60	GGAGCTCGCC	CAATATGGAC	TGAACCTCT	ACTCAACAAT	CCTCAACAGC	2000

TGAAAGTTCA	AGCTCATCAT	CAGATAGTTC	AACTTCACAG	TCTAGCTCAA	2050
CCACTCCAAG	CACAAATAAT	AGTACGACTA	CCAATCCTAA	CAATAATACG	2100
CAACAATCAA	ATACAACCCC	TGATCAACAA	AATCAGAATC	CTCAACCAGC	2150
ACAACCATAA					2160

5

2) INFORMATION FOR SEQ ID NO: 1170

10 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

15

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1170

20 ACGAATTGGA CTACGCAATT

20

2) INFORMATION FOR SEQ ID NO: 1171

25

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

30

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1171

35

ACGAGGATGA TTTGATTGTC

20

40 2) INFORMATION FOR SEQ ID NO: 1172

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1560 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

45

(ii) MOLECULE TYPE: Genomic DNA

50 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
- (B) STRAIN: 64147
- (C) ACCESSION NUMBER: X13136

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1172

GATCCTCTAA	ATGATTCTCA	GGTGGCTGTT	ATTGCCTCTA	TTTCAAAGGA	50
GATGCCTGGC	ATTAGTATTT	CTACTTCTTG	GGATAGAAAG	GTTTTGGAAA	100
CTTCCCTTTC	TTCTATAGTT	GGGAGTGTAT	CCAGTGAAAA	AGCTGGTCTC	150
60 CCAGCGGAAG	AAGCAGAAGC	CTATCTTAA	AAAGGCTATT	CTCTAAATGA	200

	CCGTGTAGGA	ACCTCCTATT	TGGAAAAGCA	ATATGAAGAG	ACCTTACAAG	250
	GAAAACGCTC	GGTAAAAGAA	ATCCATCTGG	ACAAATATGG	CAACATGGAA	300
	AGCGTGGATA	CAATTGAGGA	AGGTAGTAAG	GGAAACAATA	TCAAGCTGAC	350
	CATTGATTTG	GCCTTCCAAG	ATAGCGTGGA	TGCTTTGCTG	AAAAGTTATT	400
5	TCAATTCAGA	GTTGGGAAAT	GGTGGAGCCA	AGTATTCTGA	AGGTGTCCTAT	450
	GCAGTCGCCC	TTAACCCAAA	AACAGGTGCT	GTTTTGTCTA	TGTCAGGAAT	500
	TAAACATGAC	TTGAAAACAG	GAGAGTTGAC	GCCGGATTCC	TTGGGAACGG	550
	TAACCAATGT	CTTTGTCCCA	GGTTCGGTTG	TCAAAGCAGC	GACCATCAGC	600
	TCTGGTTGGG	AAAATGGAGT	CTTGTCAGGA	AATCAGACCT	TGACAGACCA	650
10	GTCCATTGTC	TTTCAAGGTT	CAGCTCCAAT	TAATTCTTGG	TATCCTGCCT	700
	TTTCTAGACC	AATGCCGATT	ACGGCGGTTT	AGGCTCTAGA	GTATTCTATCC	750
	AATGCTTATA	TGGTCCAAAC	AGCCTAGGT	CTTATGGGCG	AGACCTATCA	800
	ACCCAATATG	TTTGTGCGCA	CCAGCAATCT	AGAGTCTGCT	ATGGGGAAAT	850
	TGCGTTCAAC	CTTTGGTGAA	TATGGTTTGG	GTTCTGCGAC	CGGAATTGAC	900
15	CTACCAGATG	AATCTACTGG	ATTTGTTCCC	AAAGAGTATA	GCTTTGCTAA	950
	TTTCATTACC	AATGCCTTTG	GGCAGTTTGA	TAATAATACG	CCGATGCAGT	1000
	TGGCTCAGTA	TGTAGCAACT	ATTGCAAAATG	ATGGTGTTCTG	TGTGGCTCCT	1050
	CGTATTGTTG	AAGGCATTTA	TGGTAATAAT	GATAAGGGAG	GACTGGGTGA	1100
	CTTGATTGAG	CAACTGCAAC	CGACAGAGAT	GAATAAGGTC	AATATATCCG	1150
20	ACTCCGATAT	GAGCATCTTG	CACCAAGGTT	TTTATCAGGT	TGCCCATGGT	1200
	ACTAGTGAAT	TGACAACCTG	ACGTGCCTTT	TCAAATGGCG	CCTTGGTATC	1250
	CATTAGCGGA	AAAACAGGTA	CAGCCGAAAG	CTATGTGGCA	GATGGTCAGC	1300
	AAGCAACCAA	TACCAATGCG	GTGGCCTATG	CCCCATCTGA	TAATCCCCAA	1350
	ATCGCTGTAG	CTGTTGTCTT	CCCTCATAAC	ACCAACCTTA	CAAATGGTGT	1400
25	CGGACCTTCC	ATTGCGCGCG	ATATTATCAA	CCTCTATAAC	CAACATCATC	1450
	CAATGAATTA	GAAAGGAACA	TATGCTTTAT	CCAACACCTA	TTGCTAAGCT	1500
	AATTGACAGT	TATTCGAAGT	TACCGGGTAT	CGGGATTAAG	ACGGCTACCC	1550
	GTTTGGCCTT					1560

30

2) INFORMATION FOR SEQ ID NO: 1173

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 2007 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

40 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
 (B) STRAIN: CS109
 45 (C) ACCESSION NUMBER: Z49096

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1173

	GAGTCCCGAT	TGCTGAGGAT	GCAACCTCCT	ATAATGTCTA	TGCGGTCATT	50
50	GATGAGAACT	ATAAGTCAGC	AACGGGTAAG	ATTCTTTACG	TAGAAAAAAC	100
	ACAATTTAAC	AAGGTTGCAG	AGGTCTTTCA	TAAGTATCTG	GACATGGAAG	150
	AATCCTATGT	AAGAGAGCAA	CTCTCGCAAC	CTAATCTCAA	GCAAGTTTCC	200
	TTTGGAGCAA	AGGGAAATGG	GATTACCTAT	GCCAATATGA	TGACTATCAA	250
	AAAAGAGTTG	GAAACTGCAG	AGGTCAAGGG	GATTGATTTT	ACAACCAGTC	300
55	CCAATCGTAG	TTATCCAAAC	GGACAATTG	CTTCTAGTTT	TATCGGTCTA	350
	GCTCAGCTCC	ATGAAAATGA	AGATGGCAGC	AAGAGCTTGC	TGGGAACCTC	400
	TGGAATGGAG	AGTTCCTTGA	ACAGTATTCT	TGCAGGGACA	GACGGCATT	450
	TTACCTATGA	AAAGGATCGT	CTGGGCAATA	TTGTACCCGG	AACAGAACTG	500
	GTATCGCAAC	AAACTGTGGA	TGGCAAGGAT	GTTTATACAA	CATTGTCTAG	550
60	TCCGCTACAA	TCTTTCATGG	AAACTCAGAT	GGATGCCTTT	CTAGAAAAAG	600

	TAAAAGGTAA	GTATATGACC	GCGACCTTGG	TCAGTGCAA	GACCGGTGAA	650
	ATTCTCGCTA	CCACCCAACG	ACCTACCTTT	AATGCAGATA	CTAAAGAAGG	700
	AATCACTGAG	GACTTTGTTT	GGCGTGATAT	TCTTTATCAA	AGTAACTATG	750
	AACCAGGATC	AGCCTTTAAG	GTCATGATGT	TAGCTTCTTC	TATTGATAAT	800
5	AATACCTTCC	CAAGTGGAGA	ATACTTCAAT	AGCAGTGAAT	TCAAAATAGC	850
	GGATGCGACG	ACTCGAGATT	GGGATGTTAA	TGAGGGTTTG	ACTACTGGTG	900
	GGATGATGAC	TTTCTCACAA	GGTTTCGCTC	ACTCCAGTAA	TGTTGGAACG	950
	AGTCTACTTG	AACAAAAAAT	GGGAGATGCT	ACTTGGTTGG	ATTATCTAAA	1000
	ACGCTTTAAA	TTTGGGGTTC	CAACTCGCTT	TGGCTTGACA	GATGAATACG	1050
10	CTGGTCAACT	TCCAGCTGAT	AATATTGTTA	GTATTGCTCA	AAGCTCATTT	1100
	GGGCAAGGAA	TTTCAGTGAC	ACAAACACAA	ATGCTTCGTG	CCTTTACAGC	1150
	TATTGCTAAT	GATGGAGTTA	TGCTGGAGCC	AAAATTTATA	AGTGCTATTT	1200
	ATGATACTAA	CAATCAGTCT	GTACGTAAGT	CACAAAAAGA	AATAGTAGGA	1250
	AATCCTGTTT	CCAAAGAGGC	AGCAAGCACA	ACTCGAAATC	ACATGATCTT	1300
15	AGTTGGGACG	GACCCCTCTAT	ATGGAACAT	GTATAATCAC	TACACAGGAA	1350
	AGCCAATTAT	AACAGTTCCT	GGACAAAATG	TAGCAGTTAA	ATCCGGTACG	1400
	GCTCAAATCG	CTGATGAGAA	AAATGGAGGA	TACTTGGTTG	GTTCTACCAA	1450
	TTATATTTTC	TCAGTTGTGA	CTATGAATCC	TGCTGAAAAT	CCTGATTTTA	1500
	TCTTGATATG	AACGGTTCAA	CAGCCTGAGC	ATTATTCAGG	TATCCAGTTG	1550
20	GGAGAATTTG	CCACCCAAT	CTTGAGCGG	GCTTCAGCTA	TGAAAGAATC	1600
	TCTCAATCTT	CAATCTCCAG	CCAAAAATTT	AGATAAAGTT	ACGACAGAAT	1650
	CTTCTTATGC	AATGCCTAGC	ATCAAGGATA	TTTCACCTGG	TGAGTTGGCG	1700
	GAAGCCTTAC	GCCGAAATAT	TGTGCAACCA	ATCGTTGTAG	GTACTGGAAC	1750
	AAAGATTAAA	GAGACTTCTG	TAGAAGAAGG	GACCAATCTT	GCACCAAACC	1800
25	AACAAGTTCT	CCTTTTATCG	GATAAGGTAG	AAGAAATTC	AGACATGTAT	1850
	AGCTGGAAAA	AAGAGACTGC	CGAGACCTTT	GCTAAATGGT	TGGATATTGA	1900
	ACTGGAATTT	GAAGGTTTCA	GTTCCGTTGT	TCAGAAGCAA	GATGTTTCGA	1950
	CTAATACAGC	TATCAAAAAC	ATTAAAAAAA	TTAAATTAAC	TTTAGGAGAC	2000
	TAATATG					2007
30						

2) INFORMATION FOR SEQ ID NO: 1174

- 35 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 18 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

40

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1174

45 GAACGTGGTG AAGTTTCGC

18

2) INFORMATION FOR SEQ ID NO: 1175

50

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 21 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

55

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1175

60

5 2) INFORMATION FOR SEQ ID NO: 1176

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 bases
(B) TYPE: Nucleic acid
10 (C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1176

TACTGGTGTA GAAATGTTC

19

20

2) INFORMATION FOR SEQ ID NO: 1177

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
25 (B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1177

GCTCAACAAG TTCCAGATTA

20

35

2) INFORMATION FOR SEQ ID NO: 1178

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2456 bases
40 (B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

45 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Staphylococcus aureus
(B) STRAIN: NCTC8325
50 (C) ACCESSION NUMBER: X52593

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1178

ATGAACTGAT TATACTTAAC ATTAAAAAAG ATGATAACAC CTTCTACACC 50
55 TCCATATCAC AAAAAATTAT AACATTATTT TGACATAAAT ACTACATTTG 100
TAATATACTA CAAATGTAGT CTTATATAAG GAGGATATTG ATGAAAAAGA 150
TAAAAATTGT TCCACTTATT TTAATAGTTG TAGTTGTCGG GTTTGGTATA 200
TATTTTTATG CTTCAAAAGA TAAAGAAATT AATAATACTA TTGATGCAAT 250
TGAAGATAAA AATTTCAAAC AAGTTTATAA AGATAGCAGT TATATTTCTA 300
60 AAAGCGATAA TGGTGAAGTA GAAATGACTG AACGTCCGAT AAAAATATAT 350

	AATAGTTTAG	GCGTTAAAGA	TATAAACATT	CAGGATCGTA	AAATAAAAAA	400
	AGTATCTAAA	AATAAAAAAC	GAGTAGATGC	TCAATATAAA	ATTAAAAACAA	450
	ACTACGGTAA	CATTGATCGC	AACGTTCAAT	TTAATTTTGT	TAAAGAAGAT	500
	GGTATGTGGA	AGTTAGATTG	GGATCATAGC	GTCATTATTC	CAGGAATGCA	550
5	GAAAGACCAA	AGCATACATA	TTGAAAATTT	AAAATCAGAA	CGTGGTAAAA	600
	TTTtagaccg	AAACAATGTG	GAATTGGCCA	ATACAGGAAC	ACATATGAGA	650
	TTAGGCATCG	TTCCAAAGAA	TGTATCTAAA	AAAGATTATA	AAGCAATCGC	700
	TAAAGAACTA	AGTATTTCTG	AAGACTATAT	CAACAACAAA	TGGATCAAAA	750
	TTGGGTACAA	GATGATACCT	TCGTTCCACT	TAAAAACCGT	TAAAAAAATG	800
10	GATGAATATT	TAAGTGATTT	CGCAAAAAAA	TTTCATCTTA	CAACTAATGA	850
	AACAGAAAGT	CGTAACTATC	CTCTAGAAAA	AGCGACTTCA	CATCTATTAG	900
	GTTATGTTGG	TCCCATTAAAC	TCTGAAGAAT	TAAAACAAAA	AGAATATAAA	950
	GGCTATAAAG	ATGATGCAGT	TATTGGTAAA	AAGGGACTCG	AAAAACTTTA	1000
	CGATAAAAAG	CTCCAACATG	AAGATGGCTA	TCGTGTCACA	ATCGTTGACG	1050
15	ATAATAGCAA	TACAATCGCA	CATACATTAA	TAGAGAAAAA	GAAAAAGAT	1100
	GGCAAAGATA	TTCAACTAAC	TATTGATGCT	AAAGTTCAAA	AGAGTATTTA	1150
	TAACAACATG	AAAAATGATT	ATGGCTCAGG	TACTGCTATC	CACCCTCAAA	1200
	CAGGTGAATT	ATTAGCACTT	GTAAGCACAC	CTTCATATGA	CGTCTATCCA	1250
	TTTATGTATG	GCATGAGTAA	CGAAGAATAT	AATAAATTAA	CCGAAGATAA	1300
20	AAAAGAACCT	CTGCTCAACA	AGTTCAGAT	TACAACTTCA	CCAGGTTCAA	1350
	CTCAAAAAAT	ATTAACAGCA	ATGATTGGGT	TAAATAACAA	AACATTAGAC	1400
	GATAAAACAA	GTTATAAAAT	CGATGGTAAA	GGTTGGCAAA	AAGATAAATC	1450
	TTGGGGTGGT	TACAACGTTA	CAAGATATGA	AGTGGTAAAT	GGTAATATCG	1500
	ACTTAAACAA	AGCAATAGAA	TCATCAGATA	ACATTTTCTT	TGCTAGAGTA	1550
25	GCACTCGAAT	TAGGCAGTAA	GAAATTTGAA	AAAGGCATGA	AAAAACTAGG	1600
	TGTTGGTGAA	GATATACCAA	GTGATTATCC	ATTTTATAAT	GCTCAAATTT	1650
	CAAACAAAAA	TTTAGATAAT	GAAATATTAT	TAGCTGATTC	AGGTTACGGA	1700
	CAAGGTGAAA	TACTGATTAA	CCCAGTACAG	ATCCTTTCAA	TCTATAGCGC	1750
	ATTAGAAAAT	AATGGCAATA	TTAACGCACC	TCACTTATTA	AAAGACACGA	1800
30	AAAACAAAGT	TTGGAAGAAA	AATATTATTT	CCAAAGAAAA	TATCAATCTA	1850
	TTAAATGATG	GTATGCAACA	AGTCGTAAAT	AAAACACATA	AAGAAGATAT	1900
	TTATAGATCT	TATGCAAACT	TAATTGGCAA	ATCCGGTACT	GCAGAACTCA	1950
	AAATGAAACA	AGGAGAAAGT	GGCAGACAAA	TTGGGTGGTT	TATATCATAT	2000
	GATAAAGATA	ATCCAAACAT	GATGATGGCT	ATTAATGTTA	AAGATGTACA	2050
35	AGATAAAGGA	ATGGCTAGCT	ACAATGCCAA	AATCTCAGGT	AAAGTGTATG	2100
	ATGAGCTATA	TGAGAACGGT	AATAAAAAAT	ACGATATAGA	TGAATAACAA	2150
	AACAGTGAAG	CAATCCGTAA	CGATGGTTGC	TTCACGTGTT	TATTATGAAT	2200
	TATTAATAAG	TGCTGTTACT	TCTCCCTTAA	ATACAATTTT	TTCATTTTCA	2250
	TTGTATGTTG	AAAGTGACAC	TGTAACGAGT	CCATTTTCTT	TTTTTATGGA	2300
40	TTTCTTATTT	GTAATTTTCA	CGATAACGTA	CAATGTATTA	CCTGGTATAC	2350
	AGTTTAATAA	ATTTAACGTT	ATTCATTTGT	GTTCCTGCTA	CAACTTCTTC	2400
	TCCGTATTTA	CCTTCTTCTA	CCCATAATTT	AAATGATATT	GAAAGTGTAT	2450
	GCATGC					2456

45

2) INFORMATION FOR SEQ ID NO: 1179

- (i) SEQUENCE CHARACTERISTICS:
- 50 (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

55 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1179

60 ATTTGGTGAC GGGTGACTTT

20

2) INFORMATION FOR SEQ ID NO: 1180

- 5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

10

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1180

15 TCCACCGTTG CCAATCGCA

19

2) INFORMATION FOR SEQ ID NO: 1181

20

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
25 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1181

30

AGCAGCTTAC TAGATGCCGT

20

35 2) INFORMATION FOR SEQ ID NO: 1182

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
40 (C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1182

AACTGCAAGA GATCCTTTGG

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50

2) INFORMATION FOR SEQ ID NO: 1183

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2535 bases
55 (B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

60

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
 (B) STRAIN: 175
 (C) ACCESSION NUMBER: M18729

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(xii) SEQUENCE DESCRIPTION: SEQ ID NO: 1183

	ATGGCGATAG	AAAAGCTATC	ACCCGGCATG	CAACAGTATG	TGGATATTAA	50
10	AAAGCAATAT	CCAGATGCTT	TTTTGCTCTT	TCGGATGGGT	GATTTTATG	100
	AATTATTTTA	TGAGGATGCG	GTCAATGCTG	CGCAGATTCT	GGAAATTTCC	150
	TTAACGAGTC	GCAACAAGAA	TGCCGACAAT	CCGATCCCCTA	TGGCGGGTGT	200
	TCCCTATCAT	TCTGCCCAAC	AGTATATCGA	TGTCTTGATT	GAGCAGGGTT	250
	ATAAGGTGGC	TATCGCAGAG	CAGATGGAAG	ATCCTAAACA	AGCAGTTGGG	300
15	GTTGTAAAC	GAGAGGTTGT	TCAGGTCATT	ACGCCAGGGA	CAGTGGTCGA	350
	TAGCAGTAAG	CCGGACAGTC	AGAATAATTT	TTTGGTTTCC	ATAGACCGCG	400
	AAGGCAATCA	ATTTGGCCTA	GCTTATATGG	ATTTGGTGAC	GGGTGACTTT	450
	TATGTGACAG	GTCTTTTGA	TTTCACGCTG	GTTTGTGGGG	AAATCCGTAA	500
	CCTCAAGGCT	CGAGAAGTGG	TGTTGGGTTA	TGACTTGTCT	GAGGAAGAAG	550
20	AACAAATCCT	CAGCCGCCAG	ATGAATCTGG	TACTCTCTTA	TGAAAAAGAA	600
	AGCTTTGAAG	ACCTTCATTT	ATTGGATTGT	CGATTGGCAA	CGGTGGAGCA	650
	AACGGCATCT	AGTAAGCTGC	TCCAGTATGT	TCATCGGACT	CAGATGAGGG	700
	AATTGAACCA	CCTCAAACCT	GTTATCCGCT	ACGAAATTAA	GGATTTCTTG	750
	CAGATGGATT	ATGCGACCAA	GGCTAGTCTG	GATTTGGTTG	AGAATGCTCG	800
25	CTCAGGTAAG	AAACAAGGCA	GTCTTTTCTG	GCTTTTGGAT	GAAACCAAAA	850
	CGGCTATGGG	GATGCGTCTC	TTGCGTTCTT	GGATTCATCG	CCCCTTGATT	900
	GATAAGGAAC	GAATCGTCCA	ACGTCAAGAA	GTAGTGCAGG	TCTTTCTCGA	950
	CCATTTCTTT	GAGCGTAGTG	ACTTGACAGA	CAGTCTCAAG	GGTGTTTATG	1000
	ACATTGAGCG	CTTGCTAGT	CGTGTTCCTT	TTGGCAAAAC	CAATCCAAAG	1050
30	GATCTCTTGC	AGTTGGCGAC	TACCTTGTCT	AGTGTGCCAC	GGATTCGTGC	1100
	GATTTTAGAA	GGGATGGAGC	AACCTACTCT	AGCCTATCTC	ATCGCACAAAC	1150
	TGGATGCAAT	CCCTGAGTTG	GAGAGTTTGA	TTAGCGCAGC	GATTGCTCCT	1200
	GAAGCTCCTC	ATGTGATTAC	AGATGGGGGA	ATTATCCGGA	CTGGATTGGA	1250
	TGAGACTTTA	GACAAGTATC	GTTGCGTTC	CAGAGAAGGG	ACTAGCTGGA	1300
35	TTGCTGAGAT	TGAGGCTAAG	GAGCGAGAAA	ACTCTGGTAT	CAGCACGCTC	1350
	AAGATTGACT	ACAATAAAAA	GGATGGCTAC	TATTTTCATG	TGACCAATTC	1400
	GCAACTGGGA	AATGTGCCAG	CCCCTTTTTT	CCGCAAGGCG	ACGCTGAAAA	1450
	ACTCAGAACG	CTTTGGAACC	GAAGAATTAG	CCCGTATCGA	GGGAGATATG	1500
	CTTGAGGCGC	GTGAGAAGTC	AGCCAACCTC	GAATACGAAA	TATTTATGCG	1550
40	CATTCGTGAA	GAGGTCGGCA	AGTACATCCA	GCGTTTACAA	GCTCTAGCCC	1600
	AAGGAATTGC	GACGGTTGAT	GTCTTACAGA	GTCTGGCGGT	TGTGGCTGAA	1650
	ACCCAGCATT	TGATTGAC	TGAGTTTGGT	GACGATTCAC	AAATTGATAT	1700
	CCGGAAAGGG	CGCCATGCTG	TCGTTGAAAA	GGTTATGGGG	GCTCAGACCT	1750
	ATATTCCAAA	TACGATTGAG	ATGGCAGAAG	ATACCAGTAT	TCAATTGGTT	1800
45	ACAGGGCCAA	ACATGAGTGG	GAAGTCTACC	TATATGCGTC	AGTTAGCCAT	1850
	GACGGCGGTT	ATGGCCCAGC	TGGGTTCCCTA	TGTTCTTGCT	GAAAGCGCCC	1900
	ATTTACCGAT	TTTTGATGCG	ATTTTATACC	GTATCGGAGC	AGCAGATGAC	1950
	TTGGTTTCGG	GTCAGTCAAC	CTTTATGGTG	GAGATGATGG	AGGCCAATAA	2000
	TGCCATTTTCG	CATGCGACCA	AGAACTCTCT	CATTCTCTTT	GATGAATTGG	2050
50	GACGTGGAAC	TGCAACTTAT	GACGGGATGG	CTCTTGCTCA	GTCCATCATC	2100
	GAATATATCC	ATGAGCACAT	CGGAGCTAAG	ACCCTCTTTG	CGACCCACTA	2150
	CCATGAGTTG	ACTAGTCTGG	AGTCTAGTTT	ACAACACTTG	GTCAATGTCC	2200
	ACGTGGCAAC	TTTGGAGCAG	GATGGGCAGG	TCACCTTCCT	TCACAAGATT	2250
	GAACCGGGAC	CAGCTGATAA	ATCCTACGGT	ATCCATGTTG	CCAAGATTGC	2300
55	TGGCTTGCCA	GCAGACCTTT	TAGCAAGGGC	GGATAAGATT	TTGACTCAGC	2350
	GTCAGAATCA	AGGAACAGAG	AGTCCTCCTC	CCATGAGACA	AACTAGTGCT	2400
	GTCAGTGAAC	AGATTTCACT	CTTTGATAGG	GCAGAAGAGC	ATCCTATCCT	2450
	AGCAGAATTA	GCTAAACTGG	ATGTGTATAA	TATGACACCT	ATGCAGGTTA	2500
60	TGAATGTCTT	AGTAGAGTTA	AAACAGAAAC	TATAA		2535

2) INFORMATION FOR SEQ ID NO: 1184

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 623 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

10 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
 (B) STRAIN: StrR-05

15 (xiii) SEQUENCE DESCRIPTION: SEQ ID NO: 1184

	TGACGGGTGA	CTTTTATGTG	ACAGGTCTTT	TGGATTTCAC	GCTGGTTTGT	50
	GGGGAAATCC	GTAACCTCAA	GGCTCGAGAA	GTGGTGTG	GTTATGACTT	100
20	GTCTGAGGAA	GAAGAACAAA	TCCTCAGCCG	CCAGATGAAT	CTGGTACTCT	150
	CTTATGAAAA	AGAAAGCTTT	GAAGACCTTC	ATTTATTGGA	TTTGCGATTG	200
	GCAACGGTGG	AGCAAACGGC	ATCTAGTAAG	CTGCTCCAGT	ATGTTTCATCG	250
	GACTCAGATG	AGGGAATTGA	ACCACCTCAA	ACCTGTTATC	CGATACGAAA	300
	TTAAGGATTT	CTTGCAGATG	GATTATGCGA	CCAAGGCTAG	TCTGGATTG	350
25	GTTGAGAATG	CTCGCTCAGG	TAAGAAACAA	GGCAGTCTTT	TCTGGCTTTT	400
	GGATGAAACC	AAAACGGCTA	TGGGGATGCG	TCTCTTGCGT	TCTTGGAATC	450
	ATCGCCCCTT	GATTGATAAG	GAACGAATCG	TCCAACGTCA	AGAAGTAGTG	500
	CAGGTCTTTC	TCGACCATTT	CTTTGAGCGT	AGTGACTTGA	CAGACAGTCT	550
	CAAGGGTGTT	TATGACATTG	AGCGCTTGGC	TAGTCGTGTT	TCTTTTGGCA	600
30	AAACCAATCC	AAAGGATCTC	TTG			623

2) INFORMATION FOR SEQ ID NO: 1185

35

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 621 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 40 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 45 (A) ORGANISM: *Streptococcus pneumoniae*
 (B) STRAIN: StrR-06

(xiv) SEQUENCE DESCRIPTION: SEQ ID NO: 1185

50	TGACGGGTGA	CTTTTATGTG	ACAGGTCTTT	TGGATTTCAC	GCTGGTTTGT	50
	GGGGAAATCC	GTAACCTCAA	GGCTCGAGAA	GTGGTGTG	GTTATGACTT	100
	GTCTGAGGAA	GAAGAACAAA	TCCTCAGCCG	CCAGATGAAT	CTGGTACTCT	150
	CTTATGAAAA	AGAAAGCTTT	GAAGACCTTC	ATTTATTGGA	TTTGCGATTG	200
	GCAACGGTGG	AGCAAACGGC	ATCTAGTAAG	CTGCTCCAGT	ATGTTTCATCG	250
55	GACTCAGATG	AGGGAATTGA	ACCACCTCAA	ACCTGTTATC	CGATACGAAA	300
	TTAAGGATTT	CTTGCAGATG	GATTATGCGA	CCAAGGCTAG	TCTGGATTG	350
	GTTGAGAATG	CTCGCTCAGG	TAAGAAACAA	GGCAGTCTTT	TCTGGCTTTT	400
	GGATGAAACC	AAAACGGCTA	TGGGGATGCG	TCTCTTGCGT	TCTTGGAATC	450
	ATCGCCCCTT	GATTGATAAG	GAACGAATCG	TCCAACGTCA	AGAAGTAGTG	500
60	CAGGTCTTTC	TCGACCATTT	CTTTGAGCGT	AGTGACTTGA	CAGACAGTCT	550

CAAGGGTGTT TATGACATTG AGCGCTTGGC TAGTCGTGTT TCTTTTGGCA 600
 AAACCAATCC AAAGGATCTC T 621

5

2) INFORMATION FOR SEQ ID NO: 1186

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 622 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
 (B) STRAIN: StrR-11

(xv) SEQUENCE DESCRIPTION: SEQ ID NO: 1186

TGACGGGTGA CTTTATGTG ACAGGTCTTT TGGATTTCAC GCTGGTTTGT 50
 GGGGAAATCC GTAACCTCAA GGCTCGAGAA GTGGTGTTGG GTTATGACTT 100
 GTCTGAGGAA GAAGAACAAA TCCTCAGCCG CCAGATGAAT CTGGTACTCT 150
 25 CTTATGAAAA AGAAAGCTTT GAAGACCTTC ATTTATTGGA TTTGCGATTG 200
 GCAACGGTGG AGCAAACGGC ATCTAGTAAG CTGCTCCAGT ATGTTTCATCG 250
 GACTCAGATG AGGGAATTGA ACCACCTCAA ACCTGTTATC CGCTACGAAA 300
 TTAAGGATTT CTTGCAGATG GATTATGCGA CCAAGGCTAG TCTGGATTG 350
 GTTGAGAATG CTCGCTCAGG TAAGAAACAA GGCAGTCTTT TCTGGCTTTT 400
 30 GGATGAAACC AAAACGGCTA TGGGGATGCG TCTCTTGCGT TCTTGGATTG 450
 ATCGCCCCCTT GATTGATAAG GAACGAATCG TCCAACGTCA AGAAGTAGTG 500
 CAGGTCTTTC TCGACCATT CTTTGAGCGT AGTGAATTGA CAGACAGTCT 550
 CAAGGGTGTT TATGACATTG AGCGCTTGGC TAGTCGTGTT TCTTTTGGCA 600
 AAACCAATCC AAAGGATCTC TT 622

35

2) INFORMATION FOR SEQ ID NO: 1187

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 622 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

45

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
 50 (B) STRAIN: StrR-55

(ix) SEQUENCE DESCRIPTION: SEQ ID NO: 1187

TGACGGGTGA CTTTATGTG ACAGGTCTTT TGGATTTCAC GCTGGTTTGT 50
 55 GGGGAAATCC GTAACCTCAA GGCTCGAGAA GTGGTGTTGG GTTATGACTT 100
 GTCTGAGGAA GAAGAACAAA TCCTCAGCCG CCAGATGAAT CTGGTACTCT 150
 CTTATGAAAA AGAAAGCTTT GAAGACCTTC ATTTATTGGA TTTGCGATTG 200
 GCAACGGTGG AGCAAACGGC ATCTAGTAAG CTGCTCCGGT ATGTTTCATCG 250
 GACTCAGATG AGGGAATTGA ACCACCTCAA ACCTGTTATC CGCTACGAAA 300
 60 TTAAGGATTT CTTGCAGATG GATTATGCGA CCAAGGCTAG TCTGGATTG 350

	GTTGAGAATG	CTCGCTCAGG	TAAGAAACAA	GGCAGTCTTT	TCTGGCTTTT	400
	GGATGAAACC	AAAACGGCTA	TGGGGATGCG	TCTCTTGCGT	TCTTGATTTC	450
	ATCGCCCCTT	GATTGATAAG	GAACGAATCG	TCCAACGTCA	AGAAGTAGTG	500
	CAGGTCTTTC	TCGACCATT	CTTTGAGCGT	AGTGACTTGA	CAGACAGTCT	550
5	CAAGGGTGTT	TATGACATTG	AGCGCTTGGC	TAGTCGTGTT	TCTTTTGGCA	600
	AAACCAATCC	AAAGGATCTC	TT			622

10 2) INFORMATION FOR SEQ ID NO: 1188

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 599 bases
 - (B) TYPE: Nucleic acid
 - 15 (C) STRANDEDNESS: Double
 - (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Streptococcus oralis*
 - (B) STRAIN: ATCC 35037

25 (ix) SEQUENCE DESCRIPTION: SEQ ID NO: 1188

25	GGGTGACTTT	TATGTAACGG	GGCTATTGGA	TTTCACGTTG	GTTTGTGGGG	50
	AAATTTCGAA	TCTCAAGGCT	AGAGAAGTGG	TGCTGGGTTA	TGACTTGTCT	100
	GAGGAAGAAG	AACAAATCCT	CAGTCGTCAG	ATGAATCTGG	TGCTTTCTTA	150
	TGAGAAGGAA	GGCTTTGAGG	ACCTTCATTT	ACTGGATCCA	CGACTGGCAG	200
30	CTGTGGAGCA	AGCGGCAGCT	AGTAAGCTCC	TCCAGTATGT	TCACCGGACC	250
	CAGATGCGGG	AATTGAACCA	CCTCAAACCA	GTTATCCGCT	ATGAAATCAA	300
	AGATTTCTTA	CAGATGGACT	ATGCGACCAA	GGCTAGTCTG	GATTTGGTTG	350
	AGAATGCCCG	TTCAGGCAAG	AAGCAAGGCA	GTCTTTTCTG	GCTTTTAGAT	400
	GAAACCAAGA	CGGCTATGGG	AATGCGTCTC	TTGCGTTCTT	GGATTCATCG	450
35	TCCTTTGATT	GATAAGGAGC	GAATCGTCCA	GCGTCAAGAG	GTGGTGCAGG	500
	TCTTTCTTGA	CCACTTCTTT	GAGCGTAGTG	ATTTAACGGA	CAGTCTTAAG	550
	GGTGTTTATG	ATATCGAACG	CTTGCGTAGT	CGGGTTTCTT	TTGGCAAGA	599

40

2) INFORMATION FOR SEQ ID NO: 1189

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 624 bases
 - 45 (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Double
 - (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Streptococcus mitis*
 - (B) STRAIN: ATCC 49456

55 (x) SEQUENCE DESCRIPTION: SEQ ID NO: 1189

55	GGTGACGGGT	GACTTTTATG	TGACAGGTCT	TTTGGATTTT	ACGCTGGTTT	50
	GTGGGGAAAT	CCGCAATCTC	AAGGCTCGAG	AAGTGGTGCT	GGGTATGAC	100
	TTGTCTGAGG	AAGAAGAACA	GATCCTTAGT	CGTCAGATGA	ATCTGGTACT	150
60	TTCCTATGAA	AAAGAAGGCT	TTGAAGACCT	TCATTTACTG	GATTCACGAT	200

	TGGCAGCTGT	GGAGCAAGCG	GCATCTAGTA	AACTGCTTCA	GTATGTTTCAT	250
	CGGACTCAGA	TGAGGGAATT	GAACCACCTC	AAGCCTGTTA	TCCGCTATGA	300
	AATCAAAGAT	TTTTTGAGAA	TGGATTATGC	GACCAAGGCT	AGTCTGGATT	350
	TGGTTGAGAA	TGCCCCGTTCA	GGCAAGAAGC	AAGGTAGTCT	TTTTTGGCTT	400
5	TTGGATGAAA	CCAAAACAGC	TATGGGAATG	CGTCTCTTGC	GGTCTTGAT	450
	TCATCGCCCC	CTGATTGATA	AGGAACGAAT	TGTCCAACGC	CAAGAAGTTG	500
	TGCAGGTCTT	TCTCGACCAT	TTCTTTGAGC	GTAGTGATTT	GACAGACAGT	550
	CTCAAGGGTG	TTTATGACAT	TGAGCGCTTG	GCTAGTCGTG	TTTCTTTTGG	600
	CAAAACCAAT	CCAAAGGATC	TCTT			624

10

2) INFORMATION FOR SEQ ID NO: 1190

15 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 599 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

20 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus mitis*
- (B) STRAIN: LSPQ 2583

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1190

	TGACGGGTGA	CTTTCAGGTG	ACTAGTTTAG	AGGACTTTGT	CTTGGTCTGC	50
30	GGGGAATCC	GCAATTTGAA	AGCTAGGGAA	GTGGTGCTGG	GCTATGCCTT	100
	GCCAGAAGCT	GAGGAGCAGG	TTTTGGCTGG	ACAGATGAAC	CTTTTACTGT	150
	CCTATGTGGA	GAAGGTTTTG	GAGGATGTTT	AGCTGCTGGG	CGAGGAGCTG	200
	TCTCCTATGG	AGCGTCAGGC	AGCAGGGAAA	CTGCTGGAGT	ATGTGCACCG	250
	GACCCAGATG	AGGGAGCTCA	GCCATTTGAA	GAAGGCTCAG	CATTATGAAA	300
35	TCAAGGACTT	CCTGCAAATG	GACTATGCCA	CCAAGGCGAG	TCTGGATTTG	350
	ACAGAAAATG	CTCGCTCGGG	CAAGAAGCAC	GGCAGTCTTT	ATTGGCTGAT	400
	GGACGAGACT	AAGACGGCCA	TGGGCGGCCG	CATGCTGCGC	TCTTGGATCC	450
	AGCGTCCGCT	GATTGATGAA	GCGCGAATTA	GCCAGCGACA	GAATGTCGTT	500
	GAGGTTTTTC	TGGATCATTT	CTTTGAGCGG	AGTGATTGTA	CGGAGAGCCT	550
40	CAAGGGGGTC	TATGATATCG	AGCGGCTGGC	TAGTCGGGTG	TCTTTTGGC	599

2) INFORMATION FOR SEQ ID NO: 1191

45 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 622 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

50 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus mitis*
- (B) STRAIN: ATCC 903

55

(ix) SEQUENCE DESCRIPTION: SEQ ID NO: 1191

60	TGACGGGTGA	CTTTCAGGTG	ACTAGTTTAG	AGGACTTTGC	CCTGGTCTGC	50
----	------------	------------	------------	------------	------------	----

	GGGGAATCC	GTAATTTGAA	GGCTAGGGAA	GTGGTGCTGG	GCTATGCTTT	100
	GCCAGAAGCT	GAGGAGCAGG	TCTTGGCTGG	ACAGATGAAT	CTTTTGCTGT	150
	CCTATGTACA	GACGGCCTTG	GACGATGTCC	AGCTGCTGGG	CGAGGAACCTG	200
	TCTCCTATGG	AGCGTCAGGC	AGCGGGGAAA	TTGCTAGAGT	ATGTGCACCG	250
5	GACCCAGATG	AGGGAGCTCA	GCCATTTGAA	GAAGGCCAG	CATTATGAAA	300
	TCAAGGACTT	TCTGCAAATG	GATTATGCTA	CCAAGGCGAG	TCTGGATTG	350
	ACAGAAAATG	CTCGCTCGGG	TAAGAAACAC	GGCAGTCTTT	ATTGGCTGAT	400
	GGACGAGACC	AAGACGGCCA	TGGGCGGCCG	TATGCTGCGC	TCTTGATCC	450
	AGCGTCCGTT	GATTGATGAA	GTGCGAATTA	GCCAGCGGCA	GAATGTCGTC	500
10	GAGGTTTTTC	TGGAACATTT	CTTTGAGCGG	AGTGATTGTA	CGGAGAGCCT	550
	CAAGGGAGTC	TATGATATCG	AGCGGCTGGC	TAGTCGGGTG	TCTTTTGGCA	600
	AGACCAATCC	AAAGGATCTC	TT			622

15

2) INFORMATION FOR SEQ ID NO: 1192

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1192

GGTAAAACAG GAACCTCTAA CT

22

30

2) INFORMATION FOR SEQ ID NO: 1193

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1193

GGTAAGACAG GTACTTCTAA CT

22

45

2) INFORMATION FOR SEQ ID NO: 1194

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1194

60

5 2) INFORMATION FOR SEQ ID NO: 1195

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 24 bases
 (B) TYPE: Nucleic acid
10 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1195

CATTTC AAGT AACACAAC TGAATC

24

20

2) INFORMATION FOR SEQ ID NO: 1196

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 24 bases
25 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1196

GCCATTTC AAGT GTAATACAAC AGAA

24

35

2) INFORMATION FOR SEQ ID NO: 1197

- (i) SEQUENCE CHARACTERISTICS:
40 (A) LENGTH: 25 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

45 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1197

CAAACGCCAT TTCAAGTAAT ACAAC

25

50

2) INFORMATION FOR SEQ ID NO: 1198

- 55 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 381 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
60 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 5 (A) ORGANISM: *Staphylococcus saprophyticus*
(B) STRAIN: ATCC 43867

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1198

```
10 AACGGGCGTC TCGATAGAAA AACACGTGAA AATCCCAATG ATTATAAACA 50
    ATCAATATAC GATTTTGCTG AAGCTGTAAC AAAAGGTATT AAGGAACAAA 100
    CAAATAAAAA TTAATAGGCA ACTTAACCAG AATCGTTAAA ACTATATGAC 150
    GATTCTGGTT TTTTAAATTC AAAAAGTTT CTAAAAAATT TACTTGCTTC 200
    TTAAAGTAT AGGTATGAAA TACAATTGAT TAAAATAGTA AAGGAAATGA 250
    ATCATGAAAC AATTAATAA GCCTTTATAC TTTTACCTAT TACTTTTAT 300
15 TACAACAACG CTGATTGGCG CGTTACTATT ATATTGCCA ATCACAKGTA 350
    AACATCCTAT TGATTTTGTG GACGCCCCGT A 381
```

20 2) INFORMATION FOR SEQ ID NO: 1199

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 25 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1199

GTATTAAAGA AGATATCCAA AAAGC 25

35 2) INFORMATION FOR SEQ ID NO: 1200

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 25 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1200

TCAAAGAAGA AACTAAAAA GCTGT 25

50

2) INFORMATION FOR SEQ ID NO: 1201

(i) SEQUENCE CHARACTERISTICS:

- 55 (A) LENGTH: 19 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

60 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1201

AACGTAGGTG TCCTTCTTC

19

5

2) INFORMATION FOR SEQ ID NO: 1202

10 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

15

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1202

20 GTGTTGAAAT GTCCGTAAA CA

22

2) INFORMATION FOR SEQ ID NO: 1203

25

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

30

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1203

35

GGIGARMGIG GIAAYGARAT G

21

40 2) INFORMATION FOR SEQ ID NO: 1204

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

45

(ii) MOLECULE TYPE: DNA

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1204

GCIAAYAACI TCIWMYATGC C

21

55

2) INFORMATION FOR SEQ ID NO: 1205

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid

60

(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1205

AAYACITCIA WYATGCCIGT

20

10

2) INFORMATION FOR SEQ ID NO: 1206

(i) SEQUENCE CHARACTERISTICS:

15

(A) LENGTH: 19 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1206

CKISRIGTIG ARTCIGCCA

19

25

2) INFORMATION FOR SEQ ID NO: 1207

(i) SEQUENCE CHARACTERISTICS:

30

(A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1207

40

CCITCITCWC CIGGCATYTC

20

2) INFORMATION FOR SEQ ID NO: 1208

45

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 25 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1208

55

TCAAAAAGTT TTCTAAAAAA TTTAC

25

60 2) INFORMATION FOR SEQ ID NO: 1209

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 bases
(B) TYPE: Nucleic acid
5 (C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1209

ACGGGCGTCC ACAAATCAA TAGGA

25

15

2) INFORMATION FOR SEQ ID NO: 1210

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 bases
20 (B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1210

ACCAGCTTGC CCAATACAAA GG

22

30

2) INFORMATION FOR SEQ ID NO: 1211

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 bases
35 (B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

40 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1211

ATTCTTGTA CAGGCTTTGA TCCC

24

45

2) INFORMATION FOR SEQ ID NO: 1212

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 bases
50 (B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

55

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1212

60 CCICCGIRGIG GIGAIACIGC WCC

23

2) INFORMATION FOR SEQ ID NO: 1213

5

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

10

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1213

15

AARGGIGGIA CIGCIGCIAT HCCIGG

26

20 2) INFORMATION FOR SEQ ID NO: 1214

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

25

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1214

30

GGTAAAACAG GTACCTCTAA CTA

23

35 2) INFORMATION FOR SEQ ID NO: 1215

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1337 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

40

(ii) MOLECULE TYPE: Genomic DNA

45

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pyogenes*
- (B) STRAIN: D471
- (C) ACCESSION NUMBER: X65717

50

(xii) SEQUENCE DESCRIPTION: SEQ ID NO: 1215

	AACAAAATAA	AAGAACTTAC	CTATTTTCCA	TCCAAAATGT	TTAGCAATCA	50
	TCATCTGCAA	GGCAACGTAT	TGCATGGCAT	TGATGTGATG	AGCAACTAAT	100
55	ATGTCATTAG	AACGTTGCGT	CAAACTAGCA	TCTAAATAAA	GATCGAAATG	150
	CAGTTATCAA	AAATGCAAGC	TCCTATCGGC	CCTTGTTTTA	ATTATTACTC	200
	ACATTGCCTT	AATGTATTTA	CTTGCTTATT	ATTAACTTTT	TTGCTAAGTT	250
	AGTAGCGTCA	GTTATTCATT	GAAAGGACAT	TATTATGAAA	ATTCTTGTA	300
	CAGGCTTTGA	TCCCTTTGGC	GGCGAAGCTA	TTAATCCTGC	CCTTGAAGCT	350
60	ATCAAGAAAT	TGCCAGCAAC	CATTCATGGA	GCAGAAATCA	AATGTATTGA	400

	AGTTCCAACG	GTTTTTCAAA	AATCTGCCGA	TGTGCTCCAG	CAGCATATCG	450
	AAAGCTTTC	ACCTGATGCA	GTCCTTTGTA	TTGGGCAAGC	TGGTGGCCGG	500
	ACTGGACTAA	CGCCAGAACG	CGTTGCCATT	AATCAAGACG	ATGCTCGCAT	550
	TCCTGATAAC	GAAGGGAATC	AGCCTATTGA	TACACCTATT	CGTGCAGATG	600
5	GTAAAGCAGC	TTATTTTTC	ACCTTGCCAA	TCAAAGCGAT	GGTTGCTGCC	650
	ATTCATCAGG	CTGGGCTTCC	TGCTTCTGTT	TCTAATACAG	CTGGTACCTT	700
	TGTTTGCAAT	CATTTGATGT	ATCAAGCCCT	TTACTTAGTG	GATAAATATT	750
	GTCCAAATGC	CAAAGCTGGG	TTTATGCATA	TTCCCTTTAT	GATGGAACAG	800
	GTTGTTGATA	AACCTAATAC	AGCTGCCATG	AACCTCGATG	ATATTACAAG	850
10	AGGAATTGAG	GCTGCTATTT	TTGCCATTGT	CGATTTCAAA	GATCGTTCCG	900
	ATTTAAAACG	TGTAGGGGGC	GCTACTCACT	GACTGTGACG	CTACTAAACC	950
	TATTTTAAAA	AAACAGAGAT	ATGAACCTAAC	TCTGTTTTTT	TTGTGCTAAA	1000
	AATGAAAGAC	CTAGGGAAC	TTTTCATCGG	TCTTTCTCAA	TTGTCATCTT	1050
	AATCTAATAC	TACTTCTAAC	ATCAGCGGGT	ATAGTTTGCC	AGTAATTAAG	1100
15	AAACGTTGTT	GATCTAAATG	AGCAATCCCA	TTCAAAACAT	TAAGGTCAGG	1150
	GTAATGGGAC	TTATCAAGAT	TTAAGGCTTT	TAACAAAGGA	CTAATATCAT	1200
	AGGTGGCTAC	CACCTTTCCA	GAATCAGGTT	GGAGTTTGAC	AATAGTATTG	1250
	GTTTGCCAAA	TATTGGCATA	GAGATAACCA	TCTACATACT	CTAATTCGTT	1300
	AAGCATTGAG	ATAGGGACAC	TTTCTATAGC	AACTAGT		1337

2) INFORMATION FOR SEQ ID NO: 1216

- 25 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 23 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

30 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1216

35 GGTAAGACTG GTACATCAAA CTA

23

2) INFORMATION FOR SEQ ID NO: 1217

- 40 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 25 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1217

50 CAAATGCCAT TTCAAGTAAC ACAAC

25

55 2) INFORMATION FOR SEQ ID NO: 1218

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 25 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1218

CAAACGCCAT TTCAAGTAAC ACAAC

25

10

2) INFORMATION FOR SEQ ID NO: 1219

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 25 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1219

CAAATGCTAT TTCAAGTAAT ACAAC

25

25

2) INFORMATION FOR SEQ ID NO: 1220

(i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 25 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1220

CAAACGCCAT TTCAAGTAAT ACGAC

25

40

2) INFORMATION FOR SEQ ID NO: 1221

(i) SEQUENCE CHARACTERISTICS:

45 (A) LENGTH: 23 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1221

55 GAYACICCCIG GICAYGTIGA YTT

23

60

2) INFORMATION FOR SEQ ID NO: 1222

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1222

10

ATYGAYACIC CIGGICAYGT IGAYTT

26

15 2) INFORMATION FOR SEQ ID NO: 1223

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1223

AYITCIARRT GIARYTCRCC CATICC

26

30

2) INFORMATION FOR SEQ ID NO: 1224

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1224

CCIGYIHTIY TIGARCCIAT IATG

24

45

2) INFORMATION FOR SEQ ID NO: 1225

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

55 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1225

TAICCRAACA TYTCISMIAR IGGIAC

26

60

2) INFORMATION FOR SEQ ID NO: 1226

- 5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

10

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1226

15 GTIRMRTAIC CRAACATYTC

20

2) INFORMATION FOR SEQ ID NO: 1227

20

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 26 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
25 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1227

30

GTICCIYTIK CIGARATGTT YGGITA

26

35 2) INFORMATION FOR SEQ ID NO: 1228

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 29 bases
 (B) TYPE: Nucleic acid
40 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1228

GTICCIYTIK CIGARATGTT YGGITAYGC

29

50 2) INFORMATION FOR SEQ ID NO: 1229

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 26 bases
 (B) TYPE: Nucleic acid
55 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

60 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1229

TCCATYTGIG CIGCICCI GT IATCAT

26

5 2) INFORMATION FOR SEQ ID NO: 1230

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2145 bases
 (B) TYPE: Nucleic acid
 10 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

15 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Escherichia coli*
 (D) ACCESSION NUMBER: X00415

(xiii) SEQUENCE DESCRIPTION: SEQ ID NO: 1230

20 TGAACGCCTA AAAGATAAAC GAGGAAACAA ATGGCTCGTA CAACACCCAT 50
 CGCACGCTAC CGTAACATCG GTATCAGTGC GCACATCGAC GCCGGTAAAA 100
 CCACTACTAC CGAACGTATT CTGTTCTACA CCGGTGTAAC CCATAAAATC 150
 GGTGAAGTTC ATGACGGCGC TGCAACCATG GACTGGATGG AGCAGGAGCA 200
 25 GGAACGTGGT ATTACCATCA CTTCCGCTGC GACTACTGCA TTCTGGTCTG 250
 GTATGGCTAA GCAGTATGAG CCGCATCGCA TCAACATCAT CGACACCCCG 300
 GGGCACGTTG ACTTCACAAT CGAAGTAGAA CGTTCATGCG GTGTTCTCGA 350
 TGGTGCGGTA ATGGTTTACT GCGCAGTTGG TGGTGTTCAG CCGCAGTCTG 400
 AAACCGTATG GCGTCAGGCA AACAAATATA AAGTTCCGCG CATTGCGTTC 450
 30 GTTAACAAAA TGGACCGCAT GGGTGCGAAC TTCCTGAAAG TTGTTAACCA 500
 GATCAAAACC CGTCTGGGCG CGAACCCGGT TCCGCTGCAG CTGGCGATTG 550
 GTGCTGAAGA ACATTTCACC GGTGTTGTTG ACCTGGTGAA AATGAAAGCT 600
 ATCAACTGGA ACGACGCTGA CCAGGGCGTA ACCTTCGAAT ACGAAGATAT 650
 CCCGGCAGAC ATGGTTGAAC TGGCTAACGA ATGGCACCAG AACCTGATCG 700
 35 AATCCGCAGC TGAAGCTTCT GAAGAGCTGA TGGAAAAATA CCTGGGTGGT 750
 GAAGAAGCTA CTGAAGCAGA AATCAAAGGT GCTCTGCGTC AGCGCGTTCT 800
 GAACAACGAA ATCATCCTGG TAACCTGTGG TTCTGCGTTC AAGAACAAAG 850
 GTGTTTCAGG GATGCTGGAT GCGGTAATTG ATTACCTGCC ATCCCCGGTT 900
 GACGTACCTG CGATCAACGG TATCCTGGAC GACGGTAAAG ACACTCCGGC 950
 40 TGAACGTCAC GCAAGTGATG ACGAGCCGTT CTCTGCACTG GCGTTCAAAA 1000
 TCGCTACCGA CCCGTTTGTT GGTAACCTGA CCTTCTTCCG TGTTTACTCC 1050
 GGTGTGGTTA ACTCTGGTGA TACCGTACTG AACTCCGTGA AAGCTGCACG 1100
 TGAGCGTTTC GGTGCTATCG TTCAGATGCA CGCTAACAAA CGTGAAGAGA 1150
 TCAAAGAAGT TCGCGCGGGC GACATCGCTG CTGCTATCGG TCTGAAAGAC 1200
 45 GTAACCACTG GTGACACCCT GTGTGACCCG GATGCGCCGA TCATTCTGGA 1250
 ACGTATGGAA TTCCCTGAGC CGGTAATCTC CATCGCAGTT GAACCGAAAA 1300
 CCAAAGCTGA CCAGGAAAAA ATGGGTCTGG CTCTGGGCCG TCTGGCTAAA 1350
 GAAGACCCGT CTTTCCGTGT ATGGACTGAC GAAGAATCTA ACCAGACCAT 1400
 CATCGCGGGT ATGGGCGAAC TGCACCTCGA CATCATCGTT GACCGTATGA 1450
 50 AGCGTGAATT CAACGTTGAA GCGAACGTAG GTAAACCGCA GGTTGCTTAC 1500
 CGTGAAACTA TCCGCCAGAA AGTTACCGAT GTTGAAGGTA AACACGCGAA 1550
 ACAGTCTGGT GGTGCTGGTC AGTATGGTCA TGTGTGTTATC GACATGTACC 1600
 CGCTGGAGCC GGGTTCAAAC CCGAAAGGCT ACGAGTTCAT CAACGACATT 1650
 AAAGGTGGTG TAATCCCTGG CGAATACATC CCGGCCGTTG ATAAAGGTAT 1700
 55 CCAGGAACAG CTGAAAGCAG GTCCGCTGGC AGGCTACCCG GTAGTAGACA 1750
 TGGGTATTCT TCTGCACTTC GGTTCTTACC ATGACGTTGA CTCCTCTGAA 1800
 CTGGCGTTTA AACTGGCTGC TTCTATCGCC TTTAAAGAAG GCTTTAAGAA 1850
 AGCGAAACCA GTTCTGCTTG AGCCGATCAT GAAGGTTGAA GTAGAAACTC 1900
 CGGAAGAGAA CACCGGTGAC GTTATCGGTG ACTTGAGCCG TCGTCGTGGT 1950
 60 ATGCTCAAAG GTCAGGAATC TGAAGTTACT GGCCTTAAGA TCCACGCTGA 2000

AGTACCGCTG TCTGAAATGT TCGGATACGC AACTCAGCTG CGTTCTCTGA 2050
CCAAAGGTCG TGCATCATAC ACTATGGAAT TCCTGAAAGTA TGATGAAGCG 2100
CCGAGTAACG TTGCTCAGGC CGTAATTGAA GCCCGTGGTA AATAA 2145

5

2) INFORMATION FOR SEQ ID NO: 1231

(i) SEQUENCE CHARACTERISTICS:
10 (A) LENGTH: 37 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

15 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1231

20 GCGAGCCCGA AGATAAAAAA GAACCTCTGC TGCTCGC 37

2) INFORMATION FOR SEQ ID NO: 1232

25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 42 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

30 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1232

35 GGAGCCGCGC GATTTTATAA ATGAATGTTG ATAACCGGCT CC 42

2) INFORMATION FOR SEQ ID NO: 1233

40 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 35 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
45 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1233

50 GCGAGCGTTA CTGGTGTAGA AATGTTCCGG CTCGC 35

55 2) INFORMATION FOR SEQ ID NO: 1234

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
60 (C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1234

ACTAAATAAA CGCTCATTCG

20

10

2) INFORMATION FOR SEQ ID NO: 1235

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 38 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

20 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1235

GCGAGCCGAA GTTGAAGTTG TTGGTATTGC TGGCTCGC

38

25

2) INFORMATION FOR SEQ ID NO: 1236

(i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 34 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

35 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1236

GCGAGCCGTG GTGAAGTTGC CGTTGGTGGC TCGC

34

40

2) INFORMATION FOR SEQ ID NO: 1237

(i) SEQUENCE CHARACTERISTICS:

45 (A) LENGTH: 38 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1237

55 GCGAGCCGCG AAATCGAAGT TGCTGTATTA GGGCTCGC

38

60

2) INFORMATION FOR SEQ ID NO: 1238

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 38 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
5 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1238

10 GCGAGCGGCG TTAATTTTGG CACCGAAGAA GAGCTCGC 38

15 2) INFORMATION FOR SEQ ID NO: 1239

 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 33 bases
 (B) TYPE: Nucleic acid
20 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

 (ii) MOLECULE TYPE: DNA

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1239

 GCGAGCGCAG ACCTTTCAGC AGAGGAGGCT CGC 33

30 2) INFORMATION FOR SEQ ID NO: 1240

 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 38 bases
35 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

 (ii) MOLECULE TYPE: DNA

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1240

 GCGAGCCGGC AAGACAATAT GACAGCAAAA TCGCTCGC 38

45 2) INFORMATION FOR SEQ ID NO: 1241

 (i) SEQUENCE CHARACTERISTICS:
50 (A) LENGTH: 35 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

55 (ii) MOLECULE TYPE: DNA

 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1241

60 GCGAGCGGGG AACGAGGATG ATTTGATTGG CTCGC 35

2) INFORMATION FOR SEQ ID NO: 1242

5 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 600 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

10

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus faecium*
 (E) STRAIN: BM4147-1
 (F) ACCESSION NUMBER: U39790

(xiv) SEQUENCE DESCRIPTION: SEQ ID NO: 1242

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20 TTCTTAGAGA CATTGAATAT GCCTTATGTC GGCGCAGGCG TATTGACCAG      50
   TGCATGTGCC ATGGATAAAA TCATGACCAA GTATATTTTA CAAGCTGCTG      100
   GTGTGCCGCA AGTTCCTTAT GTACCAGTAC TTAAGAATCA ATGGAAAGAA      150
   AATCCTAAAA AAGTATTTGA TCAATGTGAA GGTTCCTTGC TTTATCCGAT      200
   GTTTGTCAAA CCTGCGAATA TGGGTTCTAG TGTCGGCATT ACAAAGGCAG      250
25 AAAACCGAGA AGAGCTGCAA AATGCTTTAG CAACAGCCTA TCAGTATGAT      300
   TCTCGAGCAA TCGTTGAACA AGGAATTGAA GCGCGCGAAA TCGAAGTTGC      350
   TGTATTAGGA AATGAAGATG TTCGGACGAC TTTGCCTGGC GAAGTCGTAA      400
   AAGACGTAGC ATTCTATGAT TATGAAGCCA AATATATCAA TAATAAAATC      450
   GAAATGCAGA TTCCAGCCGA AGTGCCGGAA GAAGTTTATC AAAAAGCGCA      500
30 AGAGTACGCG AAGTTAGCTT ACACGATGTT AGGTGGAAGC GGATTGAGCC      550
   GGTGCGATTT CTTTTTGACA AATAAAATG AATTATTCCT GAATGAATTA      600

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35 2) INFORMATION FOR SEQ ID NO: 1243

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2275 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

40

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus faecalis*
 (C) ACCESSION NUMBER: M38386

(xv) SEQUENCE DESCRIPTION: SEQ ID NO: 1243

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50 GGTACCAAAG AAAAAAACGA ACGCCACAAC CAACAGCCTC TAAAGCAACA      50
   CCTGCTTCTG AAATTGAGGG AGATTTAGCA AATGTCAATG AGATTCTTTT      100
   GGTTACGAT GATCGTGTCG GGTCAGCAAC GATGGGAATG AAAGTCTTAG      150
   AAGAAATTTT AGATAAAGAG AAAATTTCAA TGCCGATTCTG AAAAATTAAT      200
55 ATTAATGAAT TAACTCAACA AACACAGGCT TTAATTGTCA CAAAAGCTGA      250
   ACTAACGGAA CAAGCACGTA AAAAAGCACC GAAAGCGACA CACTTATCAG      300
   TAAAAAGTTA TGGTTAATCC CCAAAAATAT GAAACAGTGG GTTTCGCTCT      350
   TAAAAGAAAG TGCCTAGAGA GGAAGAAAAC AATGGAAAAT CTTACGAATA      400
   TTTCAATTGA ATTAAATCAA CAGTTTAATA CAAAAGAAGA AGCTATTTCG      450
60 TTTTCCGGCC AGAAACTAGT CGAGGCAGGC TGTGTTGAGC CCGCTTATAT      500

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	CGAAGCAATG	ATTGAAAGAG	ACCAATTGCT	ATCTGCCCAT	ATGGGGAATT	550
	TTATTGCCAT	TCCTCATGGA	ACAGAAGAAG	CCAAAAAATT	AGTGAAGAAA	600
	TCAGGAATCT	GTGTAGTGCA	AGTCCCAGAG	GGCGTTAATT	TTGGCACCGA	650
	AGAAGATGAA	AAAATTGCTA	CCGTATTATT	TGGGATTGCC	GGAGTCGGTG	700
5	AAGAACATTT	GCAATTAGTC	CAACAAATTG	CACTTTATTG	TAGTGATATG	750
	GATAACGTGG	TGCAACTTGC	CGATGCATTA	AGTAAAGAAG	AAATAACAGA	800
	AAATTTAGCC	ATTGCTTAAA	GGAGAGAATA	AGAATGAACG	CAGTACATTT	850
	TGGAGCAGGA	AATATTGGAC	GCGGCTTTAT	TGGCGAAATT	TTAGCTAAAA	900
	CGGGTTTCAT	ATTACCGTTT	GTGGATGTTA	ATGGAAACCA	TCATCAAGCG	950
10	TTAAAAGAAC	GTAAAAGTTA	TACAATTGAA	TTGGCCGATG	CCTCACATCA	1000
	ACAAATTAAC	GTTGAAAATG	TGACCGGGTT	AAATAACATG	ACAGAACCAG	1050
	AAAAAGTAGT	AGAAGCAATT	GCGGAAGCCG	ATTTAGTCAC	GACGGCAATT	1100
	GGTCCTAATA	TTTTACCAAG	AATTGCTGAA	TTAATTGCTC	AAGGAATTGA	1150
	TGCACGTGCC	GAAGCAAATT	GTCAAAACGG	CCCCTGGAT	ATTATCGCTT	1200
15	GTGAAAATAT	GATTGGTGGT	TCAAACTTTT	TAGCAGAAGA	AGTGGCCATA	1250
	ATATTTGAAA	AACCCAGCTT	ATCTGAACAA	TGGATTGGTT	TTCTGTATGC	1300
	GGCAGTTGAT	CGGATTGTTC	CATTACAAAA	ACATAAAGAT	CCACTTTTTG	1350
	TTCAAGTTGA	GCCTTTTTGT	GAATGGGTCA	TTGATGATAC	CAACCGAAAA	1400
	GCCAAAGAGA	TTCAGTTAGA	AGGCGTCATT	ACTTGTCGAT	TAGAGCCGTA	1450
20	TATTGAACGA	AAATTATTTA	GTGTAACCAG	TGGCCATGCT	ACAGTTGCCT	1500
	ATACAGGGGC	GTTGTTAGGC	TATCAAACCA	TTGACGAAGC	GATGCAGGAC	1550
	GCCTTAGTGG	TAGCGCAACT	CAAATCAGTT	TTGCAGGAAA	CCGGTAAACT	1600
	TTTAGTGGCC	AAATGGAATT	TTGATGAACA	AGAACATGCA	GCCTATATTG	1650
	AAAAAATTAT	CAACCGTTTC	CAAATAAAT	ATATTTTACA	TGCTATTACA	1700
25	CGTGTAGCAC	GGACACCAAT	CAGAAAATTA	GGTGCACAAG	AACGGTTTAT	1750
	TCGACCAATC	CGTGAATTAC	AGGAACGCAA	TCTAGTGTCT	GCCGCATTTA	1800
	TAGCAATGAT	TGGTATTGTC	TTTAATTATC	ATGATCCAGA	AGATGAACAA	1850
	AGCCGTCAAT	TACAGGAAAT	GCTTGACCAA	GAAAGTGTTG	ATACAGTGGA	1900
	TCGCTGAAGT	AACGGGCATT	GAAGATCCAG	AAACGGTTAA	AAATATTAAA	1950
30	CAAAACGTAG	AACTGCTATG	CGCGACCACA	AGTAGCATAA	TTAACAAAAT	2000
	CCTTCTACCA	AGATACTTCA	CATTTCTTAA	TTAAAGAAAA	AACAACCGCG	2050
	CCTCACCTGA	GCCGACCCCC	AAAAGTTAGA	CCTAGAAATC	TAACCTTTGG	2100
	AGGTTTTTTT	GTATGGCAAA	ATACAGTTTT	GAAATTTAAA	CTTAAACTTG	2150
	TTTATGACTA	CTTATATGGT	CAAGGAGGTC	TAAGGTTTCT	CGCAAAGAAG	2200
35	TATGGGTTTA	AAGATAGTCT	CAAATAAGCA	AATGGATAAA	TGCCTATAAA	2250
	GAACTTGGTG	AAGAAGGGGG	GATCC			2275

40 2) INFORMATION FOR SEQ ID NO: 1244

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 442 bases
 (B) TYPE: Nucleic acid
 45 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

50 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus aureus* subsp. *aureus*
 (B) STRAIN: ATCC 25923

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1244

55	GATCAATCTT	TGTCGGTACA	CGATATTCTT	CACGACTAAA	TAAACGCTCA	50
	TTTCGCGATTT	TATAAATGAA	TGTTGATAAC	AATGTTGTAT	TATCTACTGA	100
	AATCTCATTA	CGTTGCATCG	GAAACATTGT	GTTCTGTATG	TAAAAGCCGT	150
	CTTGATAATC	TTTAGTAGTA	CCGAAGCTGG	TCATACGAGA	GTTATATTTT	200
60	CCAGCCAAAA	CGATATTTTT	ATAATCATTA	CGTGAAAAAG	GTTTCCCTTC	250

ATTATCACAC	AAATATTTTA	GCTTTTCAGT	TTCTATATCA	ACTGTAGCTT	300
CTTTATCCAT	ACGTTGAATA	ATTGTACGAT	TCTGACGCAC	CATCTTTTGC	350
ACACCTTTAA	TGTTATTTGT	TTTAAAAGCA	TGAATAAGTT	TTTCAACACA	400
ACGATGTGAA	TCTTCTAAGA	AGTCACCGTA	AAATGAAGGA	TC	442

2) INFORMATION FOR SEQ ID NO: 1245

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 845 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

10

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacillus anthracis*
(B) STRAIN: CIP 9444

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1245

GATGGCGGAA AGCTACCAGA AATCTACAAC GCCCTTACGG TAAAACAGAG 50
CAACGAAAAC GGAACAAGCA TTAActTAAc ATTTGAAGTT GCACTTCATT 100
TAGGTGATGA CACAGTTCGT ACAGTTGCAA TGCTTCCAC AGATGGACTT 150
20 GTTCGTGGCA CAGAAGTAGA AGATACTGGT AAAGCAATCT CTGTACCAGT 200
TGGTGATGCA ACACTTGGTC GTGTATTTAA CGTATTAGGT GATGCAATTG 250
ACTTAGATGG TGAGGTTCCCT GCGGATGTAC GTCGTGATCC AATTCACCGT 300
CAAGCACCTG CATTGGAAGA ATTATCTACT AAAGTAGAAA TTCTTGAAAC 350
TGGTATTAAA GTAGTAGACT TACTTGCTCC TTACATTAAG GGTGGTAAGA 400
25 TCGGTCTATT CGGTGGTGCC GGTGTAGGTA AAACGGTATT AATTCAGGAA 450
TTAATCAATA ACATCGCACA AGAACACGGT GGTATCTCTG TATTCGCTGG 500
TG TAGGTGAG CGTACTCGTG AGGGTAATGA CTTATACCAC GAAATGAGCG 550
ATTCTGGCGT AATTAAGAAA ACTGCGATGG TATTCGGACA AATGAACGAG 600
CCACCTGGAG CACGTCAACG TGTTGCGTTA ACAGGTTTAA CAATGGCTGA 650
30 GCATTTCCGT GATGAGCAAG GACAAGATGT ACTTCTGTTC ATCGATAATA 700
TCTTCCGTTT CACGCAAGCA GGTTCTGAAG TATCTGCCCT TCTTGCCCGT 750
ATGCCATCTG CGGTAGGTTA CCAACCAACA CTTGCAACAG AAATGGGTCA 800
ATTACAAGAG CGTATTACAT CTACAAATAA AGGGTCTATC ACGTC 845

35

2) INFORMATION FOR SEQ ID NO: 1246

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 656 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

45 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacillus mycoides*
(B) STRAIN: ATCC 11986

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1246

TGCACTTCAT TTAGGTGATG ACACAGTTCG TACAGTTGCA ATGTCTTCCA 50

	CAGATGGACT	TGTTTCGTGGC	ACAGAAAGTAG	AAGATACTGG	TAAAGCAATC	100
	TCTGTACCAG	TTGGTGATGT	AACACTTGGT	CGTGTATTTA	ACGTATTAGG	150
	TGATGCAATT	GACTTAGATG	GTGATGTTCC	TGCGGATGTA	CGTCGTGATC	200
	CAATTCACCG	TCAAGCGCCT	GCATTCGAAG	AGTTATCTAC	TAAAGTAGAA	250
5	ATTCTTGAAA	CTGGTATTAA	AGTAGTAGAC	TTACTTGCTC	CTTACATTAA	300
	GGGTGGTAAG	ATTGGTCTAT	TCGGTGGTGC	CGGCGTAGGT	AAAACAGTAT	350
	TAATTCAGGA	ATTAATTAAT	AACATCGCAC	AAGAGCACGG	TGGTATCTCT	400
	GTATTCGCTG	GTGTAGGTGA	GCGTACTCGT	GAAGGTAACG	ACTTATACCA	450
	CGAAATGAGC	GATTCTGGCG	TAATTAAGAA	AACTGCGATG	GTATTCGGAC	500
10	AAATGAACGA	GCCACCTGGA	GCACGTCAAC	GTGTTGCATT	AACAGGTTTA	550
	ACAATGGCTG	AACATTTCCG	TGATGAGCAA	GGACAAGACG	TACTATTGTT	600
	CATCGATAAC	ATCTTCCGTT	TCACGCAAGC	GGGTTCTGAA	GTATCTGCCC	650
	TTCTTG					656

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2) INFORMATION FOR SEQ ID NO: 1247

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 791 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

25 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacillus thuringiensis*
 (B) STRAIN: ATCC 10792

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1247

	CGAAAACGGA	AGTATTAAC	TAACATTTGA	AGTTGCACTT	CATTTAGGTG	50
	ATGATACAGT	TCGTACAGTT	GCGATGTCTT	CCACAGATGG	ACTTGTTCTG	100
35	GGCACAGAAG	TAGAAGATAC	TGGTAAACCA	ATCTCTGTAC	CAGTTGGTGA	150
	TGTAACACTT	GGTCGCGTAT	TTAACGTATT	AGGTGATGCA	ATTGACTTAG	200
	ATGGTGAGGT	TCCTGCAGAT	GTACATCGTG	ATCCAATTCA	CCGTCAAGCA	250
	CCTGCATTCTG	AAGAATTATC	TACTAAAGTA	GAAATTCTTG	AAACTGGTAT	300
	TAAAGTAGTA	GACTTACTTG	CTCCTTACAT	TAAGGGTGGT	AAGATCGGCC	350
40	TATTCGGTGG	TGCCGGCGTA	GGTAAAACAG	TATTAATTCA	GGAATTAATT	400
	AACAACATCG	CACAAGAGCA	CGGTGGTATC	TCTGTATTCTG	CTGGTGTAGG	450
	TGAGCGTACT	CGTGAGGGTA	ATGACTTATA	CCACGAAATG	AGCGATTCTG	500
	GCGTAATCAA	GAAAACGCG	ATGGTATTCTG	GACAAATGAA	CGAGCCACCT	550
	GGAGCACGTC	AACGTGTTGC	ATTAACAGGT	TTAACAATGG	CTGAGCATTT	600
45	CCGTGATGAG	CAAGGACAAG	ACGTACTTCT	GTTTCATCGAT	AACATCTTCC	650
	GTTTCACGCA	AGCGGGTTCT	GAAGTATCTG	CCCTTCTTGG	TCGTATGCCA	700
	TCTGCGGTAG	GTTACCAACC	AACACTTGCA	ACAGAAATGG	GTCAATTACA	750
	AGAGCGTATT	ACATCTACAA	ATAAAGGGTC	TATCACGTCT	A	791

50

2) INFORMATION FOR SEQ ID NO: 1248

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 825 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 5 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 10 (A) ORGANISM: *Bacillus thuringiensis*
 (B) STRAIN: BGSC 4AC1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1248

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15 ATCTACAATG CCCTTACGGT AAAACAAAGC AACGAAAACG GAAGCATGAA      50
   CTTAACATTT GAAGTTGCAC TTCATTTAGG TGATGATACA GTTCGTACAG      100
   TTGCGATGTC TTCCACAGAT GGAAGTTGTC GTGGCACAGA AGTAGAAGAT      150
   ACTGGTAAAG CAATCTCTGT ACCAGTTGGT GATGCAACAC TTGGACGTGT      200
   ATTCAACGTA TTAGGTGATG CAATTGACTT AGATGGTGAA CTCCTGCGG      250
20 ATGTACACCG TGATCCAATT CACCGTCAAG CACCTGCATT CGAAGAATTA      300
   TCTACTAAAG TAGAAATTCT TGAAACTGGT ATTAAAGTAG TAGACTTACT      350
   TGCTCCTTAC ATTAAGGGTG GTAAGATCGG CCTATTCGGT GGTGCCGGCG      400
   TAGGTAAAAC AGTATTAATT CAGGAGTTAA TCAATAACAT CGCACAAGAG      450
   CACGGTGGTA TCTCTGTATT CGCTGGTGTA GGTGAGCGTA CTCGTGAGGG      500
25 TAATGACTTA TACCACGAAA TGAGCGATTC TGGCGTAATC AAGAAAACCTG      550
   CGATGGTATT CGGACAAATG AACGAGCCAC CTGGAGCACG TCAACGTGTT      600
   GCATTAACAG GTTTAACAAT GGCTGAGCAT TTCCGTGATG AGCAAGGACA      650
   AGACGTACTT CTGTTTCATCG ATAACATCTT CCGTTTCACG CAAGCGGGTT      700
   CTGAAGTATC TGCCCTTCTT GGTCGTATGC CATCTGCGGT AGGTTACCAA      750
30 CCAACACTTG CAACAGAAAT GGGTCAATTA CAAGAGCGTA TTACATCTAC      800
   AAATAAAGGG TCTATCACGT CTATC      825

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35 2) INFORMATION FOR SEQ ID NO: 1249

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 775 bases
 (B) TYPE: Nucleic acid
 40 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 45 (A) ORGANISM: *Bacillus thuringiensis*
 (B) STRAIN: HER 1236

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1249

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50 ATCTACAACG CCCTTACGGT AAAACAAAGC AACGAAAACG GAAGTATTAA      50
   CTTAACATTT GAAGTTGCAC TTCATTTAGG TGATGATACA GTTCGTACAG      100
   TTGCGATGTC TTCCACAGAT GGAAGTTGTC GTGGCACAGA AGTAGAAGAT      150

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	ACTGGTAAAC	CAATCTCTGT	ACCAGTTGGT	GATGTAACAC	TTGGTCGCGT	200
	ATTTAACGTA	TTAGGTGATG	CAATTGACTT	AGATGGTGAG	GTTCCTGCAG	250
	ATGTACATCG	TGATCCAATT	CACCGTCAAG	CACCTGCATT	CGAAGAATTA	300
	TCTACTAAAG	TAGAAATTCT	TGAAACTGGT	ATTAAAGTAG	TAGACTTACT	350
5	TGCTCCTTAC	ATTAAGGGTG	GTAAGATCGG	CCTATTCGGT	GGTGCCGGCG	400
	TAGGTAAAAC	AGTATTAATT	CAGGAATTAA	TTAACAACAT	CGCACAAGAG	450
	CACGGTGGTA	TCTCTGTATT	CGCTGGTGTA	GGTGAGCGTA	CTCGTGAGGG	500
	TAATGACTTA	TACCACGAAA	TGAGCGATTG	TGGCGTAATC	AAGAAAACGTG	550
	CGATGGTATT	CGGACAAATG	AACGAGCCAC	CTGGAGCACG	TCAACGTGTT	600
10	GCATTAACAG	GTTTAAACAAT	GGCTGAGCAT	TTCCGTGATG	AGCAAGGACA	650
	AGACGTACTT	CTGTTTCATCG	ATAACATCTT	CCGTTTTCACG	CAAGCGGGTT	700
	CTGAAGTATC	TGCCCTTCTT	GGTCGTATGC	CATCTGCGGT	AGGTTACCAA	750
	CCAACACTTG	CAACAGAAAT	GGGTC			775

15

2) INFORMATION FOR SEQ ID NO: 1250

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 832 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

25 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacillus weihenstephanensis*
 (B) STRAIN: WSBC 10204

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1250

	CCAGCAATCT	ACAACGCCCT	TACGGTAAAA	CAAAGCAACG	AAAACGGAGC	50
	GAGCATCAAC	TTAACATTTG	AAGTTGCACT	TCATTTAGGT	GATGACACAG	100
35	TTCGTACAGT	TGCGATGTCT	TCCACAGATG	GACTTGTTCTG	TGGCACAGAA	150
	GTAGAAGATA	CTGGTAAAGC	AATCTCTGTA	CCAGTTGGTG	ATGTAACACT	200
	TGGTCGCGTA	TTCAACGTAT	TAGGTGATGC	AATTGACTTA	GATGGTGATG	250
	TTCCTGCGGA	TGTACGTCGT	GATCCAATTC	ACCGTCAAGC	ACCTGCATTC	300
	GAAGAACTAT	CTACAAGAAT	AGAAATTCTT	GAAACTGGTA	TTAAAGTAGT	350
40	AGATTTACTT	GCTCCTTACA	TTAAGGGTGG	TAAGATCGGT	CTATTCGGTG	400
	GTGCCGGTGT	AGGTAAAACG	GTATTAATTC	AGGAATTAAT	TAACAACATC	450
	GCACAAGAGC	ACGGTGGTAT	CTCTGTATTC	GCTGGTGTAG	GTGAGCGTAC	500
	TCGTGAGGGT	AATGACTTAT	ACCACGAAAT	GAGCGATTCT	GGCGTAATTA	550
	AGAAAACGTC	GATGGTATTT	GGACAAATGA	ACGAGCCACC	TGGAGCACGT	600
45	CAACGTGTTG	CATTAACAGG	TTTAACAATG	GCTGAACATT	TCCGTGATGA	650
	GCAAGGACAA	GACGTACTAT	TGTTTCATCGA	TAACATCTTC	CGTTTCACGC	700
	AAGCAGGTTC	TGAAGTATCT	GCCCTTCTTG	GTCGTATGCC	ATCTGCGGTA	750
	GGTTACCAAC	CAACACTTGC	AACAGAAATG	GGTCAATTAC	AAGAGCGTAT	800
50	TACATCTACA	AATAAAGGGT	CTATCACGTC	TA		832

2) INFORMATION FOR SEQ ID NO: 1251

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 802 bases
 (B) TYPE: Nucleic acid
 5 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

10 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacillus thuringiensis*
 (B) STRAIN: HER 1418

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1251

15 AAATCTACAA CGCCCTTACG GTAAACAAA GCAACGAAAA CGGAAGTATT 50
 AACTTAACAT TTGAAGTTGC ACTTCATTTA GGTGATGATA CAGTTCGTAC 100
 AGTTGCGATG TCTTCCACAG ATGGACTTGT TCGTGGCACA GAAGTAGAAG 150
 ATACTGGTAA ACCAATCTCT GTACCAGTTG GTGATGTAAC ACTTGGTCGC 200
 20 GTATTTAACG TATTAGGTGA TGCAATTGAC TTAGATGGTG AGGTTCCCTGC 250
 AGATGTACAT CGTGATCCAA TTCACCGTCA AGCACCTGCA TTCGAAGAAT 300
 TATCTACTAA AGTAGAAATT CTTGAAACTG GTATTAAAGT AGTAGACTTA 350
 CTTGCTCCTT ACATTAAGGG TGGTAAGATC GGCCTATTCG GTGGTGCCGG 400
 CGTAGGTAAA ACAGTATTAA TTCAGGAATT AATTAACAAC ATCGCACAAAG 450
 25 AGCACGGTGG TATCTCTGTA TTCGCTGGTG TAGGTGAGCG TACTCGTGAG 500
 GGTAATGACT TATACCACGA AATGAGCGAT TCTGGCGTAA TCAAGAAAAC 550
 TGCGATGGTA TTCGGACAAA TGAACGAGCC ACCTGGAGCA CGTCAACGTG 600
 TTGCATTAAC AGGTTTAAAC ATGGCTGAGC ATTTCCGTGA TGAGCAAGGA 650
 CAAGACGTAC TTCTGTTTCA CGATAACATC TTCCGTTTCA CGCAAGCGGG 700
 30 TTCTGAAGTA TCTGCCCTTC TTGGTCGTAT GCCATCTGCG GTAGGTTACC 750
 AACCAACACT TGCAACAGAA ATGGGTCAAT TACAAGAGCG TATTACATCT 800
 AC 802

35

2) INFORMATION FOR SEQ ID NO: 1252

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 823 bases
 40 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

45

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacillus thuringiensis*
 (B) STRAIN: HER 1410

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1252

AAATCTACAA CGCCCTTACG GTAAACAAA GCAACGAAAA CGGAAGTATT 50
 AACTTAACAT TTGAAGTTGC ACTTCATTTA GGTGATGATA CAGTTCGTAC 100

	AGTTGCAATG	TCTTCCACAG	ATGGACTTGT	TCGTGGCACA	GAAGTAGAAG	150
	ATACTGGTAA	ACCAATCTCT	GTACCAGTTG	GTGATGTAAC	ACTTGGTGCG	200
	GTATTTAACG	TATTAGGTGA	TGCAATTGAC	TTAGATGGTG	AGGTTCCTGC	250
	AGATGTACAT	CGTGATCCAA	TTCACCGTCA	AGCACCTGCA	TTCGAAGAAT	300
5	TATCTACTAA	AGTAGAAATT	CTTGAAACTG	GTATTAAAGT	AGTAGACTTA	350
	CTTGCTCCTT	ACATTAAGGG	TGGTAAGATC	GGCCTATTCT	GTGGTGCCGG	400
	CGTAGGTAAA	ACAGTATTAA	TTCAGGAATT	AATTAACAAC	ATCGCACAAAG	450
	AGCACGGTGG	TATCTCTGTA	TTCGCTGGTG	TAGGTGAGCG	TACTCGTGAG	500
	GGTAATGACT	TATACCACGA	AATGAGCGAT	TCTGGCGTAA	TCAAGAAAAC	550
10	TGCGATGGTA	TTCGGACAAA	TGAACGAGCC	ACCTGGAGCA	CGTCAACGTG	600
	TTGCATTAAC	AGGCTTAACA	ATGGCTGAGC	ATTTCCGTGA	TGAGCAAGGA	650
	CAAGACGTAC	TTCTGTTCAT	CGATAACATC	TTCCGTTTCA	CGCAAGCGGG	700
	TTCTGAAGTA	TCTGCCCTTC	TTGGTCGTAT	GCCATCTGCG	GTAGGTTACC	750
	AACCAACACT	TGCAACAGAA	ATGGGTCAAT	TACAAGAGCG	TATTACATCT	800
15	ACAAATAAAG	GGTCTATCAC	GTC			823

2) INFORMATION FOR SEQ ID NO: 1253

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 798 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

25

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

30

- (A) ORGANISM: *Bacillus cereus*
 (B) STRAIN: ATCC 13472

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1253

35	CCAGAAATCT	ACAATGCCCT	TACGGTAAAA	CAAAGCAACG	AAAACGGAAG	50
	CATGAACTTA	ACATTTGAAG	TTGCACTTCA	TTTAGGTGAT	GATACAGTTC	100
	GTACAGTTGC	GATGTCTTCC	ACAGATGGAC	TTGTTCGTGG	CACAGAAGTA	150
	GAAGATACTG	GTAAAGCAAT	CTCTGTACCA	GTTGGTGATG	CAACACTTGG	200
	ACGTGTATTC	AACGTATTAG	GTGATGCAAT	TGACTTAGAT	GGTGAAC TTC	250
40	CTGCGGATGT	ACACCGTGAT	CCAATTCACC	GTCAAGCACC	TGCATTTCGAA	300
	GAATTATCTA	CTAAAGTAGA	AATTCTTGAA	ACTGGTATTA	AAGTAGTAGA	350
	CTTACTTGCT	CCTTACATTA	AGGGTGGTAA	GATCGGCCTA	TTCGGTGGTG	400
	CCGGCGTAGG	TAAAACAGTA	TTAATTCAGG	AATTAATCAA	TAACATCGCA	450
	CAAGAGCATG	GTGGTATCTC	TGTATTTCGT	GGTGTAGGTG	AGCGTACTCG	500
45	TGAGGGTAAT	GACTTATACC	ACGAAATGAG	CGATTCTGGC	GTAATCAAGA	550
	AAACTGCGAT	GGTATTCGGA	CAAATGAACG	AGCCACCTGG	AGCACGTCAA	600
	CGTGTTGCAT	TAACAGGTTT	AACAATGGCT	GAGCATTTCC	GTGATGAGCA	650
	AGGACAAGAC	GTA CTCTGT	TCATCGATAA	CATCTTCCGT	TTCACGCAAG	700
	CGGGTTCTGA	AGTATCTGCC	CTTCTTGGTC	GTATGCCATC	TGCGGTAGGT	750
50	TACCAACCGA	CACCTGCAAC	AGAAATGGGT	CAATTACAAG	AGCGTATT	798

2) INFORMATION FOR SEQ ID NO: 1254

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 767 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

10

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacillus cereus*
(B) STRAIN: ATCC 7064

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1254

CATTTGAAGT TGCAC TTCAT TTAGGTGATG ACACAGTTCG TACAGTTGCA 50
ATGTCTTCCA CAGATGGACT TGTTCGTGGC ACAGAAGTAG AAGATACTGG 100
TAAAGCAATC TCTGTACCAG TTGGTGATGC AACACTTGGT CGTGTATTTA 150
20 ACGTATTAGG TGATGCAATT GACTTAGATG GTGAGGTTCC TGC GGATGTA 200
CGTCGTGATC CAATTCACCG TCAAGCACCT GCATT CGAAG AATTATCTAC 250
TAAAGTAGAA ATTCTTGAAA CTGGTATTAA AGTAGTAGAC TTACTTGCTC 300
CTTACATTAA GGGTGGTAAG ATCGGTCTAT TCGGTGGTGC CGGTGTAGGT 350
AAAACGGTAT TAATTCAGGA ATTAATCAAT AACATCGCAC AAGAACACGG 400
25 TGGTATCTCT GTATTCGCTG GTGTAGGTGA GCGTACTCGT GAGGGTAATG 450
ACTTATACCA CGAAATGAGC GATTCTGGCG TAATTAAGAA AACTGCGATG 500
GTATTCGGAC AAATGAACGA GCCACCTGGA GCACGTCAAC GTGTTGCGTT 550
AACAGGTTTA ACAATGGCTG AGCATTTCCG TGATGAGCAA GGACAAGACG 600
TACTTCTGTT CATCGATAAT ATCTTCCGTT TCACGCAAGC AGGTTCTGAA 650
30 GTATCTGCCC TTCTTGGCCG TATGCCATCT GCGGTAGGTT ACCAACCAAC 700
ACTTGCAACA GAAATGGGTC AATTACAAGA GCGTATTACA TCTACAAATA 750
AAGGGTCTAT CACGTCT 767

35

2) INFORMATION FOR SEQ ID NO: 1255

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 1174 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

45

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus aureus*
(B) STRAIN: C-14

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1255

GAAATGCGTG AATCATTTTT AGATTATGCG ATGAGTGTTA TCGTTGCTCG 50
TGCATTGCCA GATGTTCTGT ACGGTTTAAA ACCAGTACAT CGTCGTATAC 100

	TATATGGATT	AAATGAACAA	GGTATGACAC	CGGATAAATC	ATATAAAAAA	150
	TCAGCACGTA	TCGTTGGTGA	CGTAATGGGT	AAATATCACC	CTCATGGTGA	200
	CTTATCTATT	TATGAAGCAA	TGGTACGTAT	GGCTCAAGAT	TTCAGTTATC	250
	GTTATCCGCT	TGTTGATGGC	CAAGGTAAC	TTGGTTCAAT	GGATGGAGAT	300
5	GGCGCAGCAG	CAATGCGTTA	TACTGAAGCG	CGTATGACTA	AAATCACACT	350
	TGAACTGTTA	CGTGATATTA	ATAAAGATAC	AATAGATTTT	ATCGATAACT	400
	ATGATGGTAA	TGAAAGAGAG	CCGTCAGTCT	TACCTGCTCG	ATTCCCTAAC	450
	TTATTAGCCA	ATGGTGCATC	AGGTATCGCG	GTAGGTATGG	CAACGAATAT	500
	TCCACCACAT	AACTTAACAG	AATTAATCAA	TGGTGTACTT	AGCTTAAGTA	550
10	AGAACCCTGA	TATTTCAATT	GCTGAGTTAA	TGGAGGATAT	TGAAGGTCCT	600
	GATTTCCCAA	CTGCTGGACT	TATTTTAGGT	AAGAGTGGTA	TTAGACGTGC	650
	ATATGAAACA	GGTCGTGGTT	CAATTCAAAT	GCGTTCCTCG	GCAGTTATTG	700
	AAGAACGTGG	AGNCGGACGT	CAACGTATTG	TTGTCACTGA	AATTCCTTTC	750
	CAAGTGAATA	AGGCTCGTAT	GATTGAAAAA	ATTGCAGAGC	TCGTTCTGTA	800
15	CAAGAAAATT	GACGGTATCA	CTGATTTACG	TGATGAAACA	AGTTTACGTA	850
	CTGGTGTGCG	TGTCGTTATT	GATGTGCGTA	AGGATGCAA	TGCTAGTGTC	900
	ATTTTAAATA	ACTTATACAA	ACAAACACCT	CTTCAAACAT	CATTTGGTGT	950
	GAATATGATT	GCACTTGTA	ATGGTAGACC	GAAGCTTATT	AATTTAAAAG	1000
	AAGCGTTGGT	ACATTATTTA	GAGCATCAAA	AGACAGTTGT	TAGAAGACGT	1050
20	ACGCAATACA	ACTTACGTAA	AGCTAAAGAT	CGTGCCCACA	TTT TAGAAGG	1100
	ATTACGTATC	GCACTTGACC	ATATCGATGA	AATTATTTCA	ACGATTCGTG	1150
	AGTCAGATAC	AGATAAAGTT	GCAA			1174

25

2) INFORMATION FOR SEQ ID NO: 1256

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 780 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

35

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacillus weihenstephanensis*
 (B) STRAIN: WSBC 10209

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1256

	ATCTACAACG	CCCTTACGGT	AAAACAAAGC	AACGAAAACG	GAGCAAGCAT	50
	TAACCTAACA	TTTGAAGTTG	CACTTCATTT	AGGTGATGAC	ACAGTTCGTA	100
	CAGTTGCAAT	GTCTTCCACA	GATGGACTTG	TTCGTGGCAC	AGAAGTAGAA	150
45	GATACTGGTA	AAGCAATCTC	TGTACCAGTT	GGTGATGTAA	CACTTGGTGC	200
	TGTATTTAAC	GTATTAGGTG	ATGCAATTGA	CTTAGATGGA	GATGTTCTCG	250
	CGGATGTACG	TCGTGATCCA	ATTCACCGTC	AAGCGCCTGC	ATTCGAAGAG	300
	TTATCTACTA	AAGTAGAAAT	TCTTGAAACT	GGTATTAAAG	TAGTAGACTT	350
	ACTTGCTCCT	TACATTAAGG	GTGGTAAGAT	CGGTCTATTC	GGTGGTGCCG	400
50	GTGTAGGTAA	AACAGTATTA	ATTCAGGAAT	TAATTAACAA	CATCGCACAA	450
	GAGCACGGTG	GTATCTCTGT	ATTCGCTGGT	GTAGGTGAGC	GTA CTCTGTA	500
	AGGTAACGAC	TTATACCACG	AAATGAGCGA	TTCTGGCGTA	ATTAAGAAAA	550
	CTGCGATGGT	ATTTCGACAA	ATGAACGAGC	CACCTGGAGC	ACGTCAACGT	600

GTTGCATTAA	CAGGTTTAAC	AATGGCTGAA	CATTTCCTGT	ATGAGCAAGG	650
GCAAGACGTA	CTATTGTTCA	TCGATAACAT	CTTCCGTTTC	ACGCAAGCGG	700
GTTCTGAAGT	ATCTGCCCTT	CTTGGTCGTA	TGCCATCTGC	GGTAGGTTAC	750
CAGCCAACAC	TTGCAACAGA	AATGGGTCAA			800

5

2) INFORMATION FOR SEQ ID NO: 1257

10 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 817 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

15

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacillus anthracis*
- (B) STRAIN: CIP 7700

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1257

CTACCAGAAA	TCTACAACGC	CCTTACGGTA	AAACAGAGCA	ACGAAAACGG	50
25 AACAAGCATT	AACTTAACAT	TTGAAGTTGC	ACTTCATTTA	GGTGATGACA	100
CAGTTCGTAC	AGTTGCAATG	TCTTCCACAG	ATGGACTTGT	TCGTGGCACA	150
GAAGTAGAAG	ATACTGGTAA	AGCAATCTCT	GTACCAGTTG	GTGATGCAAC	200
ACTTGGTCGT	GTATTTAACG	TATTAGGTGA	TGCAATTGAC	TTAGATGGTG	250
AGGTTTCCTGC	GGATGTACGT	CGTGATCCAA	TTCACCGTCA	AGCACCTGCA	300
30 TTCGAAGAAT	TATCTACTAA	AGTAGAAATT	CTTGAAACTG	GTATTAAAGT	350
AGTAGACTTA	CTTGCTCCTT	ACATTAAGGG	TGGTAAGATC	GGTCTATTCTG	400
GTGGTGCCGG	TGTAGGTAAA	ACGGTATTAA	TTCAGGAATT	AATCAATAAC	450
ATCGCACAAG	AACACGGTGG	TATCTCTGTA	TTGCTGGTG	TAGGTGAGCG	500
TACTCGTGAG	GGTAATGACT	TATACCACGA	AATGAGCGAT	TCTGGCGTAA	550
35 TTAAGAAAAC	TGCGATGGTA	TTCGGACAAA	TGAACGAGCC	ACCTGGAGCA	600
CGTCAACGTG	TTGCGTTAAC	AGGTTTAAACA	ATGGCTGAGC	ATTTCCGTGA	650
TGAGCAAGGA	CAAGATGTAC	TTCTGTTCAT	CGATAATATC	TTCCGTTTCA	700
CGCAAGCAGG	TTCTGAAGTA	TCTGCCCTTC	TTGGCCGTAT	GCCATCTGCG	750
GTAGGTTACC	AACCAACACT	TGCAACAGAA	ATGGGTCAAT	TACAAGAGCG	800
40 TATTACATCT	ACAAATA				817

2) INFORMATION FOR SEQ ID NO: 1258

45

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 829 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Bacillus thuringiensis*

(B) STRAIN: HER 1404

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1258

```

CCAGAAATCT ACAACGCCCT TACGGTAAAA CAAAGCAACG AAAACGGAAG      50
TATTAAGTTA ACATTTGAAG TTGCACTTCA TTTAGGTGAT GATACAGTTC      100
GTACAGTTGC GATGTCTTCC ACAGATGGAC TTGTTTCGTGG CACAGAAGTA      150
10 GAAGATACTG GTAAACCAAT CTCTGTACCA GTTGGTGATG TAACACTTGG      200
TCGCGTATTT AACGTATTAG GTGATGCAAT TGAAGTAGAT GGTGAGGTTT      250
CTGCAGATGT ACATCGTGAT CCAATTCACC GTCAAGCACC TGCATTCGAA      300
GAATTATCTA CTAAAGTAGA AATTCTTGAA ACTGGTATTA AAGTAGTAGA      350
CTTACTTGCT CCTTACATTA AGGGTGGTAA GATCGGCCTA TTCGGTGGTG      400
15 CCGGCGTAGG TAAAACAGTA TTAATTCAGG AATTAATTAA CAACATCGCA      450
CAAGAGCAGC GTGGTATCTC TGTATTCGCT GGTGTAGGTG AGCGTACTCG      500
TGAGGGTAAT GACTTATACC ACGAAATGAG CGATTCTGGC GTAATCAAGA      550
AAACTGCGAT GGTATTCGGA CAAATGAACG AGCCACCTGG AGCACGTCAA      600
CGTGTTCGAT TAACAGGTTT AACAAATGGCT GAGCATTTCG GTGATGAGCA      650
20 AGGACAAGAC GACTTCTGTG TCATCGATAA CATCTTCCGT TTCACGCAAG      700
CGGGTTCTGA AGTATCTGCC CTTCTTGGTC GTATGCCATC TGCGGTAGGT      750
TACCAACCAA CACTTGCAAC AGAAATGGGT CAATTACAAG AGCGTATTAC      800
ATCTACAAAT AAAGGGTCTA TCACGTCTA      829

```

25

2) INFORMATION FOR SEQ ID NO: 1259

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 844 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

35 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Bacillus cereus*

(B) STRAIN: ATCC 15816

40 (C) ACCESSION NUMBER:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1259

```

TGGCGGAAAG CTACCAGAAA TCTACAACGC CCTTACGGTA AAACAGAGCA      50
45 ACGAAAACGG TGAACCTAAC TTAACATTG AAGTTGCACT TCATTTAGGT      100
GATGATACAG TTCGTACAGT TGCGATGTCT TCCACAGATG GACTTGTTTCG      150
TGGCACAGAA GTAGAAGATA CTGGTAAAGC AATCTCTGTA CCAGTTGGTG      200
ATGCAACACT TGGTCGCGTA TTTAACGTAT TAGGTGATGC TATTGACTTA      250
GATGGTGAGG TTCCTGCGGA TGTACGTCGT GATCCAATTC ACCGTCAAGC      300
50 ACCTGCATTC GAAGAATTAT CTAATAAGT AGAAATTCTT GAAACTGGTA      350
TTAAAGTAGT AGACTTACTT GCTCCTTACA TTAAGGGTGG TAAGATCGGC      400
CTATTCGGTG GTGCCGGTGT AGGTAAACA GTATTAATTC AGGAGTTAAT      450
CAACAACATC GCACAAGAGC ACGGTGGTAT CTCTGTATTC GCTGGTGTAG      500

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	GTGAGCGTAC	TCGTGAGGGT	AATGACTTAT	ACCACGAAAT	GAGCGATTCT	550
	GGCGTAATTA	AGAAACTGC	GATGGTATTC	GGACAAATGA	ACGAGCCACC	600
	TGGAGCACGT	CAACGTGTTG	CATTAACAGG	CTTAACAATG	GCTGAATATT	650
	TCCGTGATGA	GCAAGGACAA	GACGTACTTC	TGTTTCATCGA	TAATATCTTC	700
5	CGTTTCACGC	AAGCAGGTTC	TGAAGTATCT	GCCCTTCTTG	GCCGTATGCC	750
	ATCTGCGGTA	GGTTACCAAC	CAACACTTGC	AACAGAAATG	GGTCAATTAC	800
	AAGAGCGTAT	TACATCTACA	AATAAAGGGT	CTATCACGTC	TATC	844

-10-

2) INFORMATION FOR SEQ ID NO: 1260

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 840 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

20 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacillus cereus*
(B) STRAIN: ATCC 49064

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1260

	AAGCTACCAG	AAATCTACAA	CGCCCTTACG	GTAAACAGAG	GCAACGAAAA	50
	CGGAACAAGC	ATTAACCTAA	CATTTGAAGT	TGCACTTCAT	TTAGGTGATG	100
	ACACAGTTCG	TACAGTTGCA	ATGTCTTCCA	CAGATGGACT	TGTTCGTGGC	150
30	ACAGAAGTAG	AAGATACTGG	TAAAGCAATC	TCTGTACCAG	TTGGTGATGC	200
	AACACTTGGT	CGTGTATTTA	ACGTATTAGG	TGATGCAATT	GACTTAGATG	250
	GTGAGGTTCC	TGCGGATGTA	CGCCGTGATC	CAATTCACCG	TCAAGCACCT	300
	GCATTGGAAG	AATTATCTAC	TAAAGTAGAA	ATTCTTGAAA	CTGGTATTAA	350
	AGTAGTAGAC	TTACTTGCTC	CTTACATTAA	GGGTGGTAAG	ATCGGTCTAT	400
35	TCGGTGGTGC	CGGTGTAGGT	AAAACAGTAT	TAATTCAGGA	ATTAATCAAC	450
	AACATCGCAC	AAGAACACGG	TGGTATCTCT	GTATTGCTG	GTGTAGGTGA	500
	GCGTACTCGT	GAGGGTAATG	ACTTATACCA	CGAAATGAGC	GATTCAGGCG	550
	TAATTAAGAA	AACTGCGATG	GTATTGCGAC	AAATGAACGA	GCCACCTGGA	600
	GCGCGTCAAC	GTGTTGCGTT	AACAGGTTTA	ACAATGGCTG	AGCATTTCGG	650
40	TGATGAGCAA	GGACAAGACG	TTCTTCTGTT	CATCGATAAT	ATCTTCCGTT	700
	TCACGCAAGC	AGGTTCTGAA	GTATCTGCCC	TTCTTGGTG	TATGCCATCT	750
	GCGGTAGGTT	ACCAACCAAC	ACTTGCAACA	GAAATGGGTC	AATTACAAGA	800
	GCGTATTACA	TCTACAAATA	AAGGGTCTAT	CACGTCTATC		840

45

2) INFORMATION FOR SEQ ID NO: 1261

(i) SEQUENCE CHARACTERISTICS:

- 50 (A) LENGTH: 839 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 5 (A) ORGANISM: *Bacillus thuringiensis*
(B) STRAIN: BGSC 4AZ1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1261

```

10 GCGGAAAGCT ACCAGAAATC TACAATGCCC TTACGGTAAA ACAAAGCAAC 50
   GAAAACGGAA GCATGAACTT AACATTTGAA GTTGCACTTC ATTTAGGTGA 100
   TGATACAGTT CGTACAGTTG CGATGTCTTC CACAGATGGA CTTGTTTCGTG 150
   GCACAGAAGT AGAAGATACT GGTAAAGCAA TCTCTGTACC AGTTGGTGAT 200
   GCAACACTTG GACGTGTATT CAACGTATTA GGTGATGCAA TTGACTTAGA 250
15 TGGTGAACCT CCTGCGGATG TACACCGTGA TCCAATTCAC CGTCAAGCAC 300
   CTGCATTCTG AGAATTATCT ACTAAAGTAG AAATTCTTGA AACTGGTATT 350
   AAAGTAGTAG ACTTACTTGC TCCTTACATT AAGGGTGGTA AGATCGGCCT 400
   ATTCGGTGGT GCCGGCGTAG GTAAACAGT ATTAATTCAG GAGTTAATCA 450
   ATAACATCGC ACAAGAGCAC GGTGGTATCT CTGTATTCGC TGGTGTAGGT 500
20 GAGCGTACTC GTGAGGGTAA TGACTTATAC CACGAAATGA GCGATTCTGG 550
   CGTAATCAAG AAAACTGCGA TGGTATTCGG ACAAATGAAC GAGCCACCTG 600
   GAGCACGTCA ACGTGTTGCA TTAACAGGTT TAACAATGGC TGAGCATTTC 650
   CGTGATGAGC AAGGACAAGA CGTACTTCTG TTCATCGATA ACATCTTCCG 700
   TTTCACGCAA GCGGGTTCTG AAGTATCTGC CCTTCTTGGT CGTATGCCAT 750
25 CTGCGGTAGG TTACCAACCA ACACTTGCAA CAGAAATGGG TCAATTACAA 800
   GAGCGTATTA CATCTACAAA TAAAGGGTCT ATCACGTCT 839

```

30 2) INFORMATION FOR SEQ ID NO: 1262

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 833 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

40 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacillus thuringiensis*
(B) STRAIN: BGSC 4H2

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1262

```

45 AAGCTACCAG AAATCTACAA TGCCCTTACG GTAAAACAAA GCAACGAAAA 50
   CGGAAGCATG AACTTAACAT TTGAAGTTGC ACTTCATTTA GGTGATGATA 100
   CAGTTCGTAC AGTTGCGATG TCTTCCACAG ATGGACTTGT TCGTGGCACA 150
   GAAGTAGAAG ATACTGGTAA AGCAATCTCT GTACCAGTTG GTGATGCAAC 200
50 ACTTGGACGT GTATTCAACG TATTAGGTGA TGCAATTGAC TTAGATGGTG 250
   AACTTCCTGC GGATGTACAC CGTGATCCAA TTCACCGTCA AGCACCTGCA 300
   TTCGAAGAAT TATCTACTAA AGTAGAAATT CTTGAAACTG GTATTAAAGT 350
   AGTAGACTTA CTTGCTCCTT ACATTAAGGG TGGTAAGATC GGCCTATTTCG 400

```

	GTGGTGCCGG	CGTAGGTAAA	ACAGTATTAA	TTCAGGAATT	AATCAATAAC	450
	ATCGCACAAAG	AGCACGGTGG	TATCTCTGTA	TTCGCTGGTG	TAGGTGAGCG	500
	TACTCGTGAG	GGTAATGACT	TATACCACGA	AATGAGCGAT	TCTGGCGTAA	550
	TCAAGAAAAC	TGCGATGGTA	TTCGGACAAA	TGAACGAGCC	ACCTGGAGCA	600
5	CGTCAACGTG	TTGCATTAAC	AGGTTTAAACA	ATGGCTGAGC	ATTTCCGTGA	650
	TGAGCAAGGA	CAAGACGTAC	TTCTGTTCAT	CGATAACATC	TTCCGTTTCA	700
	CGCAAGCGGG	TTCTGAAGTA	TCTGCCCTTC	TTGGTCGTAT	GCCATCTGCG	750
	GTAGGTTACC	AACCAACACT	TGCAACAGAA	ATGGGTCAAT	TACAAGAGCG	800
	TATTACATCT	ACAAATAAAG	GGTCTATCAC	GTC		833

2) INFORMATION FOR SEQ ID NO: 1263

- 15 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 790 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Double
 - (D) TOPOLOGY: Linear
- 20 (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Bacillus thuringiensis*
 - 25 (B) STRAIN: BGSC 4Q1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1263

	CGAAAACGGA	AGCATGAACT	TAACATTTGA	AGTTGCACTT	CATTTAGGTG	50
30	ATGATACAGT	TCGTACAGTT	GCGATGTCTT	CCACAGATGG	ACTTGTTTCGT	100
	GGCACAGAAG	TAGAAGATAC	TGGTAAAGCA	ATTTCTGTAC	CAGTTGGTGA	150
	TGTAACACTT	GGACGTGTAT	TCAACGTATT	AGGTGATGCA	ATTGACTTAG	200
	ATGGTGAACT	TCCTGCGGAT	GTACACCGTG	ATCCAATTCA	CCGTCAAGCA	250
	CCTGCATTCG	AAGAATTATC	TACTAAAGTA	GAAATTCTTG	AAACTGGTAT	300
35	TAAAGTAGTA	GACTTACTTG	CTCCTTACAT	TAAGGGTGGT	AAGATCGGCC	350
	TATTCGGTGG	TGCCGGTGTA	GGTAAAACAG	TATTAATTCA	GGAATTAATT	400
	AACAACATCG	CACAAGAGCA	CGGTGGTATC	TCTGTATTCT	CTGGTGTAGG	450
	TGAGCGTACT	CGTGAGGGTA	ATGACTTATA	CCACGAAATG	AGCGATTCTG	500
	GCGTAATCAA	GAAAACTGCG	ATGGTATTCT	GACAAATGAA	CGAGCCACCT	550
40	GGAGCACGTC	AACGTGTTGC	ATTAACAGGT	TTAACAATGG	CTGAGCATTT	600
	CCGTGATGAG	CAAGGACAAG	ACGTACTTCT	GTTTCATCGAT	AACATCTTCC	650
	GTTTCACGCA	AGCGGGTCT	GAAGTATCTG	CCCTTCTTGG	TCGTATGCCA	700
	TCTGCGGTAG	GTTACCAACC	AACACTTGCA	ACAGAAATGG	GTCAATTACA	750
45	AGAGCGTATT	ACATCTACAA	ATAAAGGGTC	TATCACGTCT		790

2) INFORMATION FOR SEQ ID NO: 1264

- 50 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 644 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

5 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Bacillus thuringiensis*

(B) STRAIN: HER 1232

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1264

```

10 AGTTGCACTT CATTAGGTG ATGATACAGT TCGTACAGTT GCGATGTCTT 50
   CCACAGATGG ACTTGTCGT GGCACAGAAG TAGAAGATAC TGGTAAACCA 100
   ATCTCTGTAC CAGTTGGTGA TGTAACACTT GGTCCGCTAT TTAACGTATT 150
   AGGTGATGCA ATTGACTTAG ATGGTGAGGT TCCTGCAGAT GTACATCGTG 200
15 ATCCAATTCA CCGTCAAGCA CCTGCATTCG AAGAATTATC TACTAAAGTA 250
   GAAATTCTTG AAAGTGGTAT TAAAGTAGTA GACTTACTTG CTCCTTACAT 300
   TAAGGGTGGT AAGATCGGCC TATTCGGTGG TGCCGGCGTA GGTAAAACAG 350
   TATTAATTCA GGAATTAATT AACAACATCG CACAAGAGCA CGGTGGTATC 400
   TCTGTATTCG CTGGTGTAGG TGAGCGTACT CGTGAGGGTA ATGACTTATA 450
20 CCACGAAATG AGCGATTCTG GCGTAATCAA GAAAGTGGC ATGGTATTCG 500
   GACAAATGAA CGAGCCACCT GGAGCACGTC AACGTGTTGC ATTAACAGGT 550
   TTAACAATGG CTGAGCATTT CCGTGATGAG CAAGGACAAG ACGTACTTCT 600
   GTTCATCGAT AACATCTTCC GTTTCACGCA AGCGGGTTCT GAAG 644

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25

2) INFORMATION FOR SEQ ID NO: 1265

(i) SEQUENCE CHARACTERISTICS:

```

30 (A) LENGTH: 823 bases
   (B) TYPE: Nucleic acid
   (C) STRANDEDNESS: Double
   (D) TOPOLOGY: Linear

```

35 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Bacillus anthracis*

(B) STRAIN: ATCC 4229

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1265

```

   GGCAGAAAGC TACCAGAAAT CTACAACGCC CTTACGGTAA AACAGAGCAA 50
   CGAAACGGA ACAAGCATT ACTTAACATT TGAAGTTGCA CTTCAATTTAG 100
45 GTGATGACAC AGTTCGTACA GTTGCAATGT CTTCCACAGA TGGACTTGTT 150
   CGTGGCACAG AAGTAGAAGA TACTGGTAAA GCAATCTCTG TACCAGTTGG 200
   TGATGCAACA CTTGGTCGTG TATTTAACGT ATTAGGTGAT GCAATTGACT 250
   TAGATGGTGA GGTTCCTGCG GATGTACGTC GTGATCCAAT TCACCGTCAA 300
   GCACCTGCAT TCGAAGAATT ATCTACTAAA GTAGAAATTC TTGAAACTGG 350
50 TATTAAAGTA GTAGACTTAC TTGCTCCTTA CATTAAAGGT GGTAAGATCG 400
   GTCTATTCGG TGGTGCCGGT GTAGGTAAAA CGGTATTAAT TCAGGAATTA 450
   ATCAATAACA TCGCACAAGA ACACGGTGGT ATCTCTGTAT TCGCTGGTGT 500
   AGGTGAGCGT ACTCGTGAGG GTAATGACTT ATACCACGAA ATGAGCGATT 550

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	CTGGCGTAAT	TAAGAAACT	GCGATGGTAT	TCGGACAAAT	GAACGAGCCA	600
	CCTGGAGCAC	GTCAACGTGT	TGCGTTAACA	GGTTTAACAA	TGGCTGAGCA	650
	TTTCCGTGAT	GAGCAAGGAC	AAGATGTACT	TCTGTTTCATC	GATAATATCT	700
	TCCGTTTCAC	GCAAGCAGGT	TCTGAAGTAT	CTGCCCTTCT	TGGCCGTATG	750
5	CCATCTGCGG	TAGGTTACCA	ACCAACACTT	GCAACAGAAA	TGGGTCAATT	800
	ACAAGAGCGT	ATTACATCTA	CAA			823

10 2) INFORMATION FOR SEQ ID NO: 1266

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 715 bases
 (B) TYPE: Nucleic acid
 15 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

20 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Paracoccidioides brasiliensis*
 (B) STRAIN: ATCC 200443

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1266

25	TGGTCCGAGR	CCCGATTCTMA	TGAAATTATC	AAGGAAACCT	CCAAYTTCAT	50
	TAAGAAGGTC	GGATATAACC	CCAAGACTGT	TCCTTTCGTT	CCCATTTCTG	100
	GTTTCCAGGG	TGACAACATG	ATCGATSCCT	CTGCCAACTG	CCCATGGTAC	150
	AAGGGCTGGT	ACMAKGAGAC	TGCCGACAGG	CAAGYACTCT	GGCAAGACCC	200
30	TTCTTGAGGC	CATTGACGSC	ATTGAGCCCC	CCAMSCGTCC	TWCCGATAAA	250
	CCTCTCCGTC	TTCCTCTCCA	GGATGTCTAC	AAGATCTCCG	GTATTGGMAC	300
	TGTTCTTGTC	GGACGTRTTG	AGACTGGAGT	CATCAAGCCC	GGTATGGTCG	350
	TGACCTTCGC	TCCCGCCAAC	GTCACCACTG	AAGTCAAGTC	CGTTGAAATG	400
	CACCACCAGC	AGCTTTCCGA	CGGTAWCCCC	GGTGACAACG	TCGGCTTCAA	450
35	CGTCAAGAAT	GTTTCCGTCA	AAGAAGTCCG	CCGTGGTAAC	GTTGCCTGGT	500
	GACTCTAAGA	ATGATCCCGC	MAWGGGCTGC	GATTCCTTCA	ATGCYCAGGT	550
	CATCGTCCTC	AACCACCCTG	GTCAGGTTGG	CGCTGGTTAT	GCCCCAGTCC	600
	TCGAYTGCCA	TACTGCCCAC	ATTGCTTGCA	ARTTCGCTGA	GMTCMAGAG	650
	AAGATTGAYC	GCCGAACCGG	MAAGTCTGTT	GAGAACGCCC	CCAAGTTCAT	700
40	CAAGTCCGGT	GATGC				715

2) INFORMATION FOR SEQ ID NO: 1267

45 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 875 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 50 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Blastomyces dermatitidis*

(B) STRAIN: ATCC 56220

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1267

```

GAGTCCTCTT ATTTACTTTT GTCATGACTA CCTTACTAAT CTGTCATAGA      50
TCGTTACAAC GAAATCGTCA AGGAGACTTC CAACTTCATC AAGAAGGTCG      100
GATACAACCC CAAGAACGTT CCTTTCGTTT CTATCTCCGG TTTCAACGGC      150
10 GACAACATGC TTGAGCCCTC- CCCCAACTGC CCCTGGTACA AGGGTTGGGA      200
GAAGGAGACC AAGGCCGGTA AGGTCACCTG TAAGACCCTC CTCGAGGCCA      250
TCGACGCCAT TGAGCCCCCT ACCCGTCCCG CCAACAAGGT CAGTACTACC      300
TCAATTACTT GAACTCTCTT CATACGTTCC GATTACTGAC TGCTTCACAG      350
CCCCTCCGTC TTCCCCTCCA GGACGTTTAC AAGATCGGTG GTATTGGAAC      400
15 GGTGCCCCGTC GGTTCGTGTTG AGACCGGTAC CATCTCCCCT GGTATGGTCG      450
TTACCTTGTA TGTATCCTGA CCATCCCCCT TGGCAATCAT TACGTACTAA      500
CTCACTCTTC AGCGCTCCCG CCAACGTCAC CACTGAAGTC AAGAGTGTTG      550
AAATGCACCA CCAGCAGCTC GCTGCCGGTC AGCCCGGTGA CAACGTTGGT      600
TTCAACGTGA AGAACGTCTC CGTCAAGGAA ATCCGTCGTG GTAACGTTGC      650
20 TGGTGATAGC AAGAACGACC CCCCTGCCGG TGCTGCTTCC TTCAACGCCC      700
AGGTCATCGT CCTCAACCAC CCCGGTCAGG TCGGTGCTGG TTACGCCCCA      750
GTCCTTGACT GCCACACTGC CCACATTGCT TGCAAGTTCT CTGAATCCT      800
TGAGAAGATT GACCGTCGTA CCGGAAAGTC TGTGAGGAC CACCCCAAGT      850
TCATCAAGTC CGGTGACGCT GCCAT      875
25

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2) INFORMATION FOR SEQ ID NO: 1268

30 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1124 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Histoplasma capsulatum*

40 (B) STRAIN: WSA-377

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1268

```

GTGAGCGTGG TATCACCATC GATATTGCCC TCTGGAAATT CGAGACCCCG      50
45 AAGTACAGTG TCACTGTCAT TGGTGAGTGC TTTTACCCTT TCTTAAGCAG      100
ATTTCAACTT CCAGAGTATC TACTCTAACA TATCCGCTTA GATGCTCCCG      150
GCCATCGTGA CTTTCATCAAG AACATGATCA CTGGTACCTC CCAGGCTGAC      200
TGGCCTATCC TCATCATTCG TGCCGGTACT GGTGAGTTCG AGGCTGGTAT      250
CTCCAAGGAT GGCCAGACTC GTGAGCACGC TCTGCTTGCT TTCACCCTTG      300
50 GTGTGAGGCA ACTCATCGTT GCCATCAACA AGATGGACAC CACCAAGTGG      350
TCCGAGTCCC GTTTCAACGA AATCATCAAG GAGGTTTCCA ACTTCATCAA      400
GAAGGTCGGA TATAACCCCA AGGCTGTTCC CTTCGTGCCA ATCTCTGGTT      450
TCGAGGGTGA CAACATGATT GAACCTCCC CCAACTGCAC CTGGTACAAG      500

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GGCTGGAACA AGGAGACTGC CTCTGGCAAG TCTTCTGGTA AAACCCTTCT 550
CGATGCCATT GACGCCATTG AACCCCAAC CCGTCTACC GATAAGCCTC 600
TCCGTCTTCC CCTCCAGGAT GTTTACAAAA TCTCTGGTAT TGGCACTGTT 650
CCCGTCGGAC GTGTTGAGAC TGGTGTATC AAGCCCGGTA TGGTCGTGAC 700
5 TTTGCTCCC TCCAACGTCA CCACTGAAGT CAAGTCCGTC GAGATGCACC 750
ACCAACAACCT CCAGGCTGGT TACCCTGGTG ACAACGTCGG CTTCAACGTC 800
AAGAACGTTT CAGTCAAGGA AGTCCGCCGT GGCAACGTTG CTGGCGACTC 850
CAAAAATGAT CCCCCAAGG GCTGCGAATC CTTCAATGCC CAGGTCATCG 900
TCCTTAACCA CCCCAGCCAG GTTGGCGCTG GTTATGCCCC AGTCCTCGAC 950
10 TGCCACACTG CCCACATTGC TTGCAAGTTC TCTGAACTCA TTGAGAAGAT 1000
CGACCGCCGT ACTGGAAAGT CTGTTGAGAA CAACCCCAAG TTCATCAAGT 1050
CTGGTGATGC TGCTATCGTC AAGATGGTTC CCTCCAAGCC CATGTGCGTG 1100
GAGCCCTTCA CTGACTATCC CCCT 1124

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15

2) INFORMATION FOR SEQ ID NO: 1269

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 1043 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

25 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Trichophyton rubrum*
 (B) STRAIN: WSA-224

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1269

```

GTGAGCGTGG TATCACCATC GATATCGCCC TCTGGAAGTT CGAGACCCCC 50
AAGTACAATG TCACCGTCAT TGGTATGTTT CTTTGCCTTG TTCCCTCATG 100
35 TGGTTGTACC ATATCTAACG AGAGTAGACG CCCCCGGTCA CCGTGACTTC 150
ATCAAGAACA TGATCACTGG TACCTCCCAG GCTGACTGCG CTATTCTCAT 200
CATTGCTGCC GGTACTGGTG AGTTCGAGGC TGGTATCTCC AAGGATGGCC 250
AGACCCGTGA GCACGCTCTG CTCGCCTTCA CCCTCGGTGT CAAGCAGCTC 300
ATCGTTGCCA TCAACAAGAT GGACACCACC GGCTGGTCCG AGGATCGTTT 350
40 CAAGGAAATT ATCAAGGAAG TCACCAACTT CATCAAGAAG GTTGGCTACG 400
ACCCCAAGGG TGTTCCATTC GTTCCAATCT CTGGTTTCAA CGGTGACAAC 450
ATGATTGAGG CCTCCACCAA CTGCCCATGG TACAAGGGAT GGAACAAGGA 500
GACCAAGGCC GGTGGTGCCA AGTCCGGCAA GACCCTCCTC GAGGCCATCG 550
ATGCCATCGA CATGCCAACC CGTCCTACCG ACAAGCCCCT CCGTCTCCCA 600
45 CTCCAGGATG TCTACAAGAT CTCTGGTATC GGAAGTGTGC CAGTCGGTGC 650
TGTTGAGACC GGTATCATCA AGCCCGGTAT GGTCGTCACC TTNGCCCCCG 700
CCAACGTCAC CACTGAAGTC AAGTCCGTYK AAATGCACCA CCAGCAGCTT 750
CAGCAGGGTG TCCCCGGTGA CAACGTCGGC TTCAATGTCA AGAACGTTTC 800
CGTCAAGGAA GTCCGCCGTG GTAACGTTGC CGGTGACTCC AAGAACGACC 850
50 CACCATCCGG CTGTGCCTCC TTCAACGCCC AGGTCATYGT CCTCAACCAC 900
CCCGGCCAGA TCGGTGCTGG TTACGSTCCA GTCCTCGACT GCCACACTGS 950
TCACATTGCT TGCAAGTTCG CTGAGCTCCT CGAGAAGATT GACCGCCGTA 1000
CCGGTAAATC CGTCAAGCC AACCCCAAGT TCGTCAAGTC TGG 1043

```

2) INFORMATION FOR SEQ ID NO: 1270

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1105 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Microsporium canis*
 (B) STRAIN: WSA-217
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1270

	GCTGAGCGTG	AGCGTGGTAT	CACCATTGAT	ATCGCCCTCT	GGAAGTTCGA	50
	GACCCCCAAG	TACATGGTCA	CCGTCATCGG	TATGCTTTAT	CTGTTTCCCA	100
	TTTATAGTTG	CGACCAGTAA	CTAACAAAAA	GATAGTGCCC	CCGGGCACCG	150
20	TGACTTCATC	AAGAACATGA	TTACTGGTAC	CTCCCAGGCC	GACTGCGCTA	200
	TTCTCATCAT	TGCTGCCGGT	ACTGGTGAGT	TCGAGGCTGG	TATCTCCAAG	250
	GATGGCCAGA	CTCGTGAGCA	CGCCCTGCTC	GCTTTCACCC	TCGGTGTCAA	300
	GCAGCTCATC	GTTGCCATCA	ACAAGATGGA	CACCACCAAC	TGGTCTGAGT	350
	CCCGTTTCGG	TGAAATCATC	AAGGAAGTCA	CCAACTTCAT	CAAGAAGGTC	400
25	GGCTACGACC	CCAAGGGTGT	CCCATTCTGT	CCAATCTCTG	GCTTCAACGG	450
	TGACAACATG	ATTGAGCCCT	CCACCAACTG	CCCATGGTAC	AAGGGATGGA	500
	ACAAGGAGAC	CAAGGCCGGT	GGCAAATCCT	CTGGTAAGAC	CCTCCTTGAG	550
	GCCATCGATG	CCATTGACAT	GCCCACTCGT	CCCACCGACA	AGCCTCTCCG	600
	TCTCCCCTC	CAGGATGTCT	ACAAGATCTC	TGGTATCGGA	ACAGTACCAG	650
30	TCGGTCGTGT	TGAGACTGGT	ATCATCAAGC	CTGGTATGGT	TGTCACCTTY	700
	GCCCCCGCCA	ACGTCACCAC	TGAAGTCAAG	TCCGTCGAAA	TGCACCACCA	750
	GCAGCTYGTG	CAGGGTGTTC	CCGGTGACAA	CGTTGGCTTC	AACGTCAAGA	800
	ACGYTCTGT	CAAGGAAGTC	CGCCGTGGTA	ACGTTGCCGG	TGATTCCAAG	850
	AACGACCCAC	CAGCTGGCTG	CGCCTCTTTC	AAGGCCCAGG	TCATCGTCCT	900
35	CAACCACCCC	GGCCAGATCG	GTGCTGGTTA	CGCCCCAGTC	CTTGACTGCC	950
	ACACTGCCCA	CATTGCTTGC	AAGTTCTCTG	AGCTTCTTGA	GAAGATTGAC	1000
	CGCCGTACTG	GTAAATCCGT	CGAAACCAGC	CCTAAGTTCG	TCAAGTCTGG	1050
	TGATGCCGCT	ATTGCCACCA	TGGTTCCATC	CAAGCCCATG	TGCGTTGAGG	1100
	CTTTC					1105

2) INFORMATION FOR SEQ ID NO: 1271

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1244 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Aspergillus versicolor*

(B) STRAIN: WSA-175

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1271

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5      GAGCGTGAGC GTGGTATCAC CATCGATATC GCTCTCTGGA AGTTCCAGAC      50
      CCCTAAGTAT GAGGTCACCG TCATTGGTAT GTTGTCTTC TTGTGTTACC      100
      ATCGAAACAT ATCTAACCTA CAACTGCAGA CGCCCCCGGT CACCGTGACT      150
      TCATCAAGAA CATGATCACT GGTACCTCCC AGGCCGACTG CGCTATTCTC      200
10     ATCATTGCTT CCGGTACTGG TGAATTCGAG GCTGGTATCT CCAAGGATGG      250
      CCAGACCCGT GAGCACGCTC TGCTCGCTTT CACCCTCGGT GTCCGTCAGC      300
      TCATCGTTGC CCTCAACAAG ATGGACACTG CTGGCTGGGC TGAGGCTCGT      350
      TACAACGAAA TCGTCAAGGA AACTTCCGGT TTCATCAAGA AGGTCGGCTA      400
      CAACCCCAAG TCGGTTCCCT TCGTCCCAT CTCCGGTTTC AACGGTGACA      450
15     ACATGCTTGA GCCCTCCTCC AACTGCCCCT GGTACAAGGG TTGGGAGAAG      500
      GAGACCAAGG CTGGTAAGGC CACTGGTAAG ACCCTCCTCG AGGCCATCGA      550
      CGCCATTGAG CCTCCCGTCC GTCCCTCCAA CAAGCCTCTC CGTCTTCCCC      600
      TCCAGGATGT CTACAAGATC TCTGGTATTG GAACTGTCCC CGTCGGCCGT      650
      GTCGAGACCG GTACCATCGT CCCC GGATG GTCGTCACCT TCGTCCCGC      700
20     CAACGTCACC ACTGAAGTCA AGTCCGTTGA GATGCACCAC CAGCAGCTCA      750
      AGGAGGGTGT TCCCGGTKAC AACGTTGGTT TCAACGTGAA GAACGTTTCC      800
      GTCAAGGAAG TCCGCCGTGG TAACGTCGCT GGTGACTCCA AGAACGACCC      850
      CCCTGCCGGT GCTGCCTCTT TCACCGCCCA GGTCATCGTC CTCAACCACC      900
      CCGGTCAGGT CGGCGCTGGT TACGCTCCCG TCCTCGACTG CCACACCGCT      950
25     CACATTGCCT GCAAGTTCGC TGAGCTCCAG GAGAAGATCG ACCGCCGTAC      1000
      CGGAAAGTCT GTCGAATYTG CCCCCAAGTT CATCAAGTCT GGTGACGCCG      1050
      CTATCGTCAA GATGATTCCC TCCAAGCCCA TGTGTGTCGA GTCTTTTACT      1100
      GACTACCCTC CTYTCGGCCG TTTCGCCGTC CGTGACGTAA GTTCTTTCCC      1150
      CAGCTTTTTCG ATGCTACCCT TCTMTGAATC ACGTGTCTATG TCTTGGCACC      1200
30     CGCCCATCAC ATGACCACGC AACCCCTATAC CCCGCCACAC CCTT      1244

```

2) INFORMATION FOR SEQ ID NO: 1272

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35     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 1032 bases
          (B) TYPE: Nucleic acid
          (C) STRANDEDNESS: Double
40     (D) TOPOLOGY: Linear

```

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

```

45     (A) ORGANISM: Exophiala moniliae
          (B) STRAIN: WSA-219

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1272

```

50     GCTGAGCGTG AGCGTGGTAT CACCATCGAT ATCGCTCTCT GGAAGTTCGA      50
      GACCCCAAG TACTATGTCA CCGTCATCGA CGCCCCCGGT CATCGTGACT      100
      TCATCAAGAA CATGATCACT GGTACTTCCC AAGCTGACTG CGCCATTCTC      150
      ATCATTGCTG CCGGTACTGG TGAATTCGAA GCCGGTATCT CCAAGGATGG      200

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	TCAGACCCGT	GAGCACGCTC	TGCTTGCCTA	CACCCTGGGT	GTCAAGCAGC	250
	TCATTGTGCG	CATCAACAAG	ATGGACACTA	CCAAGTGGTC	TGAGGACCGT	300
	TTCAACGAAA	TCATCAAGGA	GACTTCCAGC	TTCATCAAGA	AGGTCGGCTA	350
	CAACCCCAAG	TCCGTTCCCT	TCGTCCCCAT	CTCCGGCTTC	AACGGTGACA	400
5	ACATGATCGA	CGTCTCCACC	AACTGCCCCT	GGTACAAGGG	CTGGGAGAAG	450
	GAGACCAAGG	CTGGCAAGGC	CTCTGGCAAG	ACTCTCCTTG	AGGCCATCGA	500
	CGCCATTGAC	CCCCCTCTC	GTCCCACCGA	CAAGCCTYTC	CGTCTCCCTC	550
	TCCAGGATGT	GTACAAGATC	TCTGGTATCG	GAACGGTGCC	CGTCGGTCGT	600
	GTCGAGACTG	GTATCATCAA	GGCCGGTATG	GTCGTTACCT	TCGCTCCTGC	650
10	CAACGTCACC	ACTGAAGTCA	AGTCCGTCGA	AATGCACCAC	GAACAGCTCG	700
	CCGAGGGTGT	TCCAGGTGAC	AACGTCGGTT	TCAACGTCAA	GAACGTYTCC	750
	GTCAAGGAGG	TTCGTCGTGG	AAACGTTTGC	GGTGACTCCA	AGAACGACCC	800
	ACCCAAGGGC	GCTGATTCCT	TCAACGCCCA	GGTCATCGTC	TTGAACCACC	850
	CTGGTCAAGT	TGGTGCTGGC	TACGCCCCAG	TGTTGGATTG	CCACACTGCC	900
15	CACATTGCTT	GCAAGTTCTC	TGAGCTTCTC	GAGAAGATCG	ATCGTCGKAC	950
	CGGAAAGTCG	ATCGAAAACA	ACCCCAAGTT	CATCAAGTCT	GGTGACGCTG	1000
	CCATCGTCAA	GATGGTTCCC	AGCAAGCCCA	TG		1032

20

2) INFORMATION FOR SEQ ID NO: 1273

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1106 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Hortaea werneckii*
 (B) STRAIN: ATCC 34944

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1273

	TAACAGCCCG	TGCGACCGTC	TCGTCCAATA	ACTAATGATT	CGCAGGTACT	50
	ATGTCGTGAG	TATCCGGTCC	TTTTTTGTTA	ATTTACCAGA	AATGACGAAA	100
	TTTTTGACTA	ATTAACACAC	TCAGACCGTC	ATTGACGCC	CGGGTCACCG	150
40	TGACTTCATC	AAGAACATGA	TCACTGGTAC	CTCCCAGGCC	GACTGCGCTG	200
	TCCTCATCAT	TGCTGCCGGT	ACTGGTGAGT	TCGAGGCTGG	TATCTCCAAG	250
	GATGGCCAGA	CCCGTGAGCA	CGCCCTGCTC	GCCTACACCC	TCGGTGTCAA	300
	GCAGCTCATC	GTCGCCATCA	ATAAGATGGA	CACCACCAAG	TGGTCCGAGG	350
	AGCGTTACGG	CGAGATCATC	AAGGAGACCT	CTGCCTTCAT	CAAGAAGGTC	400
45	GGTTTCAACC	CGAAGCACGT	CCCGTTCGTC	CCGATCTCCG	GTTTCAACGG	450
	TGACAACATG	ATCGAGGCCT	YCACCAACTG	CCCGTGGTAC	AAGGGCTGGG	500
	AGAAGGAGAC	CAAGGCCAAG	GTCACCGGCA	AGACCCTYCT	TGAGGCCATT	550
	GACAACATCG	ACCCGCCGAG	CCGTCTCTCC	GACAAGCCGC	TCCGTCTTCC	600
	CCTCCAGGAT	GTCTACAAGA	TCGGTGGTAT	TGGGACAGTC	CCAGTCGGCC	650
50	GTGTCGAGAC	CGGTACCATC	AAGGCCGGCA	TGGTCGTTAC	CTTCGCTCCG	700
	GCTGGTGTCA	CCACTGAAGT	GAAGTCCGTT	GARATGCACC	ACGAGCAGCT	750
	CGCTGAGGGT	YTGCCGGGTG	ACAACGTCGG	CTTCAACGTC	AAGAACGTTT	800
	CCGTCAAGGA	GATCCGTCGT	GGCAACGTTG	CTGGTGACAG	CAAGGCTGAC	850

	CCGCCGAAGG	GCTGCGACAG	CTTCAACGCC	CAGGTCATCG	TCCTGAACCA	900
	CCCTGGCCAG	GTCGGTGCTG	GTTACGCTCC	AGTCCTGGAC	TGCCACACTG	950
	CCCACATTGC	CTGCAAGTTC	GGCGAGCTCC	TCGAGAAGAT	CGACCGTCGC	1000
	TYTGGCAAGT	CCATTGAAGC	CTYGCCTAAG	TACATCAAGT	CTGGTGACGC	1050
5	TGCCATYGTC	AAGATGATTC	CGTCCAAGCC	GATGTGCGTT	GAGCCATTCA	1100
	CTGAGT					1106

10 2) INFORMATION FOR SEQ ID NO: 1274

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1119 bases
 (B) TYPE: Nucleic acid
 15 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

20 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Fusarium solani*
 (B) STRAIN: ATCC 32793

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1274

25	CTCAAGGCCG	AGCGTGAGCG	TGGTATCACC	ATCGACATTG	CCCTCTGGAA	50
	GTTTCGAGACT	CCCCGCTACT	ATGTCACCGT	CATTGGTATG	TTGCTGTCAC	100
	CTCTCTCACA	CATGTCTCAC	CACTAACAAT	CAACAGACGC	CCCCGGCCAC	150
	CGTGATTTCA	TCAAGAACAT	GATCACTGGT	ACTTCCCAGG	CCGACTGCGC	200
30	CATTCTCATC	ATTGCCGCCG	GTA CTGGTGA	GTTCGAGGCT	GGTATCTCCA	250
	AGGATGGCCA	GACCCGTGAG	CACGCCCTGC	TCGCCTACAC	CCTCGGTGTC	300
	AAGAACCTCA	TTGTCGCCAT	CAACAAGATG	GACACCACCA	AGTGGTCCGA	350
	GTCCCGTTAC	CAGGAGATCA	TCAAGGAGAC	CTCCAACTTC	ATCAAGAAGG	400
	TCGGCTACAA	CCCCAAGGCT	GTCGCTTTCG	TCCCCATCTC	CGGTTTCAAC	450
35	GGCGACAACA	TGCTTACTCC	CTCCACCAAC	TGCCCCTGGT	ACAAGGGCTG	500
	GGAGCGTGAG	ATCAAGTCCG	GCAAGCTCAC	TGGCAAGACC	CTCCTCGAGG	550
	CCATTGACTC	CATCGAGCCC	CCCAAGCGTC	CCGTCGACAA	GCCCCTYCGA	600
	CTTCCCCTCC	AGGATGTCTA	CAAGATCGGT	GGTATTGGCA	CGGTTCCCCT	650
	CGGCCGTATC	GAGACTGGTG	TCATCAAGCC	CGGTATGGTC	GTTACCTTMG	700
40	CCCCCTCCAA	CGTCACCACT	GAAGTCAAGT	CCGTCGARAT	GCACCACGAG	750
	CAGCTCTYTG	AGGGTCTTCC	CGGTGACAAC	GTCGGCTTCA	ACGTGAAGAA	800
	CGTYTCCGTC	AAGGAGATCC	GACGTGGCAA	CGTCGCTGGT	GACTCCAAGA	850
	ACGACCCCCC	TYTGGGTGCC	GCCTCTTTCA	CCGCCCAGGT	CATTGTCCTC	900
	AACCACCCTG	GCCAGGTCGG	TGCCGGTTAC	GCCCCCGTTY	TGGACTGCCA	950
45	CACTGCCCAC	ATTGCCTGCA	AGTTCGCCGA	GATCCAGGAG	AAGATCGACC	1000
	GCCGA ACTGG	TAAGGCTGTT	GAGTCCGCCC	CCAAGTTCAT	CAAGTCTGGT	1050
	GACTCCGCCA	TCGTCAAGAT	GGTTCCCTCC	AAGCCCATGT	GCGTTGAGGC	1100
	TTTCACTGAC	TACCCCCCT				1119

50

2) INFORMATION FOR SEQ ID NO: 1275

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1113 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

5

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Aureobasidium pullulans*
 (B) STRAIN: WSA-234

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1275

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15 CTGAAGTCTG AGCGTGAGCG TGGTATCACT ATCGATATCG CCCTCTGGAA      50
   GTTCGAGACC CCCAAGTACA TGGTCACCGT CATCGATGCC CCCGGTCACC      100
   GTGATTTTCAT CAAGAACATG ATCACTGGTA CCTCCCAGGC TGACTGCGCC      150
   ATTCTCATCA TTGCTGCCGG TACTGGTGAG TTCGAGGCTG GTATCTCCAA      200
   GGATGGCCAG ACTCGTGAGC ACGCTCTCCT CGCCTACACC CTTGGTGTCA      250
20 AGCAGCTCAT CGTTGCCATC AACAAGATGG ACACCACCAA GTGGTCTGAG      300
   GCCCGTTACC AGGAGATCAT CAAGGAGACC TCCGGTTTCA TCAAGAAGGT      350
   CGGCTACAAC CCCAAGCACG TTCCCTTCGT CCCCATCTCC GGCTTCAACG      400
   GAGACAACAT GATCGAGGTC AGCTCCAAC TCCCTTGGTA CAAGGGTTGG      450
   GAGAAGGAGA CCAAGGCCAA GGCCACTGGC AAGACCCTCC TCGAGGCCAT      500
25 TGACGCCATC GACCCTCCTT CCCGTCTAC CGACAAGCCC CTCCGTCTTC      550
   CCCTCCAGGA TGTCTACAAG ATCGGTGGTA TTGGCACGGT GCCCGTCGGT      600
   CGTGTTGAGA CCGGTAAGAT CATGGGTGGT ATGGTTGTCA CCTTCGCCCC      650
   CGCTGGTGTC ACCACCGAGG TCAAGTCCGT CGAGATGCAC CACGAGCAGC      700
   TCACCGAGGG TCTTCCCGGT GACAACGTCG GCTTCAACGT CAAGAACGTY      750
30 TCCGTCAAGG AGATCCGTCG TGGCAACGTT GCCGGTGA CTCAAGAACGA      800
   CCCCCCAAG GGTGTGACT CCTTCAACGC CCAGGTCATC GTCCTGAACC      850
   ACCCTGGTCA GGTCGGTGCT GGTTACGCAC CCGTCCTCGA CTGCCACACT      900
   GCCCACATTG CTTGCAAGTT YTCCGAGCTT GTTGAGAAGA TTGACCGCAG      950
   AACCGGCAAG TCCGTTGAGG CTGCCCCCAA GTTCATCAAG TCTGGTGACG      1000
35 CCGCCATCGT CAAGATGGTT CCTCCAAGC CCATGTGTGT TGAGGCTTTC      1050
   ACCGACTACC CTCCTYTCGG TCGTTTCGCC GTCCGGTATG TTTTCTTCT      1100
   TCAATCATTC TTC                                     1113

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40

2) INFORMATION FOR SEQ ID NO: 1276

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 731 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

45

(ii) MOLECULE TYPE: Genomic DNA

50

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Blastomyces dermatitidis*
 (B) STRAIN: ATCC 14112

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1276

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5  GGTCTGAGAC CCGTTTCAAC GAAATTATCA AGGAAGTCAG CAACTTCATC      50
   AAGAAGGTCG GATACAACCC CAAGTCTGTT CCCTTCGTGC CAATCTCCGG      100
   TTTCGAGGGT GACAACATGA TTGAGCCTTC CCCCAACTGC CTTGGGTACA      150
   AGGGCTGGAA CAAGGAGACT GCTGCTGGCA AGGCCGCCGG TAAGACTCTT      200
   CTCGATGCCA TTGACGCCAT CGACCCCCCC GTCCGTCCTA CCGAGAAGCC      250
   TCTCCGTCTT CCCCTCCAGG ATGTGTACAA GATCTCCGGT ATTGGCACTG      300
10  TTCCCGTTGG ACGTGTCTGAG ACTGGTGTCA TCAAGCCTGG TATGGTCTGT      350
   ACCTTCGCCC CTGCCAACGT CACCACTGAA GTCAAGTCCG TTGAAATGCA      400
   CCACCAGCAG CTCCAGGCTG GTTACCCTGG TGACAACGTC GGCTTCAACG      450
   TCAAGAACGT TTCCGTCAAG GAAGTCCGCC GTGGCAACGT TGCCGGTGAC      500
   TCCAAGAACG ACCCCCCCAA GGGCTGCGAG TCCTTCAACG CCCAGGTCAT      550
15  CGTCCTCAAC CACCCCGGCC AGGTTGGCGC TGGTTATGCC CCAGTCCTCG      600
   ACTGCCACAC TGCCACATT GCTTGCAAGT TCTCTGAGCT CATCGAGAAG      650
   ATTGACCGCC GTACCGGAAA GTCTGTTGAG GACAACCCCA AGTTCATCAA      700
   GTCCGGTGAT GCTGCTATCG TCAAGATGAT T                      731

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20

2) INFORMATION FOR SEQ ID NO: 1277

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 1046 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

30 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Exophiala dermatitidis*
 (B) STRAIN: ATCC 76088

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1277

```

   CCGAGCGTGA GCGTGGTATC ACCATCGATA TCGCCCTCTG GAAGTTCGAG      50
   ACCCCCAAGT ACTATGTCAC CGTCATCGAC GCCCCGGGTC ATCGTGACTT      100
40  TATCAAGAAC ATGATCACTG GTACCTCGCA GGCCGACTGC GCCATCTTGA      150
   TCATTGCCGC CGGTACCGGT GAATTCGAAG CCGGTATCTC CAAGGATGGT      200
   CAGACCCGTG AGCACGCTCT GCTCGCCTAC ACCTTGGGTG TCAAGCAGCT      250
   CATCGTCGCC ATCAACAAGA TGGACACCAC CAAGTGGTCC GAGGAGCGTT      300
   TCAACGAAAT CATCAAGGAG ACTTCCAAC TCAATCAAGAA GGTCGGCTAC      350
45  AACCCCAAGG CCGTTCCTTT CGTCCCCATC TCCGGCTTCA ACGGTGACAA      400
   CATGATTGAG GTCTCCACCA ACTGCCCGTG GTACAAGGGA TGGGAGAAGG      450
   AGTCCAAGGC TGGCAAGGCC ACCGGCAAGA CCCTCCTCGA GGCCATTGAC      500
   GCCATCGACC CACCCACCCG TCCCACCGAC AAGCCTCTCC GTCTCCCTCT      550
   CCAGGATGTC TACAAGATCT CTGGTATCGG AACGGTTCCT GTCGGTCTGT      600
50  TCGAGACCGG TACCATCAAG GCCGGTATGG TCGTCACCTT CGCTCCGGCC      650
   AACGTCACCA CTGAAGTCAA GTCCGTGCGA ATGCACCACG AGCAGCTCGC      700
   CGAGGGTYTG CCAGGTGACA ACGTTGGCTT CAACGTCAAG AACGTYTCCG      750
   TCAAGGAGGT TCGTCGTGGT AACGTTGCCG GTGACTCCAA GAACGACCCG      800

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	CCCAAGGGTG	CCGAGTCCTT	CAACGCCCAG	GTCATTGTCC	TCAACCACCC	850
	TGGTCAGATC	GGTGCCGGCT	ACGCTCCAGT	CTTGGATTGC	CACACTGCCC	900
	ACATTGCTTG	CAAGTTCGCC	GAGTTGCTCG	AGAAGATCGA	CCGTCGTACC	950
	GGAAAGTCCA	TCGAGAACAA	CCCCAAGTTC	ATCAAGTCTG	GTGATGCTGC	1000
5	CATCGTCAAG	ATGATTCCCA	GCAAGCCCAT	GTGTGTCGAG	GCTTTC	1046

2) INFORMATION FOR SEQ ID NO: 1278

10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1109 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 15 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 20 (A) ORGANISM: *Fusarium moniliforme*
 (B) STRAIN: WSA-213

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1278

25	CGTGAGCGTG	GTATCACCAT	CGATATTGCT	CTCTGGAAGT	TCGAGACTCC	50
	TCGCTACTAT	GTCACCGTCA	TTGGTATGTT	GTCGCTCATA	CCTCATCCTA	100
	CTTCCTCATA	CTAACACATC	ATTGAGACGC	TCCCGGTCAC	CGTGATTTC	150
	TCAAGAACAT	GATCACTGGT	ACTTCCCAGG	CCGATTGCGC	CATTCTCATC	200
	ATTGCCGCCG	GTA CTGGTGA	GTTGAGAGCT	GGTATCTCCA	AGGATGGCCA	250
30	GACCCGTGAG	CACGCTCTTC	TTGCCTACAC	CCTTGGTGTC	AAGAACCTCA	300
	TCGTCGCCAT	CAACAAGATG	GACACCACCA	AGTGGTCTGA	GGCCCGTTAC	350
	CAGGAGATCA	TCAAGGAGAC	CTCCTCTTTC	ATCAAGAAGG	TCGGCTACAA	400
	CCCCAAGGCT	GTCGCTTTCG	TCCCCATCTC	CGGTTTCAAC	GGTGACAACA	450
	TGCTTACCCC	CTCCACCAAC	TGCCCCCTGGT	ACAAGGGTTG	GGAGCGTGAG	500
35	ATCAAGTCCG	GCAAGCTCTC	CGGCAAGACC	CTCCTCGAGG	CCATTGACTC	550
	CATCGAGCCT	CCCAAGCGTC	CCGTTGACAA	GCCCCCTCCGT	CTTCCCCTCC	600
	AGGATGTCTA	CAAGATCGGT	GGTATTGGAA	CGGTTCCCGT	CGGCCGTATT	650
	GAGACTGGTG	TCATCAAGCC	CGGTATGGTC	GTTACCTTCG	CTCCCTCCAA	700
	CGTCACCACT	GAAGTCAAGT	CCGTCGARAT	GCACCACGAG	CAGYTCAGTK	750
40	AGGGCCAGCC	CGGTGACAAC	GTTGGTTTCA	ACGTGAAGAA	CGTTTCCGTC	800
	AAGGACATCC	GACGTGGTAA	CGTCGCTGGT	GACTCCAAGA	ACGACCCCCC	850
	CCAGGGTGCC	GCTTCTTTCA	CCGCCCAGGT	CATCGTCCTC	AACCACCCCG	900
	GCCAGGTCGG	TGCTGGTTAC	GCTCCTGTCC	TCGATTGCCA	CACTGCCCCAC	950
	ATTGCCTGCA	AGTTCGCCGA	GATCCAGGAG	AAGATCGACC	GCCGAACCGG	1000
45	TAAGGCTACT	GAGGCCGCTC	CCAAGTTCAT	CAAGTCTGGT	GACTCCGCCA	1050
	TCGTCAAGAT	GGTTCCCTCC	AAGCCCATGT	GTGTCGAGGC	TTTCACTGAC	1100
	TACCCTCCT					1109

50

2) INFORMATION FOR SEQ ID NO: 1279

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 765 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

5

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Aspergillus terreus*
- (B) STRAIN: WSA-174

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1279

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15 CCTGCAAGTG GTCTGAGGAC CGTTACAACG AAATCGTGAA GGAGACCTCC      50
   AACTTCATCA AGAAGGTCGG CTACAACCCC AAGGCCGTTT CCTTCGTCCC      100
   CATCTCCGGT TTCAACGGTG ACAACATGCT TGAGCCTTCC CCCAACTGCC      150
   CCTGGTACAA GGGTTGGGAG AAGGAGGGCA AGTCCGGCAA GGTCACCGGT      200
   AAGACTCTCC TCGAGGCCAT CGATGCCATC GAGCCCCCGG TCCGTCCTGC      250
   CAACAAGCCT CTCCGTCTTC CCCTCCAGGA TGTGTACAAG ATCTCTGGTA      300
20 TCGGAAGTGT CCCCCTCGGC CGTGTGCGAG CTGGTGTCAT CACCCCCGGC      350
   ATGGTTGTTA CCTTCGCTCC TTCCAACGTC ACCACTGAAG TGAAGTCCGT      400
   TGAGATGCAC CACCAGCAGC TCAAGGAGGG TCTCCCCGGT GACAACGTTG      450
   GTTTC AACGT CAAGAACGTC TCCGTCAAGG AGGTCCGTCG TGGTAACGTC      500
   GCTGGTGACT CCAAGAACGA CCCCCCTGCT GCGGCTGCCT CCTTCACCGC      550
25 CCAGGTCATC GTTCTCAACC ACCCCGGTCA GGTCGGCGCT GGCTACGCCC      600
   CCGTCCTCGA CTGCCACACT GCCCACATTG CCTGCAAGTT CGCTGAGCTC      650
   CAGGAGAAGA TTGACCGCCG TACCGGAAAG TCTGTTGAGT CTTCTCCCAA      700
   GTTCATCAAG TCTGGTGATG CTGCCATCGT CAAGATGATC CCTYCAAAGC      750
   CCATGTGCGT CGAAG                                           765

```

30

2) INFORMATION FOR SEQ ID NO: 1280

35 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1105 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

40

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Aspergillus fumigatus*
- (B) STRAIN: ATCC 64746

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1280

```

50 GCGTGGTATC ACCATCGACA TTGCCCTCTG GAAGTTCCAG ACTCCCAAGT      50
   ATGAGGTCAC TGTCATCGGT AAGCTCGACT CGCCCCGATA TGTTTTGGTG      100
   CTGTAGCTAA CACGATCTGA AGATGCCCCC GGTCACCGTG ACTTCATCAA      150
   GAACATGATC ACTGGTACCT CCCAGGCTGA CTGCGCTATC CTCATCATTTG      200
   CCTCCGGTAC TGGTGAGTTC GAGGCTGGTA TCTCCAAGGA TGGCCAGACC      250

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	CGTGAGCACG	CTCTGCTGGC	TTTCACCCTC	GGTGTCAAGC	AGCTCATCGT	300
	CGCCCTCAAC	AAGATGGACA	CCTGCAAGTG	GTCCGAGGAT	CGTTACAACG	350
	AAATTGTCAA	GGAAACCTCC	AACTTCATCA	AGAAGGTCGG	CTACAACCCC	400
	AAGGCCGTTT	CCTTCGTMCC	CATCKCTGGC	TTCAACGGTG	ACAACATGCT	450
5	TGAGCCCTCC	TCCAAC TGCC	CCTGGTACAA	GGGATGGGAG	AAGGAGACCA	500
	AGGCCGGCAA	GGTCACTGGT	AAGACCCTCA	TCGAGGCCAT	YGACGCCATT	550
	GAGCCCCCTG	TCCGTCCCTC	CAACAAGCCC	CTYCGTCTTC	CCCTCCAGGA	600
	TGTYTACAAG	ATCTCTGGTA	TCGGAACGGT	CCCTGTCGGC	CGTGTCGAGA	650
	CCGGTATCAT	CAAGCCCGGC	ATGGTCGTCA	CCTTTGCCCC	CGCCAACGTC	700
10	ACCACTGAAG	TCAAGTCCGT	CGAAATGCAC	CACCAGCAGC	TCCAGGAGGG	750
	TGTCCCCGGT	GACAACGTCG	GTTTCAACGT	CAAGAACGTT	TCCGTCAAGG	800
	AAGTCCSCCG	TGGTAACGTT	TGCGGTGACT	CCAAGAACGA	TCCCCCTCAG	850
	GGTGCTGCCT	CCTTCAACGC	CCAGGTCATC	GTCCTCAACC	ACCCCGGTCA	900
	GGTCGGCGCT	GGTTACGCCC	CCGTCCTCGA	CTGCCACACT	GCCCACATTG	950
15	CTTGCAAGTT	CTYTGAGCTG	CTTGAGAAGA	TTGACCGCCG	TACCGGCAAG	1000
	TCTGTTGAGA	ACAACCCCAA	GTTTCATCAAG	TCCGGTGAWG	CCGCCATCGT	1050
	GAAGATGGTT	CCTTCCAAGC	CCATGTGTGT	CGAGTCCTTC	ACTGACTACC	1100
	CCCCCT					1105

20

2) INFORMATION FOR SEQ ID NO: 1281

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 1343 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

30 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Cryptococcus laurentii*
 (B) STRAIN: ATCC 44096

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1281

	GCCGAGCGAG	AGCGAGGTAT	CACCATCGAC	ATTGCTCTCT	GGAAGTTCGA	50
	GACCCCCAAG	TACAACGTCA	CCGTCATTGA	CGCCCCCGGA	CACCGAGACT	100
40	TCATCAAGAA	CATGATCACC	GGTACCTCCC	AGGCCGACTG	CGCCATCCTT	150
	ATCATTGCCA	CCGGTATCGG	AGAGTTCGAG	GCCGGTATCT	CTAAGGACGG	200
	TCAGACCCGA	GAGCAGCCTT	TGCTCGCCTT	CACCCTCGGT	GTCAGGCAGC	250
	TCATCGTTGC	TTGCAACAAG	ATGGACACCT	GCAAGTGGTC	CGAGGACCGA	300
	TTCAACGAGA	TCGTCAAGGA	GACCAACGGT	TTCATCAAGA	AGGTCCGATA	350
45	CAACCCCAAG	GCTGTTCCCT	TCGTCCCCAT	CTCTGGATGG	CACGGAGACA	400
	AGTGAGTGCC	GTTCTTTGCG	TTGAGCCCTC	TTTGTCGCTC	CCCCTCCCTC	450
	TCAAGTGCGG	GCGGCGGTCT	CCACCCACAA	ATCGGGTGGC	GAATCCGCCA	500
	CACCCACCAC	TTCTCGCCAC	CGAGTGTGGC	ACTTCTTCCA	ACTCCTCTTT	550
	CCACTCCTCC	TCGTCTCGTC	TCTTTTTTTC	TCCGTTGTCT	TTGACAAGGG	600
50	GAGTGTGCTG	ATAGTAAAGC	ATGCTTGAGG	AGACCACCAA	CATGCCGTGG	650
	TACAAGGGAT	GGACCAAGGA	GACCAAGTCC	GGTGTCGTTA	AGGGTAAGAC	700
	CCTCCTCGAC	GCCATCGACG	CCATCGAGCC	TCCTCAACGA	CCCACCGACA	750
	AGCCCCCTCG	ACTTCCCCTC	CAGGATGTCT	ACAAGATCGG	TGGTATCGGT	800

	ACGGTGCCCG	TCGGCCGAGT	CGAGACCGGT	GTCATCAAGG	CCGGGTAAGT	850
	CACGGGAGCC	TGACGGCTGT	TGTTGCCACA	CCCAACTTAT	ATCCAGTATG	900
	GTCGTCACCT	TCGCTCCTAC	CAACGTCACC	ACTGAGGTTA	AGTCCGTTGA	950
	GATGCACCAC	GAGCAGATCC	CTGAGGGTCT	TCCCGGAGAC	AACGTTGGTT	1000
5	TCAACGTGAA	GAACGTTTCC	ATCAAGGACA	TCCGACGAGG	AAACGTYTGC	1050
	TCCGACTCCA	AGAACGACCC	CGCTAAGGAG	GCCGCTTCTT	TCAACGCCCA	1100
	GGTCATTGTC	CTCAACCACC	CTGGACAGAT	TGGTGCCGGT	TACACCCCCG	1150
	TCCTCGACTG	CCACACCGCC	CACATTGCCT	GCAAGTTCGC	CGAGCTCATC	1200
	GAGAAGATCG	ACCGACGAAC	TGGTAAGACC	ATGGAGGCCG	CCCCAAGTT	1250
10	CGTCAAGTCC	GGAGACGCCG	CCATTGTCAA	GCTCGTTGCC	CAGAAGCCCA	1300
	TCTGTGTCGA	GTCTTACTCT	GACTACCCTC	CCCTTGGACG	ATT	1343

15 2) INFORMATION FOR SEQ ID NO: 1282

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 734 bases
 (B) TYPE: Nucleic acid
 20 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

25 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Emmonsia parva*
 (B) STRAIN: ATCC 10784

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1282

30	TGGTCCGAGG	CTCGTTTCAA	CGAAATCATC	AAGGAAGTCA	CCAACTTCAT	50
	CAAGAAGGTC	GGATACAACC	CCAAGTCTGT	TCCCTTCGTG	CCAATCTCTG	100
	GTTTCGAGGG	TGATAACATG	ATTGAGCCCT	CCACCAACTG	CCCCTGGTAC	150
	AAGGGCTGGA	CCAAGGAGAC	CGCTGCCGGC	AAGTCAACCG	GTAAGACTCT	200
35	TCTTGACGCC	ATTGATGCCA	TCGATCAACC	CTCCCGTCCT	ACCGACAAGC	250
	CCCTCCGTCT	TCCCCTCCAG	GATGTGTACA	AGATCTCCGG	TATTGGCACT	300
	GTTCCCCTTG	GACGTGTTGA	GACTGGTATC	ATCAAGCCTG	GTATGGTCGT	350
	GACCTTCGCT	CCCTCCAACG	TCACCACTGA	AGTCAAGTCC	GTCGAAATGC	400
	ACCACCAACA	GCTCTTGGCT	GGTAACCCCG	GTGACAACGT	CGGTTTCAAC	450
40	GTCAAGAACG	TTTCCGTCAA	GGAAGTCCGC	CGTGGCAACG	TTGCTGGTGA	500
	CTCAAAGAAC	GACCCCCCCA	AGGGCTGCGA	CTCCTTCAAC	GCCCAGGTCA	550
	TCGTCTCTAA	TCACCCCGGT	CAAGTTGGCG	CTGGTTATGC	CCCAGTCCTC	600
	GACTGCCACA	CTGCCCACAT	TGCTTGCAAG	TTCTCTGAGC	TCCTCGAGAA	650
	GATTGACCGC	CGTACCGGAA	AGTCCACTGA	GAACAACCCC	AAGTTCATCA	700
45	AGTCTGGTGA	CGCCGCTATC	GTCAAGATGG	TTCC		734

2) INFORMATION FOR SEQ ID NO: 1283

50

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1107 bases
 (B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

5

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Fusarium solani*
(B) STRAIN: ATCC 62877

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1283

	CGTGAGCGTG	GTATCACCAT	CGACATTGCC	CTCTGGAAGT	TCGAGACTCC	50
	CCGCTACTAT	GTCACCGTCA	TTGGTATGTT	GCTGTCACCT	CTCTCACACA	100
	TGTCTCACCA	CTAACAATCA	ACAGACGCCC	CCGGCCACCG	TGACTTCATC	150
15	AAGAACATGA	TCACTGGTAC	TTCCAGGCC	GACTGCGCCA	TTCTCATCAT	200
	TGCCGCTGGT	ACTGGTGAGT	TCGAGGCTGG	TATCTCCAAG	GATGGCCAGA	250
	CCCGTGAGCA	CGCCCTGCTC	GCCTACACCC	TCGGTGTCAA	GAACCTCATT	300
	GTCGCCATCA	ACAAGATGGA	CACCACCAAG	TGGTCCGAGT	CCCGTTACCA	350
	GGAGATCATC	AAGGAGACCT	CCAACTTCAT	CAAGAAGGTC	GGCTACAACC	400
20	CCAAGGCTGT	CGCTTTCGTC	CCCATCTCCG	GTTTCAACGG	CGACAACATG	450
	CTTACTCCCT	CCACCAACTG	CCCCTGGTAC	AAGGGCTGGG	AGCGTGAGAT	500
	CAAGTCCGGC	AAGCTCACTG	GCAAGACCCT	CCTCGAGGCC	ATTGACTCCA	550
	TCGAGCCCCC	CAAGCGTCCC	GTCGACAAGC	CCCTCCGACT	TCCCCTCCAG	600
	GATGTCTACA	AGATCGGTGG	TATTGGCACG	GTTCCCGTCG	GCCGTATCGA	650
25	GACTGGTGTC	ATCAAGCCCG	GTATGGTCGT	TACCTTCGCC	CCCTCCAACG	700
	TCACCACTGA	AGTCAAGTCC	GTCGAGATGC	ACCACGAGCA	GCTCTYTGAG	750
	GGTCTTCCCG	GTGACAACGT	CGGCTTCAAC	GTKAAGAACG	TYTCCGTCAA	800
	GGAGATCCGA	CGTGGAACG	TCGCTGGTGA	CTCCAAGAAC	GACCCCCCTY	850
	TGGGTGCCGC	CTCTTTCACC	GCCCAGGTCA	TTGTCCTCAA	CCACCCTGGC	900
30	CAGGTCGGTG	CCGGTTACGC	CCCCGTTYTG	GACTGCCACA	CTGCCCACAT	950
	TGCCTGCAAG	TTCGCCGAGA	TCCAGGAGAA	GATCGACCGC	CGAACTGGTA	1000
	AGGCTGTTGA	GTCCGCCCCC	AAGTTCATCA	AGTCTGGTGA	CTCCGCCATC	1050
	GTCAAGATGG	TTCCCTCCAA	GCCCATGTGC	GTTGAGGCTT	TCACTGACTA	1100
	CCCCCT					1107

35

2) INFORMATION FOR SEQ ID NO: 1284

40 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1045 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

45

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Sporothrix schenckii*
(B) STRAIN: ATCC 14285

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1284

	GCTCAAGGCC	GAGCGTGAGC	GCGGTATCAC	CATCGATATT	GCTCTGTGGA	50
	AGTTCGAGAC	CCCCAAGTAC	TACGTCACCG	TCATTGACGC	CCCCGGTCAT	100
	CGCGATTTCA	TCAAGAACAT	GATCACTGGT	ACCTCGCAGG	CCGACTGCGC	150
	CATTCTCATC	ATTGCCGCTG	GTACTGGTGA	GTTTCGAGGCT	GGTATCTCCA	200
5	AGGATGGCCA	GACTCGTGAG	CACGCTCTGC	TCGCCTACAC	CCTGGGTGTG	250
	CGGCAGCTGA	TCGTCGCCAT	CAACAAGATG	GACACGGCCA	AGTGGGCTGA	300
	GGCTCGTTAC	CAGGAGATCA	TCAAGGAGAC	CTCCAAC TTC	ATCAAGAAGG	350
	TCGGCTACAA	CCCCAAGACT	GTTGCCTTCG	TCCCCATCTC	GGGCTTCCAC	400
	GGCGACAACA	TGCTTACTCC	CTCGACCAAC	TGCCCCCTGGT	ACAAGGGCTG	450
10	GGAGAAGGAG	GGCAAGAGCG	GCAAGGTTAC	CGGTAAGACT	CTGCTGGACG	500
	CCATTGACGC	CGTCGAGCCC	CCCAAGCGCC	CCACGGACAA	GCCCCTGCGT	550
	CTGCCCCCTCC	AGGATGTCTA	CAAGATCGGC	GGTATCGGCA	CTGTCCCTGT	600
	CGGCCGTATC	GAGACTGGTG	TCCTGAAGCC	CGGCATGGTC	GTCACCTTTG	650
	CCCCGTCCAA	CGTCACCACT	GAAGTCAAGT	CCGTCGAGAT	GCACCACGAG	700
15	CAGCTTGTTG	AGGGTGTTCC	CGGCGACAAC	GTCGGCTTCA	ACGTCAAGAA	750
	CGTYTCCGTC	AAGGAGATCC	GTGTGGCAA	CGTTGCCGGT	GACTCCAAGA	800
	ACGACCCCCC	CTCGGGCGCC	GCCACCTTCA	ACGCCCAGGT	CATTGTCCTG	850
	AACCACCCCG	GCCAGGTCGG	CAACGGCTAC	GCCCCGGTTY	TGGACTGCCA	900
	CACCGCCCAC	ATTGCCTGCA	AGTTCACCGA	GATCCTTGAG	AAGATCGACC	950
20	GCCGTACCGG	CAAGTCGGTT	GAGAACAACC	CCAAGTTCAT	CAAGTCGGGT	1000
	GACGCCGCCA	TTGTCAAGCT	GACGCCCTYG	AAGCCCATGT	GCGTT	1045

25 2) INFORMATION FOR SEQ ID NO: 1285

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 764 bases
 (B) TYPE: Nucleic acid
 30 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

35 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Aspergillus nidulans*
 (B) STRAIN: WSA-176

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1285

40	TTGCCAGTGG	TCCGAGGCCC	GTTACAACGA	AATCGTCAAG	GAGACTTCCG	50
	GTTTCATCAA	GAAGGTCGGA	TACAACCCCA	AGTCCGTTGC	CTTCGTCCCC	100
	ATCTCCGGTT	TCAACGGTGA	CAACATGCTC	GAGGCCTCTA	CCAAC TGCCC	150
	CTGGTACAAG	GGTTGGGAGA	AGGAGACCAA	GGCCGGTAAG	GCCACTGGTA	200
45	AGACCCTCCT	TGAGGCCATC	GACGCCATTG	AGCCCCCAC	CCGTCCCTCC	250
	AACAAGCCCC	TCCGTCTTCC	CCTCCAGGAT	GTCTACAAGA	TCTCCGGTAT	300
	TGGAAGCTGC	CCCGTCGGCC	GTGTCGAGAC	TGGTGTTATC	ACCCCCGGCA	350
	TGGTCGTAC	CTTCGCTCCT	GCCAACGTCA	CCACTGAAGT	CAAGTCCGTT	400
	GAGATGCACC	ACCAGCAGCT	CAAGGAGGGT	GTCCCCGGTG	ACAACGTCGG	450
50	TTTCAACGTC	AAGAACGTTT	CCGTCAAGGA	AATCCGTCGT	GGTAACGTTG	500
	CCTCCGACTC	CAAGAACGAC	CCCGCCTCCG	GCGCTGCCTC	TTTCAACGCC	550
	CAGGTCATCG	TTCTCAACCA	CCCCGGTCAG	GTCGGTGCTG	GTTACGCCCC	600
	CGTCCTCGAC	TGCCACACCG	CCCACATTGC	TTGCAAGTTC	TCTGAGCTTC	650

TTGAGAAGAT	TGACCGCCGT	ACCGGAAAGG	CTGTTGAAAC	CAGCCCCAAG	700
TTCATCAAGT	CCGGTGACGC	TGCCATCGTC	AAGATGATTC	CTTCCAAGCC	750
CATGTGCGKT	CCGA				764

5

2) INFORMATION FOR SEQ ID NO: 1286

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 971 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

15 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Cladophialophora carrionii*
 (B) STRAIN: ATCC 16264

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1286

ACCATCGATA	TCGCGCTCTG	GAAGTTCGAG	ACTCCCAAGT	ACTTCGTCAC	50
CGTCATCGAT	GCCCCTGGTC	ATCGTGACTT	CATCAAGAAC	ATGATCACTG	100
25 GTACCTCCCA	GGCTGATTGT	GCTATTCTCA	TCATTGCCGC	TGGTACTGGT	150
GAGTTCGAGG	CCGGTATCTC	CAAGGATGGC	CAGACCCGTG	AGCATGCTCT	200
GCTCGCCTAC	ACCCTGGGCG	TGAAGCAGCT	TATCGTCGCC	ATCAACAAGA	250
TGGACACCAC	CAAATGGTCT	GAGGATCGTT	TCAACGAAAT	CATCAAGGAG	300
ACTTCCAACT	TCATCAAGAA	GGTCGGATAC	AACCCCAAGT	CCGTTCCATT	350
30 CGTGCCCATC	TCCGGCTTCA	ACGGTGACAA	CATGATCGAC	GTCTCCACCA	400
ATGCCCCCTG	GTACAAGGGC	TGGGAAAAGG	AGTCCAAGGC	TGGCAAGGCC	450
ACCGGCAAGA	CCCTCCTTGA	GGCTATCGAC	TCCATCGACC	CTCCTGCTCG	500
TCCCACCGAC	AAGCCTCTCC	GTCTCCCACT	CCAGGATGTC	TACAAGATTT	550
CTGGTATCGG	CACGGTGCCC	GTCGGTCGTG	TTGAGACTGG	TACCATCAAG	600
35 GCCGGTATGG	TCGTACCTT	TGCCCCCGCC	AACGTCACCA	CTGAAGTCAA	650
GTCCGTCGAA	ATGACCACG	AACAGCTYGC	CGAGGGCGTT	CCGGGTGACA	700
ACGTCGGCTT	CAACGTCAAG	AACGTYTCCG	TGAAGGAGGT	TCGTCGTGGA	750
AACGTTGCTG	GTGACTCCAA	GAACGACCCC	CCCAAGGGTG	CCGACTCCTT	800
CAACGCCCAG	GTCATCGTCC	TCAACCACCC	TGGTCAGGTC	GGTGCTGGCT	850
40 ACGCCCCGGT	CTTGGATTGC	CACACTGCCC	ACATTGCCTG	CAAGTTCTYT	900
GAGCTCCTCG	AGAAGATCGA	TCGTCGKACC	GGCAAGTCCA	TGGAACAACAA	950
CCCCAAGTTC	ATCAAGTCTG	G			971

45

2) INFORMATION FOR SEQ ID NO: 1287

(i) SEQUENCE CHARACTERISTICS:

- 50 (A) LENGTH: 732 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Exserohilum rostratum*

5 (B) STRAIN: WSA-215

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1287

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10 GGTCTGAGGA CCGTTACCAG GAGATCATCA AGGAGACCTC CAACTTCATC      50
   AAGAAGGTCG GCTACAACCC CAAGCACGTT CCCTTCGTCC CCATCTCCGG      100
   TTTCAACGGA GACAACATGA TCGAGGCCTC CAGCAACTGC CCCTGGTACA      150
   AGGGTTGGGA GAAGGAGACC AAGGCCAAGG CCACTGGTAA GACCCTCCTT      200
   GAGGCCATTG ACGCCATCGA CCCTCCCAGC CGTCCTACCG ACAAGCCCCT      250
   CCGTCTTCCC CTCCAGGATG TCTACAAGAT TGGTGGTATT GGCACGGTTC      300
15 CCGTCGGTCG TGTCGAGACC GGTATCATCA AGGCCGGTAT GGTCGTCACC      350
   TTCGCCCCCG CTGGTGTCAC CACTGAAGTC AAGTCCGTCG AGATGCACCA      400
   CGAGCAGCTT ACCGAGGGTG TCCCCGGTGA CAACGTCGGC TTCAACGTCA      450
   AGAACGTCTC CGTCAAGGAG ATCCGTCGTG GTAACGTTGC CGGTGACTCC      500
   AAGAACGACC CCCCCAAGGG CTGCGAGTCT TTCAACGCTC AGGTCATTGT      550
20 CCTCAACCAC CCTGGTCAGG TCGGTGCCGG TTACGCGCCA GTCCTCGACT      600
   GCCACACCGC CCACATTGCC TGCAAGTTCT CTGAGCTCCT CGAGAAGATT      650
   GACCGCCGTA CCGGAAAGTC TGTCGAAGCC TCTCCCAAGT TCATCAAGTC      700
   TGGTGACGCG GCCATCGTCA AGATGGTTCC CT                          732

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25

2) INFORMATION FOR SEQ ID NO: 1288

(i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 337 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

35 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Bacillus thuringiensis*

40 (B) STRAIN: HER 1236

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1288

```

AATGGATCCT GTATACGCAC AAAAATTAGG CGTTAACATA GATGAATTRC      50
TATTATCACA GCCTGATACA GGGGAGCAAG GATTGGAAAT CGCGGAAGCA      100
45 CTTGTACGAA GTGGTGCGGT TGACATTATC GTAATTGACT CTGTAGCAGC      150
   TCTTGTACCG AAAGCAGAGA TTGAAGGCGA TATGGGTGAC TCACACGTAG      200
   GTTTACAAGC ACGTTTAATG TCACAAGCAC TTMGTAAGCT TTCAGGAGCA      250
   ATCAACAAAT CARRARCAAT WGCAATCTTT ATTAACCAA TTCGWGAAAA      300
   AGTTGGGGTT ATGTTTCGAA ACCCAGAAAC AACTCCA                      337
50

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2) INFORMATION FOR SEQ ID NO: 1289

700

WO 01/23604

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 336 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Bacillus thuringiensis*
 (B) STRAIN: HER 1232

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1289

15	AATGGATCCT GTATATGCAC AAAAATTAGG CGTTAACATA GATGAATTRC	50
	TATTATCACA GCCTGATACA GGGGAGCAAG GATTGGAAAT CGCGGAAGCA	100
	CTTGTACGAA GTGGTGCGGT TGACATTATC GTAATTGACT CTGTAGCAGC	150
	TCTTGTACCG AAAGCAGAGA TTGAAGGCGA TATGGGTGAC TCACACGTAG	200
	GTTTACAAGC ACGTTTAATG TCACAAGCAC TTMGTAAGCT TTCAGGAGCA	250
20	ATCAACAAAT CARAARCAAT TGCAATCTTT ATTAACCAA TTCGTGAAAA	300
	AGTTGGGGTT ATGTTTCGGAA ACCCAGAAAC AACTCC	336

25 2) INFORMATION FOR SEQ ID NO: 1290

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 23 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1290

GAYTAYGCIA TGISIGTIAT HGT

40

2) INFORMATION FOR SEQ ID NO: 1291

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 23 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

50 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1291

WO 01/23604
GCIYTICIG AYGTIMGIGA YGG

5 2) INFORMATION FOR SEQ ID NO: 1292

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1292

20

ARISCYTCIA RIATRTGIGC

20 2) INFORMATION FOR SEQ ID NO: 1293

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1293

20

ATGGCTGAAT TACCTCAATC

35

2) INFORMATION FOR SEQ ID NO: 1294

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 25 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

45 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1294

25

ATGATTGTTG TATATCTTCT TCAAC

50

2) INFORMATION FOR SEQ ID NO: 1295

702

WO 01/23604

- 5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

- 10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1295

20

CAGAAAGTTT GAAGCGTTGT

- 15 2) INFORMATION FOR SEQ ID NO: 1296

- 20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

- 25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1296

20

AACGATTCGT GAGTCAGATA

30

- 2) INFORMATION FOR SEQ ID NO: 1297

- 35 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 22 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

40 (ii) MOLECULE TYPE: DNA

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1297

22

CGGTCAACAT TGAGGAAGAG CT

45

- 2) INFORMATION FOR SEQ ID NO: 1298

- 50 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 23 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single

703

WO 01/23604

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1298

23

ACGAAATCGA CCGTCTCTTT TTC

10

2) INFORMATION FOR SEQ ID NO: 1299

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 2711 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

20

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Staphylococcus aureus*
 (B) STRAIN: 601055
 (C) ACCESSION NUMBER: X71437

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1299

	ATGGCTGAAT	TACCTCAATC	AAGAATAAAT	GAACGAAATA	TTACCAGTGA	50
	AATGCGTGAA	TCATTTTATAG	ATTATGCGAT	GAGTGTTATC	GTTGCTCGTG	100
	CATTGCCAGA	TGTTTCGTGAC	GGTTTAAAC	CAGTACATCG	TCGTATACTA	150
30	TATGGATTAA	ATGAACAAGG	TATGACACCG	GATAAATCAT	ATAAAAAATC	200
	AGCACGTATC	GTTGGTGACG	TAATGGGTAA	ATATCACCCCT	CATGGTGACT	250
	CATCTATTTA	TGAAGCAATG	GTACGTATGG	CTCAAGATTT	CAGTTATCGT	300
	TATCCGCTTG	TTGATGGCCA	AGGTAACCTT	GGTTCAATGG	ATGGAGATGG	350
	CGCAGCAGCA	ATGCGTTATA	CTGAAGCGCG	TATGACTAAA	ATCACACTTG	400
35	AACTGTTACG	TGATATTAAT	AAAGATACAA	TAGATTTTAT	CGATAACTAT	450
	GATGGTAATG	AAAGAGAGCC	GTCAGTCTTA	CCTGCTCGAT	TCCCTAATTT	500
	ATTAGCCAAT	GGTGCATCAG	GTATCGCGGT	AGGTATGGCA	ACGAATATTC	550
	CACCACATAA	CTTAACAGAA	TTAATCAATG	GTGTACTTAG	CTTAAGTAAG	600
	AACCCTGATA	TTTCAATTGC	TGAGTTAATG	GAAGATATTG	AAGGTCCTGA	650
40	TTTCCCAACT	GCTGGACTTA	TTTTAGGTAA	GAGTGGTATT	AGACGTGCAT	700
	ATGAAACAGG	TCGTGGTTCA	ATTCAAATGC	GTTCTCGTGC	AGTTATTGAA	750
	GAACGTGGAG	GCGGACGTCA	ACGTATTGTT	GTCAGAGCTC	TTCCCTTTCCA	800
	AGTGAATAAG	GCTCGTATGA	TTGAAAAAAT	TGCAGAGCTC	GTTTCGTGACA	850
	AGAAAATTGA	CGGTATCACT	GATTTACGTG	ATGAAACAAG	TTTACGTACT	900
45	GGTGTGCGTG	TCGTTATTGA	TGTGCGTAAG	GATGCAAATG	CTAGTGTCAAT	950
	TTTAAATAAC	TTATACAAAC	AAACACCTCT	TCAAACATCA	TTTGGTGTGA	1000
	ATATGATTGC	ACTTGTAAT	GGTAGACCGA	AGCTTATTAA	TTTAAAGAA	1050
	GCGTTGGTAC	ATTATTTAGA	GCATCAAAAG	ACAGTTGTTA	GAAGACGTAC	1100
	GCAATATAAC	TTACGTAAAG	CTAAAGATCG	TGCCCCATATT	TTAGAAGGGT	1150
50	TACGTATCGC	ACTTGACCAT	ATCGATGAAA	TTATTTCAAC	GATTCGTGAG	1200
	TCAGATACAG	ATAAAGTTGC	AATGGAAAGC	TTGCAACAAC	GCTTCAAAC	1250
	TTCTGAAAAA	CAAGCTCAAG	CTATTTTAGA	CATGCGTTTA	AGACGTCTAA	1300

WO 01/23604

	CAGGTTT	AGAGAAA	CAAAATT	GAAAGCT	GAATATA	ATGAGTT	ATTAAT	1350
	TATATT	AGTAGA	AGCATCT	AGTAGCT	GATGAAG	AGTGTAT	TATACA	1400
	GTTAGT	TAGA	GATGA	ATTG	CTGAA	ATTAG	AGATCG	1450
	GTCGT	ACAGA	AATTC	AATTA	GGTGG	ATTG	AAGACT	1500
5	TTAAT	TCCAG	AAGA	CAAA	ATAGT	AATTA	CTTGA	1550
	TAAAC	GTTTG	CCGG	TATCT	AATCG	TGTC	TCAAA	1600
	GTGTT	CAAGG	TATGA	AATAC	TTGGA	AGAAG	ATTTT	1650
	ACTTT	AAGTA	CACAT	GACCA	TGTAT	TGTT	TTTAC	1700
	ATACAA	ACTA	AAAGG	TATG	AAGT	GCTG	GTTAT	1750
10	GTATT	CCTGT	AGTGA	ATGCT	ATTGA	ACTTG	GAAAT	1800
	ACAAT	GATTG	CTGTT	AAAGA	CCTTG	AAAGT	GAAGA	1850
	TGCA	ACTAA	CGTGG	TGTTG	TTAA	ACGTT	AGCAT	1900
	GAATA	AATAG	AAATG	GTAAG	ATTGC	GATTT	CGTTC	1950
	TTAAT	TGCAG	TTCGT	TTAAC	AAGT	GGTCA	GAAGA	2000
15	ATCAC	ATGCA	TCATT	AATTC	GATTC	CCCTG	ATCA	2050
	GCCGT	ACAGC	AACGG	GTTG	AAAGG	TATTA	CACTT	2100
	GTTGT	AGGGC	TTGAT	GTAGC	TCATG	CAAAC	AGTGT	2150
	AGTTA	CTGAA	AATGG	TATG	GTAA	ACGT	GCCAG	2200
	TATCA	AATCG	TGGT	GGTAAA	GGTAT	TAAAA	CAGCT	2250
20	AATGG	TAAATG	TTGT	ATGTAT	CACTA	CAGTA	ACTGG	2300
	GATTG	TACT	AATGC	CGGTG	TCATT	TATTCG	ACTAG	2350
	CTCAA	AATGG	TCGT	GCAGCA	CAAGG	TGTT	GCTTA	2400
	GATCA	ATTTG	TTTCA	ACGGT	TGCTA	AAAGT	AGAGG	2450
	AAATG	AGAT	GAACA	ATCTA	CTGT	ATCTGA	AGATG	2500
25	GTGA	AGCGGT	TGTAA	ATGAT	GAAAC	ACCAG	GAAAT	2550
	GTGAT	TGATT	CAGA	AGAAA	TGAT	GAGAT	GGACG	2600
	AGATT	TCATG	GATCG	TGTG	AAGA	AGATAT	ACAAC	2650
	ATGA	AGAATA	A					2711

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2) INFORMATION FOR SEQ ID NO: 1300

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 2628 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

40 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 45 (A) ORGANISM: *Escherichia coli*
 (B) STRAIN: K12
 (C) ACCESSION NUMBER: X57174

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1300

50	ATGAGCGACC	TTGCGAGAGA	AATTACACCG	GTCAACATTG	AGGAAGAGCT	50
	GAAGAGCTCC	TATCTGGATT	ATGCGATGTC	GGTCATTGTT	GGCCGTGCGC	100
	TGCCAGATGT	CCGAGATGGC	CTGAAGCCGG	TACACCGTCG	CGTACTTTAC	150
	GCCATGAACG	TACTAGGCAA	TGACTGGAAC	AAAGCCTATA	AAAAATCTGC	200
	CCGTGTCGTT	GGTGACGTAA	TCGGTAAATA	CCATCCCCAT	GGTGACTCGG	250

WO 01/23604

	CGGTCTATGA	CACGATCGTC	CGCATGGCGC	AGCCATTCTC	GCTGCGTTAT	300
	ATGCTGGTAG	ACGGTCAGGG	TAACCTCGGT	TCTATCGACG	GCGACTCTGC	350
	GGCGGCAATG	CGTTATACGG	AAATCCGTCT	GGCGAAAATT	GCCCATGAAC	400
	TGATGGCCGA	TCTCGAAAAA	GAGACGGTCG	ATTTTCGTTGA	TAACATGAC	450
5	GGCACGAAA	AAATTCCGGA	CGTCATGCCA	ACCAAAATTC	CTAACCTGCT	500
	GGTGAACGGT	TCTTCCGGTA	TCGCCGTAGG	TATGGCAACC	AACATCCCGC	550
	CGCACAACCT	GACGGAAGTC	ATCAACGGTT	GTCTGGCGTA	TATTGATGAT	600
	GAAGACATCA	GCATTGAAGG	GCTGATGGAA	CACATCCCGG	AGCCGGACTT	650
	CCCGACGGCG	GCAATCATTA	ACGGTCGTCTG	CGGTATTGAA	GAAGCTTACC	700
10	GTACCGGTCTG	CGGCAAGGTG	TATATCCCGG	CTCGCGCAGA	AGTGGAAGTT	750
	GACGCCAAAA	CCGGTCGTGA	AACCATTATC	GTCCACGAAA	TTCCGTATCA	800
	GGTAAACAAA	GCGCGCCTGA	TCGAGAAGAT	TGCGGAAGT	GTAAAAGAAA	850
	AACGCGTGGA	AGGCATCAGC	GCGCTGCGTG	ACGAGTCTGA	CAAAGACGGT	900
	ATGCGCATCG	TGATTGAAGT	GAAACGCGAT	GCGGTCCGGT	AAGTTGTGCT	950
15	CAACAACCTC	TACTCCAGAG	CCCAGTTGCA	GGTTTCTTTC	GGTATCAACA	1000
	TGGTGGCATT	GCACCATGGT	CAGCCGAAGA	TCATGAACCT	GAAAGACATC	1050
	ATCGCGGCGT	TTGTTCGTCA	CCGCCGTGAA	GTGGTGACCC	GTCGTACTAT	1100
	TTTCGAACTG	CGTAAAGCTC	GCGATCGTGC	TCATATCCTT	GAAGCATTAG	1150
	CCGTGGCGCT	GGCGAACATC	GACCCGATCA	TCGAACTGAT	CCGTCATGCG	1200
20	CCGACGCCTG	CAGAAGCGAA	AACCTGCGTG	GTTGCTAATC	CGTGGCAGCT	1250
	GGGCAACGTT	GCCGCGATGC	TCGAACGTGC	TGGCGACGAT	GCTGCGCGTC	1300
	CGGAATGGCT	GGAGCCAGAG	TTCGGCGTGC	GTGATGGTCT	GTACTACCTG	1350
	ACCGAACAGC	AAGCTCAGGC	GATTCTGGAT	CTGCGTTTGC	AGAACTGAC	1400
	CGGTCTTGAG	CACGAAAAAC	TGCTCGACGA	ATACAAAGAG	CTGCTGGATC	1450
25	AGATCGCGGA	ACTGTTGCGT	ATTCTTGGA	GCGCCGATCG	TCTGATGGAA	1500
	GTGATCCGTG	AAGAGCTGGA	GCTGGTTCGT	GAACAGTTCT	GTGACAAACG	1550
	TCGTACTGAA	ATCACCGCCA	ACAGCGCAGA	CATCAACCTG	GAAGATCTGA	1600
	TCACCCAGGA	AGATGTGGTC	GTGACGCTCT	CTCACCAGGG	CTACGTAAAG	1650
	TATCAGCCGC	TTTCTGAATA	CGAAGCGCAG	CGTCTGGCG	GGAAAGGTAA	1700
30	ATCTGCCGCA	CGTATTAAAG	AAGAAGACTT	TATCGACCGA	CTGCTGGTGG	1750
	CGAACACTCA	CGACCATATT	CTGTGCTTCT	CCAGCCGTGG	TCGCGTCTAT	1800
	TCGATGAAAG	TTTATCAGTT	GCCGGAAGCC	ACTCGTGGCG	CGCGCGGTCTG	1850
	TCCGATCGTC	AACCTGCTGC	CGCTGGAGCA	GGACGAACGT	ATCACTGCGA	1900
	TCCTGCCAGT	GACCGAGTTT	GAAGAAGGCG	TGAAAGTCTT	CATGGCGACC	1950
35	GCTAACGGTA	CCGTGAAGAA	AACCTGCTCTC	ACCGAGTTCA	ACCGTCTGCG	2000
	TACCGCCGGT	AAAGTGCGGA	TCAAACCTGGT	TGACGGCGAT	GAGCTGATCG	2050
	GCGTTGACCT	GACCAGCGGC	GAAGACGAAG	TAATGCTGTT	CTCCGCTGAA	2100
	GGTAAAGTGG	TGCGCTTTAA	AGAGTCTTCT	GTCCGTGCGA	TGGGCTGCAA	2150
	CACCACCGGT	GTTCGCGGTA	TTCGCTTAGG	TGAAGGCGAT	AAAGTCGTCT	2200
40	CTCTGATCGT	GCCTCGTGCC	GATGGCGCAA	TCCTCACC GC	AACGCAAAAC	2250
	GGTTACGGTA	AACGTACCGC	AGTGGCGGAA	TACCCAACCA	AGTCGCGTGC	2300
	GACGAAAGGG	GTTATCTCCA	TCAAGTTTAC	CGAACGTAAC	GGTTTAGTTG	2350
	TTGGCGCGGT	ACAGGTAGAT	GACTGCGACC	AGATCATGAT	GATCACCAGT	2400
	GCCGGTACGC	TGGTACGTAC	TCGCGTTTTCG	GAAATCAGCA	TCGTGGGCGG	2450
45	TAACACCCAG	GGCGTGATCC	TCATCCGTAC	TGCGGAAGAT	GAAAACGTAG	2500
	TGGGTCTGCA	ACGTGTTGCT	GAACCGGTTG	ACGAGGAAGA	TCTGGATACC	2550
	ATCGACGGCA	GTGCCGCGGA	AGGGGACGAT	GAAATCGCTC	CGGAAGTGGA	2600
	CGTTGACGAC	GAGCCAGAAG	AAGAATAA			2628

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2) INFORMATION FOR SEQ ID NO: 1301

WO 01/23604

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 23 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

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(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1301

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GTIMGIAWIM GICCIIGSIAT GTA

15 2) INFORMATION FOR SEQ ID NO: 1302

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 23 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: DNA

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1302

23

TAIADIGGIG GIKKIGCIAT RTA

30 2) INFORMATION FOR SEQ ID NO: 1303

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: DNA

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1303

20

GGIGAIGAID YIMGIGARGG

45

2) INFORMATION FOR SEQ ID NO: 1304

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 19 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

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707

WO 01/23604

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1304

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CIARYTTIKY ITTIGTYTG

19

10 2) INFORMATION FOR SEQ ID NO: 1305

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 22 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1305

22

ATGGTGACTG CATTGTCAGA TG

25 2) INFORMATION FOR SEQ ID NO: 1306

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 22 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1306

22

GTCTACGGTT TTCTACAACG TC

40

2) INFORMATION FOR SEQ ID NO: 1307

(i) SEQUENCE CHARACTERISTICS:

- 45 (A) LENGTH: 1923 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

50 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Staphylococcus aureus*

WO 01/23604

(C) ACCESSION NUMBER: M86227

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1307

5	ATGGT	ACTG	CATTG	TCAGA	TGTAA	ACAAC	ACGGATA	AATT	ATGGT	GCTGG	50
	GCAA	ATACAA	GTATT	AGAAG	GTTTA	GAAAG	AGTAC	GTAAG	AGACC	AGGTA	100
	TGTAT	ATAGG	ATCGA	CTCAG	AGAGA	GTTGC	ACATT	AGTGT	GGAA	ATTGT	150
	GATA	ATAGT	TCGAT	GAAAG	ATTAG	CTGGT	TATGC	AAATA	AAATT	GGAAGT	200
	TGTT	ATTGAA	AAAGAT	AACT	GGATT	AAAGT	AACGG	ATAAC	GGACG	TGGTA	250
	TCCC	AGTTGA	TATTC	AAGAA	AAAAT	GGGAC	GTCC	AGCTGT	CGAAG	TTATT	300
10	TTAA	CTGTTT	TACAT	GCTGG	TGGTA	AATTC	GGCGG	TGGCG	GATAC	AAAGT	350
	ATCT	GGTGGT	TTACAT	GGTG	TTGGT	TCATC	AGTT	GTAAC	GCATT	GTCAC	400
	AAGAC	TTAGA	AGTAT	ATGTA	CACAG	AAATG	AGACT	TATATA	TCATC	AAGCA	450
	TATA	AAAAAG	GTGT	ACCTCA	ATTTG	ACTTA	AAAGA	AGTTG	GCACA	ACTGA	500
	TAAGA	CAGGT	ACTGT	CATTC	GTTTT	AAAGC	AGAT	GGAGAA	ATCTT	CACAG	550
15	AGACA	ACTGT	ATACAA	CTAT	GAAAC	ATTAC	AGCAG	CGTAT	TAGAG	AGCTT	600
	GCTTT	CTTAA	ACAA	AGGAAT	TCAA	ATCACA	TTAAG	AGATG	AACGT	GATGA	650
	AGAAA	ACGTT	AGAGA	AAGACT	CCTAT	CACTA	TGAGG	GCGGT	ATTAA	ATCGT	700
	ACGTT	GAGTT	ATTGA	ACGAA	AATAA	AGAAC	CTATT	CATGA	TGAGC	CAATT	750
	TATAT	TCATC	AATCT	AAAGA	TGAT	ATTGAA	GTA	AAATTG	CGATT	CAATA	800
20	TAAC	TACAG	GATAT	CCACAA	ATCTT	TTAAC	TTACG	CAAAT	AACAT	TCATA	850
	CGTAC	GGAAG	TGGT	ACGCAT	GAAG	ACGGAT	TCAA	ACGTGC	ATTA	ACGCGT	900
	GTCT	TAAATA	GTTAT	GTTTT	AAGT	AGCAGA	TATGA	AGAAG	AAA	AGATAGC	950
	TTCT	GGTGAA	GATAC	ACGAG	AAGGT	ATGAC	AGCA	ATTATA	TCTAT	CAAAC	1000
	ATGG	TGATCC	TCAAT	TTCGAA	GGTCA	AACGA	AGACA	AAATT	AGGT	AATTCT	1050
25	GAAG	TGCGTC	AAGTT	GTTAGA	TAAAT	TATTC	TCAG	AGCACT	TTGA	ACGATT	1100
	TTTAT	ATGAA	AATCC	ACAAG	TCGC	ACGTAC	AGTGG	TTGAA	AAAGG	TATTA	1150
	TGGC	GGCACG	TGCAC	GTGTT	GCTGC	GAAAA	AAGCG	CGTGA	AGTA	ACACGT	1200
	CGTAA	ATCAG	CGTTA	GATGT	AGCA	AGTCTT	CCAGG	TAAAT	TAGCC	GATTG	1250
	CTCT	AGTCAA	AGTC	CCTGAAG	AATGT	GAGAT	TTTCT	TAGTC	GAAGG	GGACT	1300
30	CTGC	CGGAGG	GTCT	ACAAAA	TCTGG	TCGTG	ACTCT	AGAAC	GCAGG	CGATT	1350
	TTAC	CATTAC	GAGG	TAAAGAT	ATTAA	ATGTT	GAAAA	AGCAC	GATT	AGATAG	1400
	AATTT	TGAAT	AACA	ATGAAA	TTCGT	CAAAT	GATCA	CAGCA	TTTGG	TACAG	1450
	GAAT	CGGTGG	CGACT	TTGAT	CTAG	CGAAAG	CAAG	ATATCA	CAAA	ATCGTC	1500
35	ATTAT	GACTG	ATGCC	GATGT	GGAT	GAGCG	CATAT	TAGAA	CATT	GTTATT	1550
	AATAT	TCTTC	TATCG	ATTTA	TGAG	ACCGTT	AATT	GAAAGCA	GGCT	ATGTGT	1600
	ATATT	GCACA	GCCAC	CGTTG	TATAA	ACTGA	CACA	AGGTAA	ACAAA	AGTAT	1650
	TATGT	ATACA	ATGAT	AGGGA	ACTTG	ATAAA	CTTAA	ATCTG	AATT	GAAATCC	1700
	AACAC	CAAAA	TGGT	CTATTG	CGCT	TATACAA	AGGT	CTTGGA	GAA	ATGAATG	1750
40	CAGAT	CAATT	ATGGG	AAACA	ACAAT	GAAACC	CTGAG	CACCG	CGCT	CTTTTA	1800
	CAAG	TAAAAC	TTGA	AGATGC	GATT	GAAAGCG	GACCA	AACAT	TTGA	AATGTT	1850
	AATGG	GTGAC	GTTGT	AGAAA	ACCGT	AGACA	ATTTA	TAGAA	GATA	ATGCAG	1900
	TTTAT	GCAAA	CTTAG	ACTTC	TAA						1923

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2) INFORMATION FOR SEQ ID NO: 1308

(i) SEQUENCE CHARACTERISTICS:

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- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1308

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ATGTAYGTIA TIATGGAYMG IGC

23

10 2) INFORMATION FOR SEQ ID NO: 1309

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 bases

(B) TYPE: Nucleic acid

15 (C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1309

ATIATYTTTTRT TICCYTTICC YTT

23

25

2) INFORMATION FOR SEQ ID NO: 1310

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 bases

30 (B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1310

ATIATITSIA TIACYTCRTC

20

40

2) INFORMATION FOR SEQ ID NO: 1311

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 bases

45 (B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

50 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1311

WO 01/23604
GARATGAARA TIMGIGGIGA RCA

5 2) INFORMATION FOR SEQ ID NO: 1312

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 23 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1312

23

AARTAYATIA TICARGARMG IGC

20 2) INFORMATION FOR SEQ ID NO: 1313

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 23 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1313

23

AMIAYICKRT GIGGITTITT YTT

35

2) INFORMATION FOR SEQ ID NO: 1314

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 23 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

45 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1314

23

TAIGAITYA CIGAISMICA RGC

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2) INFORMATION FOR SEQ ID NO: 1315

711

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 bases
(B) TYPE: Nucleic acid
5 (C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1315

ACIATIGCIT CIGCYTGIKS YTC

23

15

2) INFORMATION FOR SEQ ID NO: 1316

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 bases
20 (B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1316

GTGAGTGAAA TAATTCAAGA TT

22

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2) INFORMATION FOR SEQ ID NO: 1317

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 bases
35 (B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

40 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1317

CACCAAAATC ATCTGTATCT AC

22

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2) INFORMATION FOR SEQ ID NO: 1318

50 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1318

ACCTAYTCSA TGTACGTRAT CATGGA

26

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2) INFORMATION FOR SEQ ID NO: 1319

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 23 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

20 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1319

AGRTCCTCIA CCATCGGYAG YTT

23

25

2) INFORMATION FOR SEQ ID NO: 1320

(i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 2259 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

35 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

40 (A) ORGANISM: *Escherichia coli*
(B) STRAIN: K-12 MG1655
(C) ACCESSION NUMBER: AE000384

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1320

	ATGAGCGATA	TGGCAGAGCG	CCTTGCGCTA	CATGAATTTA	CGGAAAACGC	50
45	CTACTTAAAC	TACTCCATGT	ACGTGATCAT	GGACCGTGCG	TTGCCGTTTA	100
	TTGGTGATGG	TCTGAAACCT	GTTTCAGCGCC	GCATTGTGTA	TGCGATGTCT	150
	GAACTGGGCC	TGAATGCCAG	CGCCAAATTT	AAAAAATCGG	CCCGTACCGT	200
	CGGTGACGTA	CTGGGTAAAT	ACCATCCGCA	CGGCGATAGC	GCCTGTTATG	250
	AAGCGATGGT	CCTGATGGCG	CAACCGTTCT	CTTACCGTTA	TCCGCTGGTT	300
50	GATGGTCAGG	GGAAGTGGGG	CGCGCCGGAC	GATCCGAAAT	CGTTCGCGGC	350
	AATGCGTTAC	ACCGAATCCC	GGTTGTCGAA	ATATTCCGAG	CTGCTATTGA	400
	GCGAGCTGGG	GCAGGGGACG	GCTGACTGGG	TGCCAAACTT	CGACGGCACT	450
	TTGCAGGAGC	CGAAAATGCT	ACCTGCCCCG	CTGCCAAACA	TTTTGCTTAA	500

WO 01/23604

	CGGCACCACC	GGTATTGCCG	TCGGCATGGC	GACCGATATT	CCACCGCATA	550
	ACCTGCGTGA	AGTGGCTCAG	GCGGCAATCG	CATTAATCGA	CCAGCCGAAA	600
	ACCACGCTCG	ATCAGCTGCT	GGATATCGTG	CAGGGGCCGG	ATTATCCGAC	650
	TGAAGCGGAA	ATTATCACTT	CGCGCGCCGA	GATCCGTAAA	ATCTACGAGA	700
5	ACGGACGTGG	TTCAGTGCGT	ATGCGCGCGG	TGTGGAAGAA	AGAAGATGGC	750
	GCGGTGGTTA	TCAGCGCATT	GCCGCATCAG	GTTTCAGGTG	CGCGCGTACT	800
	GGAGCAAATT	GCTGCGCAAA	TGCGCAACAA	AAAGCTGCCG	ATGGTTGACG	850
	ATCTGCGCGA	TGAATCTGAC	CACGAGAACC	CGACCCGCCT	GGTGATTGTG	900
	CCGCGTTCCA	ACCGCGTGGA	TATGGATCAG	GTGATGAACC	ACCTCTTCGC	950
10	TACCACCGAT	CTGGAAGA	GCTATCGTAT	TAACCTTAAT	ATGATCGGTC	1000
	TGGATGGTCG	TCCGGCGGTG	AAAAACCTGC	TGGAATCCT	CTCCGAATGG	1050
	CTGGTGTTCC	GCCGCGATAC	CGTGCGCCGC	CGACTGAACT	ATCGTCTGGA	1100
	GAAAGTCCTC	AAGCGCCTGC	ATATCCTCGA	AGGTTTGCTG	GTGGCGTTTC	1150
	TCAATATCGA	CGAAGTGATT	GAGATCATTC	GTAATGAAGA	TGAACCGAAA	1200
15	CCGGCGCTGA	TGTCGCGGTT	TGGCCTTACG	GAAACCCAGG	CGGAAGCGAT	1250
	CCTCGAACTG	AAACTGCGTC	ATCTTGCCAA	ACTGGAAGAG	ATGAAGATTC	1300
	GCGGTGAGCA	GAGTGAAGT	GAAAAAGAGC	GCGACCAGTT	GCAGGGCATT	1350
	TTGGCTTCCG	AGCGTAAAT	GAATAACCTG	CTGAAGAAAG	AACTGCAGGC	1400
	AGACGCGCAA	GCCTACGGTG	ACGATCGTCG	TTCGCCGTTG	CAGGAACGCG	1450
20	AAGAAGCGAA	AGCGATGAGC	GAGCACGACA	TGCTGCCGTC	TGAACCTGTC	1500
	ACCATTGTGC	TGTCGCAGAT	GGGCTGGGTA	CGCAGCGCTA	AAGGCCATGA	1550
	TATCGACGCG	CCGGGCCTGA	ATTATAAAGC	GGGTGATAGC	TTCAAAGCGG	1600
	CGGTGAAAGG	TAAGAGCAAC	CAACCGGTAG	TGTTTGTGTA	TTCCACCGGT	1650
	CGTAGCTATG	CCATTGACCC	GATTACGCTG	CCGTCGGCGC	GTGGTCAGGG	1700
25	CGAGCCGCTC	ACCGGCAAAT	TAACGTTGCC	GCCTGGGGCG	ACCGTTGACC	1750
	ATATGCTGAT	GGAAAGCGAC	GATCAGAAAC	TGCTGATGGC	TTCCGATGCG	1800
	GGTTACGGTT	TCGTCTGCAC	CTTTAACGAT	CTGGTGGCGC	GTAACCGTGC	1850
	AGGTAAGGCT	TTGATCACCT	TACCGGAAAA	TGCCCATGTT	ATGCCGCCGG	1900
	TGGTGATTGA	AGATGCTTCC	GATATGCTGC	TGGCAATCAC	TCAGGCAGGC	1950
30	CGTATGTTGA	TGTTCCCGGT	AAGTGATCTG	CCGCAGCTGT	CGAAGGGCAA	2000
	AGGCAACAAG	ATTATCAACA	TTCCATCGGC	AGAAGCCGCG	CGTGGAGAAG	2050
	ATGGTCTGGC	GCAATTGTAC	GTTCTGCCGC	CGCAAAGCAC	GCTGACCATT	2100
	CATGTTGGGA	AACGCAAAAT	TAACTGCGC	CCGGAAGAGT	TACAGAAAGT	2150
	CACTGGCGAA	CGTGGACGCC	GCGGTACGTT	GATGCGCGGT	TTGCAGCGTA	2200
35	TCGATCGTGT	TGAGATCGAC	TCTCCTCGCC	GTGCCAGCAG	CGGTGATAGC	2250
	GAAGAGTAA					2259

40 2) INFORMATION FOR SEQ ID NO: 1321

(i) SEQUENCE CHARACTERISTICS:

- 45 (A) LENGTH: 2403 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

50 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus aureus*
(B) STRAIN: KMP9
(C) ACCESSION NUMBER: D67074

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1321

	GTGAGTGAAA	TAATTCAAGA	TTTATCACTT	GAAGATGTTT	TAGGTGATCG	50
5	CTTTGGAAGA	TATAGTAAAT	ATATTATTCA	AGAGCGTGCA	TTGCCAGATG	100
	TTCGTGATGG	TTTAAAACCA	GTACAACGTC	GTATTTTATA	TGCAATGTAT	150
	TCAAGTGAGTA	ATACACACGA	TAAAAATTTT	CGTAAAAGTG	CGAAAACAGT	200
	CGGTGATGTT	ATTGGTCAAT	ATCATCCACA	TGGAGACTTC	TCAGTGTACA	250
	AAGCAATGGT	CCGTTTAAGT	CAAGACTGGA	AGTTACGACA	TGTCTTAATA	300
10	GAAATGCATG	GTAATAATGG	TAGTATCGAT	AATGATCCGC	CAGCGGCAAT	350
	GCGTTACACT	GAAGCTAAGT	TAAGCTTACT	AGCTGAAGAG	TTATTACGTG	400
	ATATTAATAA	AGAGACAGTT	TCTTTCATTC	CAAACATGA	TGATACGACA	450
	CTCGAACCAA	TGGTATTGCC	ATCAAGATTT	CCTAACTTAC	TAGTGAATGG	500
	TTCTACAGGT	ATATCTGCAG	GTTACGCGAC	AGATATACCA	CCACATAATT	550
15	TAGCTGAAGT	GATTCAAGCA	ACACTTAAAT	ATATTGATAA	TCCGGATATT	600
	ACAGTCAATC	AATTAATGAA	ATATATTAAA	GGTCCTGATT	TTCCAACCTGG	650
	TGGTATTATT	CAAGGTATTG	ATGGTATTAA	AAAAGCTTAT	GAATCAGGTA	700
	AAGGTAGAAT	TATAGTTCGT	TCTAAAGTTG	AAGAAGAAAC	TTTACGCAAT	750
	GGACGTAAAC	AGTTAATTAT	TACTGAAATT	CCATATGAAG	TGAACAAAAG	800
20	TAGCTTAGTA	AAACGTATCG	ATGAATTACG	TGCTGACAAA	AAAGTCGATG	850
	GTATCGTTGA	AGTACGTGAT	GAAACTGATA	GAAGTGGTTT	ACGAATAGCA	900
	ATTGAATTGA	AAAAAGATGT	GAACAGTGAA	TCAATCAAAA	ATTATCTTTA	950
	TAAAACTCT	GATTTACAGA	TTTCATATAA	TTTCAACATG	GTCGCTATTA	1000
	GTGATGGTCG	TCCAAAATTG	ATGGGTATTC	GTCAAATTAT	AGATAGTTAT	1050
25	TTGAATCATC	AAATTGAGGT	TGTTGCAAAT	AGAACGAAGT	TTGAATTAGA	1100
	TAATGCTGAA	AAACGTATGC	ATATCGTTGA	AGGTTTGATT	AAAGCGTTGT	1150
	CAATTTTAGA	TAAAGTAATT	GAATTGATTC	GTAGCTCTAA	AAACAAGCGT	1200
	GACGCTAAAG	AAAACCTTAT	CGAAGTATTC	GAGTTCACAG	AAGAACAGGC	1250
	TGAAGCAATT	GTAATGTTAC	AGTTATATCG	TTTAACAAAC	ACTGACATAG	1300
30	TTGCGCTTGA	AGGTGAACAT	AAAGAACTTG	AAGCATTAAT	CAAACAATTA	1350
	CGTCATATTC	TTGATAACCA	TGATGCATTA	TTGAATGTCA	TAAAAGAAGA	1400
	ATTGAATGAA	ATTAAAAAGA	AATTCAAATC	TGAACGACTG	TCTTTAATTG	1450
	AAGCAGAAAT	TGAAGAAATT	AAAATTGACA	AAGAAGTTAT	GGTGCCTAGT	1500
	GAAGAAGTTA	TTTTAAGTAT	GACACGTCAT	GGATATATTA	AACGTACTTC	1550
35	TATTCGTAGC	TTTAATGCTA	GCGGTGTTGA	GGATATTGGT	TTAAAAGATG	1600
	GTGACAGTTT	ACTTAAACAT	CAAGAAGTAA	ATACGCAAGA	TACCGTACTA	1650
	GTATTTACAA	ATAAAGGTCG	TTATCTATTT	ATACCGGTTT	ATAAATTAGC	1700
	AGATATTCGT	TGGAAAGAAT	TGGGGCAACA	TGTATCACAA	ATAGTTCCTA	1750
	TCGAAGAAGA	TGAAGTGGTT	ATTAATGTCT	TTAATGAAAA	GGACTTTAAT	1800
40	ACAGATGCAT	TTTATGTTTT	TGCGACTCAA	AATGGCATGA	TTAAGAAAAG	1850
	TACAGTGCCT	CTATTTAAAA	CAACGCGTTT	TAATAAACCT	TTAATTGCTA	1900
	CTAAAGTTAA	AGAAAATGAT	GATTTGATTA	GTGTTATGCG	CTTTGAAAAA	1950
	GATCAATTAA	TTACCGTCAT	TACTAATAAA	GGTATGTCAT	TAACGTATAA	2000
	TACAAGTGAA	CTATCAGATA	CCGGATTAAG	GGCAGCTGGT	GTTAAATCAA	2050
45	TAAATCTTAA	AGCTGAAGAT	TTCGTTGTTA	TGACAGAAGG	TGTTTCTGAA	2100
	AATGATACTA	TATTGATGGC	CACACAACGC	GGCTCGTTAA	AACGTATTAG	2150
	TTTTTAAATC	TTACAAGTTG	CTAAAAGAGC	ACAACGTGGA	ATAACTTTAT	2200
	TAAAAGAATT	AAAGAAAAAT	CCACATCGTA	TTGTAGCTGC	ACATGTAGTG	2250
	ACAGGTGAAC	ATAGTCAATA	TACATTATAT	TCAAAATCAA	ATGAAGAACA	2300
50	TGGTTTAATT	AATGATATTC	ATAAATCTGA	ACAATATACA	AATGGCTCAT	2350
	TCATTGTAGA	TACAGATGAT	TTTGGTGAAG	TAATAGACAT	GTATATTAGC	2400
	TAA					2403

2) INFORMATION FOR SEQ ID NO: 1322

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 22 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1322

RTIGAIYAAYI SIGTIGAYGA RG

22

15

2) INFORMATION FOR SEQ ID NO: 1323

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 22 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

25 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1323

ACIAWRSAIG GIGGIACICA YG

22

30

2) INFORMATION FOR SEQ ID NO: 1324

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

40

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1324

45 CCICCGICIS WRTCICCYTC

20

50

2) INFORMATION FOR SEQ ID NO: 1325

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 bases
(B) TYPE: Nucleic acid

WO 01/23604

- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1325

21

RTTCATYTCI CCIARICCYT T

10

2) INFORMATION FOR SEQ ID NO: 1326

(i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 22 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1326

22

TGATTCAATA CAGGTTTTAG AG

25

2) INFORMATION FOR SEQ ID NO: 1327

30

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1327

22

40 CTAGATTTC TCCTCATCAA AT

2) INFORMATION FOR SEQ ID NO: 1328

45

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1992 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: Genomic DNA

717

WO 01/23604

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus aureus*
 (B) STRAIN: RN4220
 (C) ACCESSION NUMBER: D67075

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1328

	ATGAATAAAC AAAATAATTA TTCAGATGAT TCAATACAGG TTTTAGAGGG	50
	GTTAGAAGCA GTTCGTAAAA GACCTGGTAT GTATATTGGA TCAACTGATA	100
10	AACGGGGATT ACATCATCTA GTATATGAAA TTGTCGATAA CTCCGTCGAT	150
	GAAGTATTGA ATGGTTACGG TAACGAAATA GATGTAACAA TTAATAAAGA	200
	TGGTAGTATT TCTATAGAAG ATAATGGACG TGGTATGCCA ACAGGTATAC	250
	ATAAATCAGG TAAACCGACA GTCGAAGTTA TCTTTACTGT TTTACATGCA	300
	GGAGGTAAAT TTGGACAAGG CGGCTATAAA ACTTCAGGTG GTCTTCACGG	350
15	TGTTGGTGCT TCAGTTGTAA ATGCATTGAG TGAATGGCTT GAAGTTGAAA	400
	TCCATCGAGA TGGTAATATA TATCATCAAA GTTTTAAAA CGGTGGTTCG	450
	CCATCTTCTG GTTTAGTGAA AAAAGGTAAA ACTAAGAAAA CAGGTACCAA	500
	AGTAACATTT AAACCTGATG ACACAATTTT TAAAGCATCT ACATCATTTA	550
	ATTTTGATGT TTTAAGTGAA CGACTACAAG AGTCTGCGTT CTTATTGAAA	600
20	AATTTAAAA TAACGCTTAA TGATTTACGC AGTGGTAAAG AGCGTCAAGA	650
	GCATTACCAT TATGAAGAAG GAATCAAAGA GTTTGTAGT TATGTCAATG	700
	AAGGAAAAGA AGTTTTGCAT GACGTGGCTA CATTTTCAGG TGAAGCAAAT	750
	GGTATAGAGG TAGACGTAGC TTTCCAATAT AATGATCAAT ATTCAGAAAG	800
	TATTTTAAGT TTTGTAAATA ATGTACGTAC TAAAGATGGT GGTACACATG	850
25	AAGTTGGTTT TAAAACAGCA ATGACACGTG TATTTAATGA TTATGCACGT	900
	CGTATTAATG AACTTAAAC AAAAGATAAA AACTTAGATG GTAATGATAT	950
	TCGTGAAGGT TTAACAGCTG TTGTGTCTGT TCGTATTCCA GAAGAATTAT	1000
	TGCAATTTGA AGGACAAACG AAATCTAAAT TGGGTACTTC TGAAGCTAGA	1050
	AGTGCTGTTG ATTCAGTTGT TGCAGACAAA TTGCCATTCT ATTTAGAAGA	1100
30	AAAAGGACAA TTGTCTAAAT CACTTGTGAA AAAAGCGATT AAAGCACAAC	1150
	AAGCAAGGGA AGCTGCACGT AAAGCTCGTG AAGATGCTCG TTCAGGTAAG	1200
	AAAAACAAGC GTAAAGACAC TTTGCTATCT GGTAAATTAA CACCTGCACA	1250
	AAGTAAAAAC ACTGAAAAAA ATGAATTGTA TTTAGTCGAA GGTGATTCTG	1300
35	CGGGAGGTTT AGCAAACTT GGACGAGACC GCAAATTCCA AGCGATATTA	1350
	CCATTACGTG GTAAGGTAAT TAATACAGAG AAAGCACGTC TAGAAGATAT	1400
	TTTTAAAAAT GAAGAAATTA ATACAATTAT CCACACAATC GGGGCAGGCG	1450
	TTGGTACTGA CTTTAAAATT GAAGATAGTA ATTATAATCG TGTAATTATT	1500
	ATGACTGATG CTGATACTGA TGGTGCGCAT ATTCAAGTGC TATTGTAAAC	1550
	ATTCTTCTTC AAATATATGA AACCGCTTGT TCAAGCAGGT CGTGTATTTA	1600
40	TTGCTTTACC TCCACTTTAT AAATTGGAAA AAGGTAAAGG CAAAACAAAG	1650
	CGAGTTGAAT ACGCTTGGAC AGACGAAGAG CTTAATAAAT TGCAAAAAGA	1700
	ACTTGGTAAA GGCTTCACGT TACAACGTTA CAAAGGTTTG GGTGAAATGA	1750
	ACCCTGAGCA ATTATGGGAA ACGACGATGA ACCCAGAAAC ACGAACTTTA	1800
	ATTCGTGTAC AAGTTGAAGA TGAAGTGCCT TCATCTAAAC GTGTAACAAC	1850
45	ATTAATGGGT GACAAAGTAC AACCTAGACG TGAATGGATT GAAAAGCATG	1900
	TTGAGTTTGG TATGCAAGAG GACCAAAGTA TTTTAGATAA TTCTGAAGTA	1950
	CAAGTGCTTG AAAATGATCA ATTTGATGAG GAGGAAATCT AG	1992

50

2) INFORMATION FOR SEQ ID NO: 1329

(i) SEQUENCE CHARACTERISTICS:

718

WO 01/23604

- (A) LENGTH: 25 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

5

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1329

25

10 TGTAGAGCGC GGTATCATCA AAGTA

2) INFORMATION FOR SEQ ID NO: 1330

15

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1330

22

25 AGATTCTGAAC TTGGTGTGCG GG

30 2) INFORMATION FOR SEQ ID NO: 1331

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1331

30

GCCCTTGAGG TACAGAATGG TAATGAAGTT

45

2) INFORMATION FOR SEQ ID NO: 1332

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1332

5 GACCGCGGCG CAGACCATCA

20

2) INFORMATION FOR SEQ ID NO: 1333

10

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

15 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1333

20

TCATGGTGAC TTATCTATTT ATG

23

25 2) INFORMATION FOR SEQ ID NO: 1334

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 bases

(B) TYPE: Nucleic acid

30 (C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1334

CATCTATTTA TAAAGCAATG GTA

23

40

2) INFORMATION FOR SEQ ID NO: 1335

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 19 bases

45 (B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1335

CTATTTATGG AGCAATGGT

19

2) INFORMATION FOR SEQ ID NO: 1336

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 17 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1336

TGGAGACTAC TCAGTGT

17

15

2) INFORMATION FOR SEQ ID NO: 1337

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 17 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

25 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1337

TGGAGACTTC TCAGTGT

17

30

2) INFORMATION FOR SEQ ID NO: 1338

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 15 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

40

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1338

45 GTGTACGGAG CAATG

15

50

2) INFORMATION FOR SEQ ID NO: 1339

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 bases
(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1339

CCAGCGGAAA TCGGT

15

10

2) INFORMATION FOR SEQ ID NO: 1340

(i) SEQUENCE CHARACTERISTICS:

15

(A) LENGTH: 25 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1340

GAACAAGGTA TGACACCGGA TAAAT

25

25

2) INFORMATION FOR SEQ ID NO: 1341

(i) SEQUENCE CHARACTERISTICS:

30

(A) LENGTH: 25 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1341

GATAACTGAA ATCCTGAGCC ATACG

25

40

2) INFORMATION FOR SEQ ID NO: 1342

45

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1342

GATGTTATTG GTCAATATCA TCCA

24

5

2) INFORMATION FOR SEQ ID NO: 1343

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 29 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

15 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1343

AAGAAACTGT CTCTTTATTA ATATCACGT

29

20

2) INFORMATION FOR SEQ ID NO: 1344

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 24 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

30

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1344

35 AGCAGCAACG ATGTTACGCA GCAG

24

2) INFORMATION FOR SEQ ID NO: 1345

40

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
45 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1345

50

CCCGCCGAGC ATTTCAACTA TTG

23

2) INFORMATION FOR SEQ ID NO: 1346

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1346

GATGTTACGC AGCAGGGCAG TC

22

2) INFORMATION FOR SEQ ID NO: 1347

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1347

ACCAAGCAGG TTCGCAGTCA AGTA

24

2) INFORMATION FOR SEQ ID NO: 1348

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 750 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

- (vi) ORIGINAL SOURCE:
(A) ORGANISM: Unidentified bacterium
(C) ACCESSION NUMBER: X04555

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1348

ATGCGCTCAC GCAACTGGTC CAGAACCTTG ACCGAACGCA GCGGTGGTAA 50
CGGCGCAGTG GCGGTTTTCA TGGCTTGTTA TGACTGTTTT TTTGTACAGT 100
CTATGCCTCG GGCATCCAAG CAGCAAGCGC GTTACGCCGT GGGTCGATGT 150
TTGATGTTAT GGAGCAGCAA CGATGTTACG CAGCAGGGCA GTCGCCCTAA 200
AACAAAGTTA GGCCGCATGG ACACAACGCA GGTCACATTG ATACACAAAA 250

TTCTAGCTGC GGCAGATGAG CGAAATCTGC CGCTCTGGAT CGGTGGGGGC 300
 TGGGCGATCG ATGCACGGCT AGGGCGTGTA ACACGCAAGC ACGATGATAT 350
 TGATCTGACG TTTCCCGGCG AGAGGCGCGG CGAGCTCGAG GCAATAGTTG 400
 AAATGCTCGG CGGGCGCGTC ATGGAGGAGT TGGACTATGG ATTCTTAGCG 450
 5 GAGATCGGGG ATGAGTTACT TGA CTGCGAA CCTGCTTGGT GGGCAGACGA 500
 AGCGTATGAA ATCGCGGAGG CTCCGCAGGG CTCGTGCCCA GAGGCGGCTG 550
 AGGGCGTCAT CGCCGGGCGG CCAGTCCGTT GTAACAGCTG GGAGGCGATC 600
 ATCTGGGATT ACTTTTACTA TGCCGATGAA GTACCACCAG TGGACTGGCC 650
 TACAAAGCAC ATAGAGTCCT ACAGGCTCGC ATGCACCTCA CTCGGGGCGG 700
 10 AAAAGGTTGA GGTCTTGCCT GCCGCTTCA GGTGCGGATA TGCGGCCTAA 750

2) INFORMATION FOR SEQ ID NO: 1349

15

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 20 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1349

25

CAGCCGACCA ATGAGTATCT TGCC

24

30 2) INFORMATION FOR SEQ ID NO: 1350

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases
 (B) TYPE: Nucleic acid
 35 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1350

40

TAATCAGGGC AGTTGCGACT CCTA

24

45

2) INFORMATION FOR SEQ ID NO: 1351

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 531 bases
 50 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 5 (A) ORGANISM: *Pseudomonas aeruginosa*
 (B) STRAIN: Stone 130
 (C) ACCESSION NUMBER: L06157

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1351

```

10 ATGTTATGGA GCAGCAACGA TGTTACGCAG CAGGGCAGTC GCCCTAAAC 50
   AAAGTTAGGT GGCTCAATGA GCATCATTGC AACCGTCAAG ATCGGCCCTG 100
   ACGAAATTTC AGCCATGAGG GCTGTGCTCG ATCTCTTCGG CAAAGAGTTT 150
   GAGGACATTC CAACCTACTC TGATCGCCAG CCGACCAATG AGTATCTTGC 200
   CAATCTTCTG CACAGCGAGA CGTTCATCGC GCTCGCTGCT TTTGACCGCG 250
15 GAACAGCAAT AGGTGGGCTC GCCGCCTACG TTCTACCCAA GTTCGAGCAA 300
   GCGCGAAGCG AGATCTACAT TTATGACTTG GCAGTCGCTT CCAGCCATCG 350
   AAGGCTAGGA GTCGCAACTG CCCTGATTAG CCACCTGAAG CGTGTGGCGG 400
   TTGAAGTTGG CGCGTATGTA ATCTATGTGC AAGCAGACTA CGGTGACGAT 450
   CCGGCAGTCG CTCTCTACAC AAAGCTTGA GTTCGGGAAG ACGTCATGCA 500
20 CTTGCACATT GATCCAAGAA CCGCCACCTA A 531
  
```

2) INFORMATION FOR SEQ ID NO: 1352

25

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 30 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1352

35

CCACGCTGAC AGAGCCGCAC CG 22

40 2) INFORMATION FOR SEQ ID NO: 1353

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
 (B) TYPE: Nucleic acid
 45 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1353

GGCCAGCTCC CATCGGACCC TG 22

2) INFORMATION FOR SEQ ID NO: 1354

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 21 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1354

CACGCTGACA GAGCCGCACC G

21

15

2) INFORMATION FOR SEQ ID NO: 1355

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 24 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

25 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1355

ATGCCGTTGC TGTCGAAATC CTCG

24

30

2) INFORMATION FOR SEQ ID NO: 1356

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 810 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

40

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 45 (A) ORGANISM: *Serratia marcescens*
 (C) ACCESSION NUMBER: M97172

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1356

ATGAACACGA TCGAATCGAT CACGGCGGAC CTGCACGGAC TGGGCGTCCG 50
 50 GCCCGGCGAC CTGATCATGG TCCATGCATC GCTGAAAGCC GTCGGCCCCG 100
 TCGAGGGAGG TGCGGCCTCG GTGGTGTCGG CCCTTCGCGC CGCGGTCTGG 150
 TCCGCAGGGA CCCTGATGGG TTATGCCTCA TGGGACCGCT CGCCCTATGA 200
 GGAGACGCTG AACGGCGCGC GGATGGACGA AGAACTGCGC CGCCGGTGGC 250

	CACCCTTCGA	TCTGGCCACA	TCCGGTACCT	ATCCCGGCTT	CGGCCTGCTC	300
	AACCGGTTTC	TGCTTGAGGC	GCCCGACGCA	CGGCGCAGCG	CGCATCCCGA	350
	CGCCTCCATG	GTCGCGGTCTG	GCCCCCTTGC	CGCCACGCTG	ACAGAGCCGC	400
	ACCGGCTTGG	GCAGGCGCTG	GGCGAAGGCT	CGCCGCTGGA	GCGCTTCGTC	450
5	GGGCATGGCG	GAAAGGTCCT	GCTTCTGGGA	GCGCCGCTCG	ACTCCGTCAC	500
	CGTGCTGCAT	TACGCCGAGG	CCATCGCCCC	CATCCCGAAC	AAACGCCGCG	550
	TGACCTATGA	AATGCCGATG	CTCGGCCCGG	ATGGCAGGGT	CCGATGGGAG	600
	CTGGCCGAGG	ATTTTCGACAG	CAACGGCATT	CTCGATTGCT	TCGCGGTCTGA	650
	TGGGAAGCCG	GATGCCGTCG	AGACGATCGC	CAAGGCTTAT	GTGGAAGTGG	700
-10	GCCGGCATCG	GGAAGGCATC	GTCGGTCGCG	CACCCTCCTA	TCTGTTTGAA	750
	GCGCAGGATA	TCGTCTCGTT	CGGCGTCACC	TATCTCGAAC	AGCATTTCGG	800
	CGCGCCCTGA					810

15

2) INFORMATION FOR SEQ ID NO: 1357

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1357

GCCCATCCAT TTGCCTTTGC

20

30

2) INFORMATION FOR SEQ ID NO: 1358

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1358

GCGTACCAAC TTGCCATCCT GAAG

24

45

2) INFORMATION FOR SEQ ID NO: 1359

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single

50

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1359

TGCCCCCTGCC ACCTCACTC

19

10

2) INFORMATION FOR SEQ ID NO: 1360

(i) SEQUENCE CHARACTERISTICS:

15

(A) LENGTH: 24 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1360

CGTACCAACT TGCCATCCTG AAGA

24

25

2) INFORMATION FOR SEQ ID NO: 1361

(i) SEQUENCE CHARACTERISTICS:

30

(A) LENGTH: 786 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

35

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Escherichia coli*
(C) ACCESSION NUMBER: X01385

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1361

	GTGCAATACG AATGGCGAAA AGCCGAGCTC ATCGGTCAGC TTCTCAACCT	50
	TGGGGTTACC CCCGGCGGTG TGCTGCTGGT CCACAGCTCC TTCCGTAGCG	100
45	TCCGGCCCCT CGAAGATGGG CCACTTGGAC TGATCGAGGC CCTGCGTGCT	150
	GCGCTGGGTC CGGGAGGGAC GCTCGTCATG CCCTCGTGGT CAGGTCTGGA	200
	CGACGAGCCG TTCGATCCTG CCACGTCGCC CGTTACACCG GACCTTGGAG	250
	TTGTCTCTGA CACATTCTGG CGCCTGCCAA ATGTAAAGCG CAGCGCCCAT	300
	CCATTTCCTT TTGCGGCAGC GGGGCCACAG GCAGAGCAGA TCATCTCTGA	350
50	TCCATTGCCC CTGCCACCTC ACTCGCCTGC AAGCCCGGTC GCCCGTGTCC	400
	ATGAACTCGA TGGGCAGGTA CTTCTCCTCG GCGTGGGACA CGATGCCAAC	450
	ACGACGCTGC ATCTTGCCGA GTTGATGGCA AAGGTTCCCT ATGGGGTGCC	500
	GAGACACTGC ACCATTCTTC AGGATGGCAA GTTGGTACGC GTCGATTATC	550

TCGAGAATGA CCACTGCTGT GAGCGCTTTG CCTTGGCGGA CAGGTGGCTC 600
 AAGGAGAAGA GCCTTCAGAA GGAAGGTCCA GTCGGTCATG CCTTTGCTCG 650
 GTTGATCCGC TCCCGCGACA TTGTGGCGAC AGCCCTGGGT CAACTGGGCC 700
 GAGATCCGTT GATCTTCCTG CATCCGCCAG AGGGCGGGAT GCGAAGAATG 750
 5 CGATGCCGCT CGCCAGTCGA TTGGCTGAGC TCATGA 786

2) INFORMATION FOR SEQ ID NO: 1362

10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 15 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1362

20

CGCCGCCATC GCCCAAAGCT GG

22

25 2) INFORMATION FOR SEQ ID NO: 1363

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases
 (B) TYPE: Nucleic acid
 30 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1363

CGGCATAATG GAGCGCGGTG ACTG

24

40

2) INFORMATION FOR SEQ ID NO: 1364

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases
 45 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1364

TTTCTCGCCC ACGCAGGAAA AATC

24

2) INFORMATION FOR SEQ ID NO: 1365

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 22 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1365

CATCCTCGAC GAATATGCCG CG

22

15

2) INFORMATION FOR SEQ ID NO: 1366

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 900 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

25 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterobacter cloacae*
(C) ACCESSION NUMBER: M88012

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1366

	ATGACTGATC	CCCGCAAAAA	CGGCGATTTG	CACGAACCCG	CGACGGCACC	50
	CGCGACGCCC	TGGTCCAAAA	GCGAGCTGGT	CCGGCAATTG	CGCGACCTCG	100
35	GCGTGCGCTC	AGGCGATATG	GTGATGCCGC	ATGTGTCGTT	GCGCGCCGTC	150
	GGGCCGCTGG	CGGACGGACC	GCAGACACTT	GTCGATGCGC	TGATCGAGGC	200
	CGTCGGCCCC	ACCGGGAATA	TTCTCGCCTT	CGTCTCGTGG	CGCGATTTCG	250
	CCTATGAACA	GACGCTGGGT	CATGATGCGC	CGCCCGCCGC	CATCGCCCAA	300
	AGCTGGCCTG	CGTTCGACCC	CGACCATGCG	CCCGCCTACC	CCGGCTTTGG	350
40	CGCGATCAAC	GAATTTATCC	GAACCTATCC	GGGGTGTCGG	CGCACGGCCC	400
	ATCCCGACGC	ATCGATGGCG	GCGATCGGGC	CCGATGCGGC	GTGGCTGGTG	450
	GCGCCGCACG	AGATGGGCGC	CGCTTATGGC	CCCCGCTCGC	CGATCGCGCG	500
	TTTTCTCGCC	CACGCAGGAA	AAATCCTGTC	GATCGGCGCC	GGGCCCAGAT	550
	CAGTCAACGC	GCTCCATTAT	GCCGAAGCGG	TGGCGCGGAT	CGAGGGCAAG	600
45	CGCCGCGTCA	CTTATTCGAT	GCCCTTACTG	CGCGAAGGCA	AGCGCGTCTG	650
	GGTCACCACG	TCCGACTGGG	ATTCGAACGG	CATCCTCGAC	GAATATGCCG	700
	CGCCCGACGG	CCCCGACGCG	GTCGAACGGA	TCGCCCAGCA	CTATCTCGCC	750
	CGCACCAGGG	TTGCGCAAGG	CCCGGTCGGC	GGCGCGCAAT	CCCGGCTGAT	800
	CGACGCGGCC	GATATCGTTT	CCTTCGGCAT	CGAATGGCTC	GAGGCGCGCC	850
50	ACGCCGCGCC	AGCGGCGGCA	GCGCTGAAGC	CGAAACAACG	CCGCGACTGA	900

2) INFORMATION FOR SEQ ID NO: 1367

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 24 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1367

CAAATATACT AACAGAAGCG TTCA

24

15

2) INFORMATION FOR SEQ ID NO: 1368

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 22 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

25 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1368

AGGATCTTGC CAATACCTTT AT

22

30

2) INFORMATION FOR SEQ ID NO: 1369

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 24 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

40

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1369

45 AAACCTTTGT TTCGGTCTGC TAAT

24

2) INFORMATION FOR SEQ ID NO: 1370

50

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases
(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1370

AAGCGATTCC AATAATACCT TGCT

24

10

2) INFORMATION FOR SEQ ID NO: 1371

(i) SEQUENCE CHARACTERISTICS:

15

(A) LENGTH: 558 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Citrobacter diversus*

(C) ACCESSION NUMBER: M18967

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1371

	ATGAATTATC	AAATTGTGAA	TATTGCGGAA	TGCAGCAATT	ATCAGTTAGA	50
	AGCAGCAAAT	ATACTAACAG	AAGCGTTCAA	TGATCTTGGT	AACAATTCAT	100
30	GGCCAGATAT	GACGAGTGCA	ACAAAAGAAG	TAAAAGAATG	TATTGAGAGT	150
	CCAAACCTTT	GTTTCGGTCT	GCTAATAAAT	AACCTCCTAG	TTGGCTGGAT	200
	AGGCTTAAGG	CCAATGTACA	AGGAAACCTG	GGAATTGCAT	CCATTGGTTG	250
	TCAGACCAGA	TTATCAAAAT	AAAGGTATTG	GCAAGATCCT	GCTTAAGGAA	300
	TTAGAAAACA	GAGCTAGAGA	GCAAGGTATT	ATTGGAATCG	CTTTAGGAAC	350
35	AGATGATGAA	TACTATAGAA	CAAGTCTCTC	TTTAATAACT	ATAACAGAAG	400
	ATAATATATT	TGATTCAATA	AAAAATATTA	AAAATATTAA	TAAACATCCA	450
	TATGAGTTTT	ATCAGAAGAA	TGGTTATTAT	ATTGTTGGAA	TAATTCCAAA	500
	TGCCAATGGT	AAAACAAAC	CAGATATTTG	GATGTGGAAA	AGTTTAATCA	550
	AAGAGTAA					558

40

2) INFORMATION FOR SEQ ID NO: 1372

45 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1372

GCTTTCGTTG CCTTTGCCGA GGTC

24

5

2) INFORMATION FOR SEQ ID NO: 1373

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 23 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

15 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1373

CACCCCTGTT GCTTCGCCCA CTC

23

20

2) INFORMATION FOR SEQ ID NO: 1374

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 24 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

30 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1374

AGATATTGGC TTCGCCGCAC CACA

24

35

2) INFORMATION FOR SEQ ID NO: 1375

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 23 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

45

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1375

50 CCCTGTTGCT TCGCCCACTC CTG

23

2) INFORMATION FOR SEQ ID NO: 1376

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 441 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
(A) ORGANISM: *Serratia marcescens*
(C) ACCESSION NUMBER: M94066
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1376

ATGATCGTCA	TCTGCGACCA	CGACAACCTC	GACGCCTGGC	TGGCGCTGCG	50
CACCGCGCTG	TGGCCCTCCG	GCTCGCCTGA	AGATCACCGC	GCGGAAATGC	100
GCGAGATATT	GGCTTCGCCG	CACCACACCG	CGTTTATGGC	GCGGGGGCTG	150
GACGGCGCTT	TCGTTGCCTT	TGCCGAGGTC	GCGCTGCGCT	ACGATTACGT	200
CAACGGCTGC	GAATCGTCGC	CGGTGGCGTT	TTTGGAAGGA	ATTTATACCG	250
CCGAACGCGC	CCGCCGCCAG	GGCTGGGCCG	CGCGCCTGAT	CGCGCAGGTG	300
CAGGAGTGGG	CGAAGCAACA	GGGGTGCAGC	GAGCTGGCGT	CGGATACCGA	350
TATCGCCAAT	CTGGACTCCC	AGCGCCTGCA	TGCGGCGCTG	GGCTTTGCCG	400
AAACGGAGCG	AGTAGTGTTT	TACCGCAAAA	CGCTGGGCTG	A	441

2) INFORMATION FOR SEQ ID NO: 1377

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: DNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1377

GCCGTGGGTC	GATGTTTGAT	GTTA	24
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2) INFORMATION FOR SEQ ID NO: 1378

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1378

GCTCGATGAC GCCAACTACC TCTG

24

5

2) INFORMATION FOR SEQ ID NO: 1379

10 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

15

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1379

20 AGCAGCAACG ATGTTACGCA GCAG

24

2) INFORMATION FOR SEQ ID NO: 1380

25

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

30

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1380

35

CGCTCGATGA CGCCAACTAC CTCT

24

2) INFORMATION FOR SEQ ID NO: 1381

40

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 972 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

45

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

50

- (A) ORGANISM: *Escherichia coli*
- (C) ACCESSION NUMBER: X02340

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1381

```

5  GTGGTAACGG CGCAGTGGCG GTTTTTCATGG CTTCTTGTTA TGACATGTTT      50
   TTTTGGGGTA CAGTCTATGC CTCGGGCATC CAAGCAGCAA GCGCGTTACG      100
  CCGTGGGTCG ATGTTTGATG TTATGGAGCA GCAACGATGT TACGCAGCAG      150
   GGCAGTCGCC CTA AAACAAA GTTAAACATC ATGAGGGAAG CGGTGATCGC      200
   CGAAGTATCG ACTCAACTAT CAGAGGTAAGT TGGCGTCATC GAGCGCCATC      250
   TCGAACCGAC GTTGCTGGCC GTACATTTGT ACGGCTCCGC AGTGGATGGC      300
   GGCCTGAAGC CACACAGTGA TATTGATTG CTGGTTACGG TGACCGTAAG      350
  10 GCTTGATGAA ACAACGCGGC GAGCTTTGAT CAACGACCTT TTGGAAACTT      400
   CGGCTTCCCC TGGAGAGAGC GAGATTCTCC GCGCTGTAGA AGTCACCATT      450
   GTTGTGCACG ACGACATCAT TCCGTGGCGT TATCCAGCTA AGCGCGAACT      500
   GCAATTTGGA GAATGGCAGC GCAATGACAT TCTTGACAGG ATCTTCGAGC      550
   CAGCCACGAT CGACATTGAT CTGGCTATCT TGCTGACAAA AGCAAGAGAA      600
  15 CATAGCGTTG CCTTGGTAGG TCCAGCGGCG GAGGAACTCT TTGATCCGGT      650
   TCCTGAACAG GATCTATTTG AGGCGCTAAA TGAAACCTTA ACGCTATGGA      700
   ACTCGCCGCC CGACTGGGCT GCGGATGAGC GAAATGTAGT GCTTACGTTG      750
   TCCCGCATTT GGTACAGCGC AGTAACCGGC AAAATCGCGC CGAAGGATGT      800
   CGCTGCCGAC TGGGCAATGG AGCGCCTGCC GGCCCAGTAT CAGCCCGTCA      850
  20 TACTTGAAGC TAGACAGGCT TATCTTGAC AAGAAGAAGA TCGCTTGGCC      900
   TCGCGCGCAG ATCAGTTGGA AGAATTTGTC CACTACGTGA AAGGCGAGAT      950
   CACCAAGGTA GTCGGCAAAT AA                                     972

```

25

2) INFORMATION FOR SEQ ID NO: 1382

```

   (i) SEQUENCE CHARACTERISTICS:
   (A) LENGTH: 24 bases
  30 (B) TYPE: Nucleic acid
   (C) STRANDEDNESS: Single
   (D) TOPOLOGY: Linear

```

35 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1382

TAGATATGAT AGGCGGTAAA AAGC

24

40

2) INFORMATION FOR SEQ ID NO: 1383

```

   (i) SEQUENCE CHARACTERISTICS:
   (A) LENGTH: 23 bases
  45 (B) TYPE: Nucleic acid
   (C) STRANDEDNESS: Single
   (D) TOPOLOGY: Linear

```

50 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1383

CCCAAATTCG AGTAAGAGGT ATT

23

5 2) INFORMATION FOR SEQ ID NO: 1384

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 22 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1384

GATATGATAG GCGGTAAAAA GC

22

20

2) INFORMATION FOR SEQ ID NO: 1385

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 22 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1385

TCCCAAATTC GAGTAAGAGG TA

22

35

2) INFORMATION FOR SEQ ID NO: 1386

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 477 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

45 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus aureus*
(C) ACCESSION NUMBER: V01282

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1386

ATGAAAGAAA GATATGGAAC AGTATATAAA GGCTCTCAGA GGCTCATAGA

50

CGAGGAAAGT GGAGAAGTAA TAGAGGTAGA TAAGCTATAC CGTAAACAAA 100
 CGTCTGGTAA CTTTGTA AAA GCGTATATCG TCCAATTAAT AAGTATGTTA 150
 GATATGATAG GCGGTAAAA GCTCAAGATT GTTAATTATA TATTAGATAA 200
 TGTACATCTA AGTAATAACA CAATGATAGC AACTGTTAGA GAAATAGCAG 250
 5 AAGGAACAAA TACAAGCACG AAAACCGTAA ATACAACGCT TAAAATCTTA 300
 GAAGAAGGAA ATATCATTAA AAGAAGAACT GGAGCATTAA TGCTAAACCC 350
 AGAGCTACTC ATGAGAGGCG ATGACCAAAA ACAAAAATAC CTCTTACTCG 400
 AATTTGGGAA CTTTGAGCAA GAGGACGACC AAAAGCAAGA AAATGCTTTA 450
 TCAGAATATT ATTCTTTCAA GGAGTAG 477
 10

2) INFORMATION FOR SEQ ID NO: 1387

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 24 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear
 20 (ii) MOLECULE TYPE: DNA
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1387
 25 TTATGCCTCT TCCGACCATC AAGC 24

2) INFORMATION FOR SEQ ID NO: 1388

30 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 24 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 35 (D) TOPOLOGY: Linear
 (ii) MOLECULE TYPE: DNA
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1388
 40 TACGCTCGTC ATCAAATCA CTCG 24

45 2) INFORMATION FOR SEQ ID NO: 1389

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 24 bases
 (B) TYPE: Nucleic acid
 50 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear
 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1389

GAATAACGGT TTGGTTGATG CGAG

24

5

2) INFORMATION FOR SEQ ID NO: 1390

10 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

15

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1390

20 ATGGCAAGAT CCTGGTATCG GTCT

24

2) INFORMATION FOR SEQ ID NO: 1391

25

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 816 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

30

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 35 (A) ORGANISM: *Escherichia coli*
- (C) ACCESSION NUMBER: J01839

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1391

40	ATGAGCCATA TTCAACGGGA AACGTCTTGC TCGAGGCCGC GATTAAATTC	50
	CAACATGGAT GCTGATTTAT ATGGGTATAA ATGGGCTCGC GATAATGTCG	100
	GGCAATCAGG TGCACAAATC TATCGATTGT ATGGGAAGCC CGATGCGCCA	150
	GAGTTGTTTC TGAAACATGG CAAAGGTAGC GTTGCCAATG ATGTTACAGA	200
	TGAGATGGTC AGACTAAACT GGCTGACGGA ATTTATGCCT CTTCCGACCA	250
45	TCAAGCATTT TATCCGTACT CCTGATGATG CATGGTTACT CACCACTGCG	300
	ATCCCCGGA AAACAGCATT CCAGGTATTA GAAGAATATC CTGATTCAGG	350
	TGAAAATATT GTTGATGCGC TGGCAGTGTT CCTGCGCCGG TTGCATTCTGA	400
	TTCCTGTTTG TAATTGTCCT TTAAACAGCG ATCGCGTATT TCGTCTCGCT	450
	CAGGCGCAAT CACGAATGAA TAACGGTTTG GTTGATGCGA GTGATTTTGA	500
50	TGACGAGCGT AATGGCTGGC CTGTTGAACA AGTCTGGAAA GAAATGCATA	550
	AGCTTTTGCC ATTCTCACCG GATTCAGTCG TCACTCATGG TGATTTCTCA	600
	CTTGATAACC TTATTTTGA CGAGGGGAAA TTAATAGGTT GTATTGATGT	650
	TGGACGAGTC GGAATCGCAG ACCGATACCA GGATCTTGCC ATCCTATGGA	700

ACTGCCTCGG	TGAGTTTCT	CCTTCATTAC	AGAAACGGCT	TTTTCAAAAA	750
TATGGTATTG	ATAATCCTGA	TATGAATAAA	TTGCAGTTTC	ATTTGATGCT	800
CGATGAGTTT	TTCTAA				816

5

2) INFORMATION FOR SEQ ID NO: 1392

- (i) SEQUENCE CHARACTERISTICS:
- 10 (A) LENGTH: 24 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

- 15 (ii) MOLECULE TYPE: DNA

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1392

20 TGGGTGGAGA GGCTATTCGG CTAT 24

2) INFORMATION FOR SEQ ID NO: 1393

- 25 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

- 30 (ii) MOLECULE TYPE: DNA

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1393

35 CAGTCCCTTC CCGCTTCAGT GAC 23

2) INFORMATION FOR SEQ ID NO: 1394

- 40 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 24 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- 45 (D) TOPOLOGY: Linear

- (ii) MOLECULE TYPE: DNA

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1394

50 GACGTTGTCA CTGAAGCGGG AAGG 24

2) INFORMATION FOR SEQ ID NO: 1395

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 24 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1395

CTTGGTGGTC GAATGGGCAG GTAG

24

15

2) INFORMATION FOR SEQ ID NO: 1396

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 795 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

25 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Escherichia coli*
(C) ACCESSION NUMBER: V00618

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1396

ATGATTGAAC AAGATGGATT GCACGCAGGT TCTCCGGCCG CTTGGGTGGA 50
GAGGCTATTC GGCTATGACT GGGCACAACA GACAATCGGC TGCTCTGATG 100
35 CCGCCGTGTT CCGGCTGTCA GCGCAGGGGC GCCCGGTTCT TTTTGTCAAG 150
ACCGACCTGT CCGGTGCCCT GAATGAACTG CAGGACGAGG CAGCGCGGCT 200
ATCGTGGCTG GCCACGACGG GCGTTCCTTG CGCAGCTGTG CTCGACGTTG 250
TCACTGAAGC GGAAGGGAC TGGCTGCTAT TGGGCGAAGT GCCGGGGCAG 300
GATCTCCTGT CATCTCACCT TGCTCCTGCC GAGAAAGTAT CCATCATGGC 350
40 TGATGCAATG CGGCGGCTGC ATACGCTTGA TCCGGCTACC TGCCCATTCTG 400
ACCACCAAGC GAAACATCGC ATCGAGCGAG CACGTACTCG GATGGAAGCC 450
GGTCTTGTCG ATCAGGATGA TCTGGACGAA GAGCATCAGG GGCTCGCGCC 500
AGCCGAACTG TTCGCCAGGC TCAAGGCGCG CATGCCCGAC GGCGAGGATC 550
TCGTCGTGAC CCATGGCGAT GCCTGCTTGC CGAATATCAT GGTGGAAAT 600
45 GGCCGCTTTT CTGGATTCAT CGACTGTGGC CGGCTGGGTG TGGCGGACCG 650
CTATCAGGAC ATAGCGTTGG CTACCCGTGA TATTGCTGAA GAGCTTGCG 700
GCGAATGGGC TGACCGCTTC CTCGTGCTTT ACGGTATCGC CGCTCCCGAT 750
TCGCAGCGCA TCGCCTTCTA TCGCCTTCTT GACGAGTTCT TCTGA 795

50

2) INFORMATION FOR SEQ ID NO: 1397

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
5 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1397
10 GTGGGAGAAA ATGAAAACCT AT 22

15 2) INFORMATION FOR SEQ ID NO: 1398

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
20 (C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1398
ATGGAGTGAA AGAGCCTGAT 20

30 2) INFORMATION FOR SEQ ID NO: 1399

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 bases
35 (B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1399
ACCTATGATG TGGAACGGGA AAAG 24

45 2) INFORMATION FOR SEQ ID NO: 1400

(i) SEQUENCE CHARACTERISTICS:
50 (A) LENGTH: 23 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1400

5

CGATGGAGTG AAAGAGCCTG ATG

23

10 2) INFORMATION FOR SEQ ID NO: 1401

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 795 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

20 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus faecalis*
(C) ACCESSION NUMBER: V01547

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1401

25

ATGGCTAAAA	TGAGAATATC	ACCGGAATTG	AAAAAACTGA	TCGAAAAATA	50
CCGCTGCGTA	AAAGATACGG	AAGGAATGTC	TCCTGCTAAG	GTATATAAGC	100
TGGTGGGAGA	AAATGAAAAC	CTATATTTAA	AAATGACGGA	CAGCCGGTAT	150
AAAGGGACCA	CCTATGATGT	GGAACGGGAA	AAGGACATGA	TGCTATGGCT	200
30 GGAAGGAAAG	CTGCCTGTTC	CAAAGGTCCT	GCACTTTGAA	CGGCATGATG	250
GCTGGAGCAA	TCTGCTCATG	AGTGAGGCCG	ATGGCGTCCT	TTGCTCGGAA	300
GAGTATGAAG	ATGAACAAAG	CCCTGAAAAG	ATTATCGAGC	TGTATGCGGA	350
GTGCATCAGG	CTCTTTCACT	CCATCGACAT	ATCGGATTGT	CCCTATACGA	400
ATAGCTTAGA	CAGCCGCTTA	GCCGAATTGG	ATTACTTACT	GAATAACGAT	450
35 CTGGCCGATG	TGGATTGCGA	AAACTGGGAA	GAAGACACTC	CATTTAAGAA	500
TCCGCGCGAG	CTGTATGATT	TTTTAAAGAC	GGAAAAGCCC	GAAGAGGAAC	550
TTGTCTTTTC	CCACGGCGAC	CTGGGAGACA	GCAACATCTT	TGTGAAAGAT	600
GGCAAAGTAA	GTGGCTTTAT	TGATCTTGGG	AGAAGCGGCA	GGGCGGACAA	650
GTGGTATGAC	ATTGCCTTCT	GCGTCCGGTC	GATCAGGGAG	GATATCGGGG	700
40 AAGAACAGTA	TGTCGAGCTA	TTTTTTGACT	TACTGGGGAT	CAAGCCTGAT	750
TGGGAGAAAA	TAAAATATTA	TATTTTACTG	GATGAATTGT	TTTAG	795

45 2) INFORMATION FOR SEQ ID NO: 1402

(i) SEQUENCE CHARACTERISTICS:

- 50 (A) LENGTH: 24 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1402

TATTCAACAA TTTATCGGAA ACAG

24

5

2) INFORMATION FOR SEQ ID NO: 1403

10 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single,
- (D) TOPOLOGY: Linear

15

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1403

20 TCAGAGAGCC AACTCAACAT TTT

23

2) INFORMATION FOR SEQ ID NO: 1404

25

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

30

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1404

35

AAACAGCGTT TTAGAGCCAA ATAA

24

40 2) INFORMATION FOR SEQ ID NO: 1405

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

45

(ii) MOLECULE TYPE: DNA

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1405

TTCTCAGAGA GCCAACTCAA CATT

24

2) INFORMATION FOR SEQ ID NO: 1406

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 780 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

10

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Acinetobacter baumannii*
 (B) STRAIN: BM2580
 (C) ACCESSION NUMBER: X07753

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1406

ATGGAATTGC CCAATATTAT TCAACAATTT ATCGGAAACA GCGTTTTAGA 50
 GCCAAATAAA ATTGGTCAGT CGCCATCGGA TGTTTATTCT TTTAATCGAA 100
 20 ATAATGAAAC TTTTTTCTT AAGCGATCTA GCACTTTATA TACAGAGACC 150
 ACATACAGTG TCTCTCGTGA AGCGAAAATG TTGAGTTGGC TCTCTGAGAA 200
 ATTAAAGGTG CCTGAACTCA TCATGACTTT TCAGGATGAG CAGTTTGAAT 250
 TCATGATCAC TAAAGCGATC AATGCAAAAC CAATTTTCAGC GCTTTTTTTA 300
 ACAGACCAAG AATTGCTTGC TATCTATAAG GAGGCACTCA ATCTGTTAAA 350
 25 TTCAATTGCT ATTATTGATT GTCCATTTAT TTCAAACATT GATCATCGGT 400
 TAAAAGAGTC AAAATTTTTT ATTGATAACC AACTCCTTGA CGATATAGAT 450
 CAAGATGATT TTGACACTGA ATTATGGGGA GACCATAAAA CTTACCTAAG 500
 TCTATGGAAT GAGTTAACCG AGACTCGTGT TGAAGAAAGA TTGGTTTTTTT 550
 CTCATGGCGA TATCACGGAT AGTAATATTT TTATAGATAA ATTCAATGAA 600
 30 ATTTATTTTT TAGATCTTGG TCGTGCTGGG TTAGCAGATG AATTTGTAGA 650
 TATATCCTTT GTTGAACGTT GCCTAAGAGA GGATGCATCG GAGGAAACTG 700
 CGAAAATATT TTAAAGCAT TTAAAAAATG ATAGACCTGA CAAAAGGAAT 750
 TATTTTTTAA AACTTGATGA ATTGAATTGA 780

35

2) INFORMATION FOR SEQ ID NO: 1407

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 24 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1407

CCCTGTAATA GAAAAGCAAG TAGG

24

50

2) INFORMATION FOR SEQ ID NO: 1408

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 bases
(B) TYPE: Nucleic acid
5 (C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1408

TTGTCGTATC CCTCAAATCA CC

22

15

2) INFORMATION FOR SEQ ID NO: 1409

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 bases
20 (B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1409

TGGGATTACA ATGGCAATCA GCG

23

30

2) INFORMATION FOR SEQ ID NO: 1410

- (i) SEQUENCE CHARACTERISTICS:
35 (A) LENGTH: 25 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

40 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1410

GGGGAATAGG TCACAAGATC TGCTT

25

45

2) INFORMATION FOR SEQ ID NO: 1411

- 50 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 912 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

5 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Pseudomonas aeruginosa*

(C) ACCESSION NUMBER: S46063

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1411

```

10  ATGCTTTTAT ATAAAATGTG TGACAATCAA AATTATGGGG TTACTTACAT      50
    GAAGTTTTTA TTGGCATT TTGCTTTTAA ACCATCCGTG GTTTTTGCAA      100
    GTAGTTCAAA GTTTCAGCAA GTTGAACAAG ACGTTAAGGC AATTGAAGTT      150
    TCTCTTTCTG CTCGTATAGG TGTTTCCGTT CTTGATACTC AAAATGGAGA      200
15  ATATTGGGAT TACAATGGCA ATCAGCGCTT CCCGTTAACA AGTACTTTTA      250
    AAACAATAGC TTGCGCTAAA TTACTATATG ATGCTGAGCA AGGAAAAGTT      300
    AATCCCAATA GTACAGTCGA GATTAAGAAA GCAGATCTTG TGACCTATTC      350
    CCCTGTAATA GAAAAGCAAG TAGGGCAGGC AATCACACTC GATGATGCGT      400
    GCTTCGCAAC TATGACTACA AGTGATAATA CTGCGGCAAA TATCATCCTA      450
20  AGTGCTGTAG GTGGCCCCAA AGGCGTTACT GATTTTTTAA GACAAATTGG      500
    GGACAAAGAG ACTCGTCTAG ACCGTATTGA GCCTGATTTA AATGAAGGTA      550
    AGCTCGGTGA TTTGAGGGAT ACGACAAC TCAGGCAAT AGCCAGTACT      600
    TTGAATAAAC TTTTATTTGG TTCCGCGCTA TCTGAAATGA ACCAGAAAAA      650
    ATTAGAGTCT TGGATGGTGA ACAATCAAGT CACTGGTAAT TTACTACGTT      700
25  CAGTATTGCC GGCGGGATGG AACATTGCGG ATCGCTCAGG TGCTGGCGGA      750
    TTTGGTGCTC GGAGTATTAC AGCAGTTGTG TGGAGTGAGC ATCAAGCCCC      800
    AATTATTGTG AGCATCTATC TAGCTCAAAC ACAGGCTTCA ATGGCAGAGC      850
    GAAATGATGC GATTGTTAAA ATTGGTCATT CAATTTTGA CGTTTATACA      900
    TCACAGTCGC GC                                          912
30

```

2) INFORMATION FOR SEQ ID NO: 1412

35 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

40

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1412

45 GAGAAAACGC TCCAGCAGGG C

21

2) INFORMATION FOR SEQ ID NO: 1413

50

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 bases

(B) TYPE: Nucleic acid

- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1413

CATGAGGCTT TCACTGCGGG G

21

10

2) INFORMATION FOR SEQ ID NO: 1414

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

15

20

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1414

TATCGTTAAT CGCACCATCA C

21

25

2) INFORMATION FOR SEQ ID NO: 1415

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

30

35

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1415

40 ATGCAGTAAT GCGGCTTTAT C

21

2) INFORMATION FOR SEQ ID NO: 1416

45

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1146 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Double
 - (D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Klebsiella pneumoniae*
 (B) STRAIN: HEL-1
 (C) ACCESSION NUMBER: X91840

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1416

	ATGATGAAAA	AATCGTTATG	CTGCGCTCTG	CTGCTGACAG	CCTCTTTCTC	50
	CACATTTGCT	GCCGCAAAAA	CAGAACAACA	GATTGCCGAT	ATCGTTAATC	100
10	GCACCATCAC	CCCGTTGATG	CAGGAGCAGG	CTATTCCGGG	TATGGCCGTT	150
	GCCGTTATCT	ACCAGGGAAA	ACCCTATTAT	TTCACCTGGG	GTAAAGCCGA	200
	TATCGCCAAT	AACCACCCAG	TCACGCAGCA	AACGCTGTTT	GAGCTAGGAT	250
	CGGTTAGTAA	GACGTTTAAC	GGCGTGTTGG	GCGGCGATGC	TATCGCCCGC	300
	GGCGAAATTA	AGCTCAGCGA	TCCGGTCACG	AAATACTGGC	CAGAACTGAC	350
15	AGGCAAACAG	TGGCAGGGTA	TCCGCCTGCT	GCACTTAGCC	ACCTATACGG	400
	CAGGCGGCCT	ACCGCTGCAG	ATCCCCGATG	ACGTTAGGGA	TAAAGCCGCA	450
	TTACTGCATT	TTTATCAAAA	CTGGCAGCCG	CAATGGACTC	CGGGCGCTAA	500
	GCGACTTTAC	GCTAACTCCA	GCATTGGTCT	GTTTGGCGCG	CTGGCGGTGA	550
	AACCCTCAGG	AATGAGTTAC	GAAGAGGCAA	TGACCAGACG	CGTCCTGCAA	600
20	CCATTAAAAC	TGGCGCATAC	CTGGATTACG	GTTCCGCAGA	ACGAACAAAA	650
	AGATTATGCC	TGGGGCTATC	GCGAAGGGAA	GCCCCGTACAC	GTTTCTCCGG	700
	GACAACTTGA	CGCCGAAGCC	TATGGCGTGA	AATCCAGCGT	TATTGATATG	750
	GCCCCGTGGG	TTCAGGCCAA	CATGGATGCC	AGCCACGTTT	AGGAGAAAAC	800
	GCTCCAGCAG	GGCATTGCGC	TTGCGCAGTC	TCGCTACTGG	CGTATTGGCG	850
25	ATATGTACCA	GGGATTAGGC	TGGGAGATGC	TGAACTGGCC	GCTGAAAGCT	900
	GATTCGATCA	TCAACGGCAG	CGACAGCAAA	GTGGCATTGG	CAGCGCTTCC	950
	CGCCGTTGAG	GTAAACCCGC	CCGCCCCCGC	AGTGAAAGCC	TCATGGGTGC	1000
	ATAAAACGGG	CTCCACTGGT	GGATTGTGGCA	GCTACGTAGC	CTTCGTTCCA	1050
	GAAAAAACC	TTGGCATCGT	GATGCTGGCA	AACAAAAGCT	ATCCTAACCC	1100
30	TGTCCGTGTC	GAGGCGGCCT	GGCGCATTCT	TGAAAAGCTG	CAATAA	1146

2) INFORMATION FOR SEQ ID NO: 1417

35

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

40

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1417

45

TGGTTAACTA YAATCCSATT GCGGA

25

50 2) INFORMATION FOR SEQ ID NO: 1418

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases

750

- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

5 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1418

ATGCTTTACC CAGCGTCAGA TT

22

10

2) INFORMATION FOR SEQ ID NO: 1419

15 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1419

25 CGATGAATAA GCTGATTCT CACG

24

2) INFORMATION FOR SEQ ID NO: 1420

30

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1420

40

TGCTTTACCC AGCGTCAGAT TACG

24

2) INFORMATION FOR SEQ ID NO: 1421

45

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1421

AATTAGAGCG GCAGTCGGGA GGAA

24

5

2) INFORMATION FOR SEQ ID NO: 1422

10 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

15

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1422

20 GAAATCAGCT TATTCATCGC CACG

24

2) INFORMATION FOR SEQ ID NO: 1423

25

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 876 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

30

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 35 (A) ORGANISM: *Escherichia coli*
- (B) STRAIN: GRI-1
- (C) ACCESSION NUMBER: X92506

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1423

40

ATGGTTAAAA	AATCACTGCG	TCAGTTCACG	CTGATGGCGA	CGGCAACCGT	50
CACGCTGTTG	TTAGGAAGTG	TGCCGCTGTA	TGCGCAAACG	GCGGACGTAC	100
AGCAAAAAGT	TGCCGAATTA	GAGCGGCAGT	CGGGAGGAAG	ACTGGGTGTG	150
GCATTGATTA	ACACAGCAGA	TAATTCGCAA	ATACTTTATC	GTGCTGATGA	200
45 GCGCTTTGCG	ATGTGCAGCA	CCAGTAAAGT	GATGGCCGTG	GCCGCGGTGC	250
TGAAGAAAAG	TGAAAGCGAA	CCGAATCTGT	TAAATCAGCG	AGTTGAGATC	300
AAAAAATCTG	ACTTGGTTAA	CTATAATCCG	ATTGCGGAAA	AGCACGTCGA	350
TGGGACGATG	TCACTGGCTG	AGCTTAGCGC	GGCCGCGCTA	CAGTACAGCG	400
ATAACGTGGC	GATGAATAAG	CTGATTCTC	ACGTTGGCGG	CCCGGCTAGC	450
50 GTCACCGCGT	TCGCCCCACA	GCTGGGAGAC	GAAACGTTCC	GTCTCGACCG	500
TACCGAGCCG	ACGTTAAACA	CCGCCATTCC	GGGCGATCCG	CGTGATACCA	550
CTTCACCTCG	GGCAATGGCG	CAAATCTG	GTAATCTGAC	GCTGGGTAAA	600
GCATTGGGTG	ACAGCCAACG	GGCGCAGCTG	GTGACATGGA	TGAAAGGCAA	650

TACCACCGGT GCAGCGAGCA TTCAGGCTGG ACTGCCTGCT TCCTGGGTTG 700
 TGGGGGATAA AACCGGCAGC GGTGACTATG GCACCACCAA CGATATCGCG 750
 GTGATCTGGC CAAAAGATCG TGCGCCGCTG ATTCTGGTCA CTTACTTCAC 800
 CCAGCCTCAA CCTAAGGCAG AAAGCCGTCG CGATGTATTA GCGTCGGCGG 850
 5 CTAAATCGT CACCAACGGT TTGTAA 876

2) INFORMATION FOR SEQ ID NO: 1424

10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

15

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1424

20

GTTAACGGTG ATGGCGACGC TAC

23

25 2) INFORMATION FOR SEQ ID NO: 1425

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

30

(ii) MOLECULE TYPE: DNA

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1425

GAATTATCGG CGGTGTTAAT CAGC

24

40

2) INFORMATION FOR SEQ ID NO: 1426

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

45

(ii) MOLECULE TYPE: DNA

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1426

CACGCTCAAT ACCGCCATTC CA

22

2) INFORMATION FOR SEQ ID NO: 1427

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 24 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1427

TTATCGCCCA CTACCCATGA TTTC

24

15

2) INFORMATION FOR SEQ ID NO: 1428

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 876 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

25 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Salmonella typhimurium*
 (B) STRAIN: CAS-5
 30 (C) ACCESSION NUMBER: X92507

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1428

	ATGATGACTC	AGAGCATTCG	CCGCTCAATG	TTAACGGTGA	TGGCGACGCT	50
35	ACCCCTGCTA	TTTAGCAGCG	CAACGCTGCA	TGCGCAGGCG	AACAGCGTGC	100
	AACAGCAGCT	GGAAGCCCTG	GAGAAAAGTT	CGGGAGGTCG	GCTTGCGCTT	150
	GCGCTGATTA	ACACCGCCGA	TAATTCGCAG	ATTCTCTACC	GTGCCGATGA	200
	ACGTTTTTGC	ATGTGCAGTA	CCAGTAAGGT	GATGGCGGCC	GCGGCGGTGC	250
	TTAAACAGAG	CGAGAGCGAT	AAGCACCTGC	TAAATCAGCG	CGTTGAAATC	300
40	AAGAAGAGCG	ACCTGGTTAA	CTACAATCCC	ATTGCGGAGA	AACACGTTAA	350
	CGGCACGATG	ACGCTGGCTG	AGCTTGGCGC	AGCGGCGCTG	CAGTATAGCG	400
	ACAATACTGC	CATGAATAAG	CTGATTGCCC	ATCTGGGTGG	TCCCGATAAA	450
	GTGACGGCGT	TTGCTCGCTC	GTTGGGTGAT	GAGACCTTCC	GTCTGGACAG	500
	AACCGAGCCC	ACGCTCAATA	CCGCCATTCC	AGGCGACCCG	CGTGATACCA	550
45	CCACGCCGCT	CGCGATGGCG	CAGACCCTGA	AAAATCTGAC	GCTGGGTAAA	600
	GCGCTGGCGG	AAACTCAGCG	GGCACAGTTG	GTGACGTGGC	TTAAGGGCAA	650
	TACTACCGGT	AGCGCGAGCA	TTCGGGCGGG	TCTGCCGAAA	TCATGGGTAG	700
	TGGGCGATAA	AACCGGCAGC	GGAGATTATG	GCACCACCAA	CGATATCGCG	750
	GTTATCTGGC	CGGAAAACCA	CGCACCCTG	GTTCTGGTGA	CCTACTTTAC	800
50	CCAACCGGAG	CAGAAGGCGG	AAAGCCGTCG	GGATATTCTG	GCTGCGGCGG	850
	CGAAAATCGT	AACCCACGGT	TTCTGA			876

2) INFORMATION FOR SEQ ID NO: 1429

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 25 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

10 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1429

TTTACGGCTA AAGATACTGA AAAGT

25

15

2) INFORMATION FOR SEQ ID NO: 1430

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 26 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

25 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1430

GTTTAATAAAA ACAACCACCG AATAAT

26

30

2) INFORMATION FOR SEQ ID NO: 1431

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 25 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

40

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1431

45 TAATTGACAC TCCATTTACG GCTAA

25

2) INFORMATION FOR SEQ ID NO: 1432

50

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 bases
(B) TYPE: Nucleic acid

- (C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1432

ACCGAATAAT ATTTTCCTTT CAGGCA

26

10

2) INFORMATION FOR SEQ ID NO: 1433

(i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 741 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Pseudomonas aeruginosa*
(C) ACCESSION NUMBER: AJ223604

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1433

	ATGAGCAAGT TATCTGTATT CTTTATATTT TTGTTTTGCA GCATTGCTAC	50
	CGCAGCAGAG TCTTTGCCAG ATTTAAAAAT TGAAAAGCTT GATGAAGGCG	100
30	TTTATGTTCA TACTTCGTTT GAAGAAGTTA ACGGGTGGGG CGTTGTTCTT	150
	AAACATGGTT TGGTGGTTCT TGTAATGCT GAGGCTTACC TAATTGACAC	200
	TCCATTTACG GCTAAAGATA CTGAAAAGTT AGTCACTTGG TTTGTGGAGC	250
	GTGGCTATAA AATAAAAGGC AGCATTTTCT CTCATTTTCA TAGCGACAGC	300
	ACGGGCGGAA TAGAGTGGCT TAATTCTCGA TCTATCCCCA CGTATGCATC	350
35	TGAATTAACA AATGAACTGC TTAAAAAGA CGGTAAGGTT CAAGCCACAA	400
	ATTCATTTAG CGGAGTTAAC TATTGGCTAG TTAAAAATAA AATTGAAGTT	450
	TTTTATCCAG GCCC GGACAC CACTCCAGAT AACGTAGTGG TTTGGTTGCC	500
	TGAAAGGAAA ATATTATTCG GTGGTTGTTT TATTAAACCG TACGGTTTAC	550
	GCAATTTGGG TGACGCAAAT ATAGAAGCTT GGCCAAAGTC CGCCAAATTA	600
40	TTAAAGTCCA AATATGGTAA GGCAAACTG GTTGTTCCAA GTCACAGTGA	650
	AGTTGGAGAC GCATCACTCT TGAAACTTAC ATTAGAGCAG GCGGTAAAG	700
	GGTTAAACGA AAGTAAAAAA CCATCAAAC CAAGCAACTA A	741

45

2) INFORMATION FOR SEQ ID NO: 1434

(i) SEQUENCE CHARACTERISTICS:

50

- (A) LENGTH: 25 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1434

5 CACAATCAAG ACCAAGATTT GCGAT

25

2) INFORMATION FOR SEQ ID NO: 1435

10

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 25 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

15 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1435

20

GAAAGGGCAG CTCGTTACGA TAGAG

25

25 2) INFORMATION FOR SEQ ID NO: 1436

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 bases

(B) TYPE: Nucleic acid

30 (C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1436

CAGCATCAAC ATTTAAGATC CCA

24

40

2) INFORMATION FOR SEQ ID NO: 1437

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 26 bases

45 (B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1437

CTCCACTTGA TTAAGTGC GG AAATTC

26

2) INFORMATION FOR SEQ ID NO: 1438

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 828 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

10 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Escherichia coli*
 (C) ACCESSION NUMBER: X06046

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1438

ATGGCAATCC GAATCTTCGC GATACTTTTC TCCATTTTTT CTCTTGCCAC 50
 TTTCGCGCAT GCGCAAGAAG GCACGCTAGA ACGTTCTGAC TGGAGGAAGT 100
 TTTTCAGCGA ATTTCAAGCC AAAGGCACGA TAGTTGTGGC AGACGAACGC 150
 20 CAAGCGGATC GTGCCATGTT GGTTTTGTGAT CCTGTGCGAT CGAAGAAACG 200
 CTACTCGCCT GCATCGACAT TCAAGATACC TCATACACTT TTTGCACTTG 250
 ATGCAGGCGC TGTTCGTGAT GAGTTCAGAG TTTTTCGATG GGACGGCGTT 300
 AACAGGGGCT TTGCAGGCCA CAATCAAGAC CAAGATTTGC GATCAGCAAT 350
 GCGGAATTCT ACTGTTTGGG TGTATGAGCT ATTTGCAAAG GAAATTGGTG 400
 25 ATGACAAAGC TCGGCGCTAT TTGAAGAAAA TCGACTATGG CAACGCCGAT 450
 CCTTCGACAA GTAATGGCGA TTACTGGATA GAAGGCAGCC TTGCAATCTC 500
 GGCGCAGGAG CAAATTGCAT TTCTCAGGAA GCTCTATCGT AACGAGCTGC 550
 CCTTTCGGGT AGAACATCAG CGCTTGGTCA AGGATCTCAT GATTGTGGAA 600
 GCCGGTCGCA ACTGGATACT GCGTGCAAAG ACGGGCTGGG AAGGCCGTAT 650
 30 GGGTTGGTGG GTAGGATGGG TTGAGTGGCC GACTGGCTCC GTATTCTTCG 700
 CACTGAATAT TGATACGCCA AACAGAATGG ATGATCTTTT CAAGAGGGAG 750
 GCAATCGTGC GGGCAATCCT TCGCTCTATT GAAGCGTTAC CGCCCAACCC 800
 GGCAGTCAAC TCGGACGCTG CGCGATAA 828

35

2) INFORMATION FOR SEQ ID NO: 1439

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 801 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

45 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Pseudomonas aeruginosa*
 (C) ACCESSION NUMBER: J03427

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1439

ATGAAAACAT TTGCCGCATA TGTAATTATC GCGTGTCTTT CGAGTACGGC 50

	ATTAGCTGGT	TCAATTACAG	AAAATACGTC	TTGGAACAAA	GAGTTCTCTG	100
	CCGAAGCCGT	CAATGGTGTC	TTCGTGCTTT	GTAAAAGTAG	CAGTAAATCC	150
	TGCGCTACCA	ATGACTTAGC	TCGTGCATCA	AAGGAATATC	TTCCAGCATC	200
	AACATTTAAG	ATCCCCAACG	CAATTATCGG	CCTAGAAACT	GGTGTCTATA	250
5	AGAATGAGCA	TCAGGTTTTT	AAATGGGACG	GAAAGCCAAG	AGCCATGAAG	300
	CAATGGGAAA	GAGACTTGAC	CTTAAGAGGG	GCAATACAAG	TTTCAGCTGT	350
	TCCCGTATTT	CAACAAATCG	CCAGAGAAGT	TGGCGAAGTA	AGAATGCAGA	400
	AATACCTTAA	AAAATTTTCC	TATGGCAACC	AGAATATCAG	TGGTGGCATT	450
	GACAAATTCT	GGTTGGAAGG	CCAGCTTAGA	ATTTCCGCAG	TTAATCAAGT	500
10	GGAGTTTCTA	GAGTCTCTAT	ATTTAAATAA	ATTGTCAGCA	TCTAAAGAAA	550
	ACCAGCTAAT	AGTAAAAGAG	GCTTTGGTAA	CGGAGGCGGC	ACCTGAATAT	600
	CTAGTGCATT	CAAAAACCTG	TTTTTCTGGT	GTGGGAACTG	AGTCAAATCC	650
	TGGTGTGCGA	TGGTGGGTTG	GGTGGGTTGA	GAAGGAGACA	GAGGTTTACT	700
	TTTTCGCCTT	TAACATGGAT	ATAGACAACG	AAAGTAAGTT	GCCGCTAAGA	750
15	AAATCCATTC	CCACCAAAT	CATGGAAAGT	GAGGGCATCA	TTGGTGGCTA	800
	A					801

20 2) INFORMATION FOR SEQ ID NO: 1440

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 bases
- (B) TYPE: Nucleic acid
- 25 (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1440

AGACCGTTAT CGTAAACAGG GCTAAG

26

35

2) INFORMATION FOR SEQ ID NO: 1441

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 bases
- 40 (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1441

TTTTTTGCTC AACTTTTTTC AGGATC

26

50

2) INFORMATION FOR SEQ ID NO: 1442

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 927 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Pseudomonas aeruginosa*
 (B) STRAIN: RNL-1
 (C) ACCESSION NUMBER: Z21957

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1442

```

15  ATGAATGTCA TTATAAAAGC TGTAAGTTACT GCCTCGACGC TACTGATGGT      50
    ATCTTTTAGT TCATTTCGAAA CCTCAGCGCA ATCCCCACTG TTAAAAGAGC      100
    AAATTGAATC CATAGTCATT GGAAAAAAG CCACTGTAGG CGTTGCAGTG      150
    TGGGGGCGCTG ACGATCTGGA ACCTTTACTG ATTAATCCTT TTGAAAAATT      200
20  CCCAATGCAA AGTGATATTTA AATTGCATTT AGCTATGTTG GTACTGCATC      250
    AGGTTGATCA GGGAAAGTTG GATTTAAATC AGACCGTTAT CGTAAACAGG      300
    GCTAAGGTTT TACAGAATAC CTGGGCTCCG ATAATGAAAG CGTATCAGGG      350
    AGACGAGTTT AGTGTTCCAG TGCAGCAACT GCTGCAATAC TCGGTCTCGC      400
    ACAGCGATAA CGTGGCCTGT GATTGTATAT TTGAACTGGT TGGTGGACCA      450
25  GCTGCTTTGC ATGACTATAT CCAGTCTATG GGTATAAAGG AGACCGCTGT      500
    GGTGCGAAAT GAAGCGCAGA TGCACGCCGA TGATCAGGTG CAGTATCAAA      550
    ACTGGACCTC GATGAAAGGT GCTGCAGAGA TCCTGAAAAA GTTTGAGCAA      600
    AAAACACAGC TGTCTGAAAC CTCGCAGGCT TTGTTATGGA AGTGGATGGT      650
    CGAAACCACC ACAGGACCAG AGCGGTTAAA AGGTTTGTTA CCAGCTGGTA      700
30  CTGTGGTCGC ACATAAAACT GGTACTTCGG GTATCAAAGC CGGAAAAACT      750
    GCGGCCACTA ATGATTTAGG TATCATTTCTG TTGCCTGATG GACGGCCCTT      800
    GCTGGTTGCT GTTTTTGTGA AAGACTCAGC CGAGTCAAGC CGAACCAATG      850
    AAGCTATCAT TGCGCAGGTT GCTCAGACTG CGTATCAATT TGAATTGAAA      900
    AAGCTTTCTG CCCTAAGCCC AAATTAA      927
35

```

2) INFORMATION FOR SEQ ID NO: 1443

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1443

```

50  CTTCTGCTCT GCTGATGCTT GGC

```

23

2) INFORMATION FOR SEQ ID NO: 1444

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 26 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1444

GGCGACCAGG TATTTGTAA TACTGC

26

15

2) INFORMATION FOR SEQ ID NO: 1445

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 927 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

25 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Salmonella typhimurium*
(B) STRAIN: JMC
30 (C) ACCESSION NUMBER: X93314

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1445

ATGAATGTCA TCACAAAATG TGTTCACACC GCTTCTGCTC TGCTGATGCT 50
35 TGGCTTAAGT TCATTTGTAG TATCAGCCCA ATCCCCTTTG TTAAAAGAGC 100
AGATTGAAAC CATAGTGACG GGTAAAAAGG CCACTGTAGG TGTAGCAGTG 150
TGGGGGCGCTG ACGATCTGGA ACCTTTGTTG CTGAATCCAT TTGAAAAGTT 200
TCCGATGCAA AGTGTGTTTA AACTGCATTT AGCTATGTTA GTTCTGCATC 250
AGGTCGATCA GGGGAAACTG GATTTAAATC AGTCTGTTAC TGTTAATCGT 300
40 GCTGCAGTAT TACAAAATAC CTGGTCGCCA ATGATGAAAG ATCATCAGGG 350
CGATGAATTT ACTGTTGCAG TACAGCAGTT ACTGCAGTAT TCGGTGTCAC 400
ACAGCGACAA TGTGGCCTGC GATTGTATT TTTGAAGTGGT GGGCGGGCCG 450
CAAGCTTTGC ATGCTTATAT CCAGTCTTTA GCGGTTAAAG AAGCTGCCGT 500
GGTAGCAAAT GAAGCGCAA TGCATGCGGA TGATCAGGTG CAATATCAAA 550
45 ACTGGACGTC GATGAAAGCC GCAGCACAAG TTCTGCAAAA GTTTGAACAG 600
AAAAAGCAGT TGTCTGAAAC CTCTCAGGCC TTGTTATGGA AATGGATGGT 650
TGAAACCACC ACAGGACCAC AGCGGTTAAA AGGCTTGTTA CCTGCTGGTA 700
CTATAGTGGC GCATAAAACC GGTACTTCGG GCGTCAGAGC AGGAAAAACT 750
GCGGCGACTA ATGATGCGGG CGTCATTATG TTGCCTGATG GACGGCCTTT 800
50 ATTGGTGGCG GTATTTGTCA AGGATTCGGC TGAATCAGAA CGAACCAATG 850
AAGCTATTAT TGCGCAGGTT GCGCAAGCGG CTTATCAGTT TGAGCTGAAA 900
AAACTCTCTG CAGTGAGTCC GGATTGA 927

2) INFORMATION FOR SEQ ID NO: 1446

- 5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 27 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

10 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1446

GGCCTGYGAT TTGTTATTTG AACTGGT 27

15

2) INFORMATION FOR SEQ ID NO: 1447

- 20 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

25 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1447

CGCTSTGGTC CTGTGGTGGT TTC 23

30

2) INFORMATION FOR SEQ ID NO: 1448

- 35 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

40

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1448

45 GATCAGGTGC ARTATCAAAA CTGGAC 26

2) INFORMATION FOR SEQ ID NO: 1449

- 50 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 bases
(B) TYPE: Nucleic acid

- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1449

AGCWGGTAAC AAYCCTTTTA ACCGCT

26

10

2) INFORMATION FOR SEQ ID NO: 1450

(i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 26 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1450

ACCACTGGGA ATACACTTGT AATGGC

26

25

2) INFORMATION FOR SEQ ID NO: 1451

(i) SEQUENCE CHARACTERISTICS:

30

- (A) LENGTH: 26 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1451

40

ATCTACCTGG TCAATCATTG CTCGT

26

2) INFORMATION FOR SEQ ID NO: 1452

45

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 486 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus epidermidis*
(B) STRAIN: BM10393
(C) ACCESSION NUMBER: AF045472

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1452

	ATGACATTAT	CAATAATTGT	CGCTCACGAT	AAACAAAGAG	TCATTGGGTA	50
	CCAAAATCAA	TTACCTTGGC	ACTTACCAA	TGATTTAAAG	CATATTAAAC	100
10	AACTGACCAC	TGGGAATACA	CTTGTAATGG	CACGGAAAAC	TTTAAATTCT	150
	ATAGGGAAGC	CATTGCCAAA	TAGACGTAAC	GTCGTACTCA	CTAACCAAGC	200
	TTCATTTTAC	CATGAAGGGG	TAGATGTTAT	AAACTCTCTT	GATGAAATTA	250
	AAGAGTTATC	TGGTCATGTT	TTTATATTTG	GAGGACAAAC	GTTATACGAA	300
	GCAATGATTG	ACCAGGTAGA	TGATATGTAT	ATCACAGTAA	TAGATGGAAA	350
15	GTTTCAAGGA	GACACATTCT	TTCCACCATA	CACATTCGAA	AACTGGGAAG	400
	TCGAATCTTC	AGTAGAAGGT	CAACTAGATG	AAAAAAATAC	TATACCGCAT	450
	ACATTCTTAC	ATTTAGTGCG	TAGAAAAGGG	AAATAG		486

20

2) INFORMATION FOR SEQ ID NO: 1453

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1453

ATCGAAGAAT GGAGTTATCG GRAATG 26

35

2) INFORMATION FOR SEQ ID NO: 1454

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1454

CCTAAAAYTR CTGGGGATTT CWGGA 25

50

2) INFORMATION FOR SEQ ID NO: 1455

764

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 24 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1455

CAGGTGGTGG GGAGATATAC AAAA

24

15

2) INFORMATION FOR SEQ ID NO: 1456

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 26 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1456

TATGTTAGAS RCGAAGTCTT GGKTAA

26

30

2) INFORMATION FOR SEQ ID NO: 1457

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 22 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

40 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1457

CAAAGGTGAA CAGCTCCTGT TT

22

45

2) INFORMATION FOR SEQ ID NO: 1458

(i) SEQUENCE CHARACTERISTICS:

- 50 (A) LENGTH: 27 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1458

TCCGTTATTT TCTTTAGGTT GGTAA

27

10

2) INFORMATION FOR SEQ ID NO: 1459

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1459

AAGGTGAACA GCTCCTGTTT

20

25

2) INFORMATION FOR SEQ ID NO: 1460

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 22 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

35 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1460

GATCACTACG TTCTCATTGT CA

22

40

2) INFORMATION FOR SEQ ID NO: 1461

(i) SEQUENCE CHARACTERISTICS:

- 45 (A) LENGTH: 474 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Escherichia coli*

(C) ACCESSION NUMBER: AJ238350

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1461

5
GTGAAACTAT CACTAATGGT AGCTATATCG AAGAATGGAG TTATCGGGAA 50
TGGCCCTGAT ATTCCATGGA GTGCCAAAGG TGAACAGCTC CTGTTTAAAG 100
CTATTACCTA TAACCAATGG CTGTTGGTTG GACGCAAGAC TTTTGAATCA 150
ATGGGAGCAT TACCCAACCG AAAGTATGCG GTCGTAACAC GTCCAAGTTT 200
10 TACATCTGAC AATGAGAACG TAGTGATCTT TCCATCAATT AAAGATGCTT 250
TAACCAACCT AAAGAAAATA ACGGATCATG TCATTGTTTC AGGTGGTGGG 300
GAGATATACA AAAGCCTGAT CGATCAAGTA GATACACTAC ATATATCTAC 350
AATAGACATC GAGCCGGAAG GTGATGTTTA CTTTCCTGAA ATCCCCAGCA 400
ATTTTAGGCC AGTTTTTACC CAAGACTTCG CCTCTAACAT AAATTATAGT 450
15 TACCAAATCT GGCAAAAGGG TTAA 474

2) INFORMATION FOR SEQ ID NO: 1462

20

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

25

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1462

30

GCACTCCCYA ATAGGAAATA CGC

23

35 2) INFORMATION FOR SEQ ID NO: 1463

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 bases

(B) TYPE: Nucleic acid

40

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1463

AGTGTTGCTC AAAACAACCT TCG

23

50

2) INFORMATION FOR SEQ ID NO: 1464

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

5

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1464

10 ACGTTYGAAT CTATGGGMGC ACT

23

2) INFORMATION FOR SEQ ID NO: 1465

15

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1465

25

GTCGATAAGT GGAGCGTAGA GGC

23

30 2) INFORMATION FOR SEQ ID NO: 1466

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1466

40

AAGCATTGAC CTACAATCAG TGT

23

45

2) INFORMATION FOR SEQ ID NO: 1467

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1467

5 AATACAATA CATTGTCATC ATTTGAT

27

2) INFORMATION FOR SEQ ID NO: 1468

10

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 26 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

15

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1468

20

CGTTACCCGC TCAGGTTGGA CATCAA

26

25 2) INFORMATION FOR SEQ ID NO: 1469

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 bases

(B) TYPE: Nucleic acid

30

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1469

CATCCCCCTC TGGCTCGATG TCG

23

40

2) INFORMATION FOR SEQ ID NO: 1470

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 474 bases

45

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

50

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Escherichia coli*

(C) ACCESSION NUMBER: Z50804

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1470

```

5   TTGAAAGTAT CATTGATAGC TGC GAAACGA AAAAACGGCG TGATTGGTTG      50
    CGGTCCAGAC ATACCGTGGT CCGCGAAAGG GGAGCAGCTA CTTTTTAAAG      100
    CATTGACCTA CAATCAGTGT CTTCTGGTGG GTCGCAAGAC GTTTGAATCT      150
    ATGGGCGCAC TCCCCAATAG GAAATACGCG GTCGTTACCC GCTCAGGTTG      200
    GACATCAAAT GATGACAATG TAGTTGTATT TCAGTCAATC GAAGAGGCCA      250
    TGGACAGGCT AGCTGAATTC ACCGGTCACG TTATAGTGTC TGGTGGCGGA      300
10  GAAATTTACC GAGAAACATT ACCCATGGCC TCTACGCTCC ACTTATCGAC      350
    GATCGACATC GAGCCAGAGG GGGATGTTTT CTTCCCGAGT ATTCCAAATA      400
    CCTTCGAAGT TGTTTTTGAG CAACACTTTA CTTCAAACAT TAACTATTGC      450
    TATCAAATTT GGAAAAAGGG TTAA                                     474

```

15

2) INFORMATION FOR SEQ ID NO: 1471

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20  (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 26 bases
      (B) TYPE: Nucleic acid
      (C) STRANDEDNESS: Single
      (D) TOPOLOGY: Linear

```

25 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1471

```

30  GATAATGACA ACGTAATAGT ATTCCC                                     26

```

2) INFORMATION FOR SEQ ID NO: 1472

```

35  (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 23 bases
      (B) TYPE: Nucleic acid
      (C) STRANDEDNESS: Single
      (D) TOPOLOGY: Linear

```

40

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1472

```

45  GCTCAATATC AATCGTCGAT ATA                                     23

```

2) INFORMATION FOR SEQ ID NO: 1473

```

50  (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 26 bases
      (B) TYPE: Nucleic acid

```

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1473

TTAAAGCCTT GACGTACAAC CAGTGG

26

10

2) INFORMATION FOR SEQ ID NO: 1474

(i) SEQUENCE CHARACTERISTICS:

15

(A) LENGTH: 26 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1474

TGGGCAATGT TTCTCTGTAA ATCTCC

26

25

2) INFORMATION FOR SEQ ID NO: 1475

(i) SEQUENCE CHARACTERISTICS:

30

(A) LENGTH: 474 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Escherichia coli*

40

(C) ACCESSION NUMBER: X12868

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1475

	GTGAAAGTAT	CATTAATGGC	TGCAAAAGCG	AAAAACGGAG	TGATTGGTTG	50
45	CGGTCCACAC	ATACCCTGGT	CCGCGAAAGG	AGAGCAGCTA	CTCTTTAAAG	100
	CCTTGACGTA	CAACCAGTGG	CTTTTGGTGG	GCCGCAAGAC	GTTCGAATCT	150
	ATGGGAGCAC	TCCCTAATAG	GAAATACGCG	GTCGTTACTC	GCTCAGCCTG	200
	GACGGCCGAT	AATGACAACG	TAATAGTATT	CCCGTCGATC	GAAGAGGCCA	250
	TGTACGGGCT	GGCTGAACTC	ACCGATCACG	TTATAGTGTC	TGGTGGCGGG	300
50	GAGATTTACA	GAGAAACATT	GCCCATGGCC	TCTACGCTCC	ATATATCGAC	350
	GATTGATATT	GAGCCGGAAG	GAGATGTTTT	CTTTCCGAAT	ATTCCCAATA	400
	CCTTCGAAGT	TGTTTTTGAG	CAACACTTTA	GCTCAAACAT	TAATATTGTC	450
	TATCAAATTT	GGCAAAAGGG	TTAA			474

2) INFORMATION FOR SEQ ID NO: 1476

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1476

GGCGAGCAGC TCCTATTCAA AG

22

2) INFORMATION FOR SEQ ID NO: 1477

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1477

TAGGTAAGCT AATGCCGATT CAACA

25

2) INFORMATION FOR SEQ ID NO: 1478

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1478

GAGAATGGAG TAATTGGCTC TGGATT

26

2) INFORMATION FOR SEQ ID NO: 1479

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 bases
- (B) TYPE: Nucleic acid

- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1479

GCGAAATACA CAACATCAGG GTCAT

25

10

2) INFORMATION FOR SEQ ID NO: 1480

(i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 474 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Proteus mirabilis*
- (B) STRAIN: J120
- (C) ACCESSION NUMBER: Z86002

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1480

ATGAAAATAT	CTCTTATGGC	AGCTGTTTCC	GAGAATGGAG	TAATTGGCTC	50
30	TGGATTGGAT	ATACCTTGGC	ATGTACAAGG	CGAGCAGCTC	100
	CCATGACTTA	CAATCAATGG	CTTCTAGTTG	GTCGTAAAAC	150
	ATGGGTAAAC	TTCCGAATAG	AAAATATGCA	GTGGTTACTC	200
	TATCTCGAAT	GACCCTGATG	TTGTGTATTT	CGCAAGTGTT	250
	TAGCTTACCT	AAACAATGCG	ACAGCACATA	TCTTTGTTTC	300
35	GAAATATATA	AAGCTTTAAT	CGATCAAGCA	GATGTTATCC	350
	GATTCACAAG	CATATCTCTG	GCGATGTGTT	TTTTCCCTCCA	400
	GCTTCAAGCA	AACATTTGAG	CAAAGTTTCA	GTTCAAATAT	450
	TACCAAATTT	GGGCAAAGGG	CTAA		474

40

2) INFORMATION FOR SEQ ID NO: 1481

(i) SEQUENCE CHARACTERISTICS:

45

- (A) LENGTH: 24 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1481

RTTACAGATC ATKTATATGT CTCT

24

5 2) INFORMATION FOR SEQ ID NO: 1482

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 bases
- (B) TYPE: Nucleic acid
- 10 (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1482

TAATTTATAT TAGACAWAAA AAACGTG

26

20

2) INFORMATION FOR SEQ ID NO: 1483

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- 25 (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1483

CARYGTCAGA AAATGGCGTA ATC

23

35

2) INFORMATION FOR SEQ ID NO: 1484

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 26 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

45 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1484

TKCAAAGCRW TTTCTATTGA AGGAAA

26

50

2) INFORMATION FOR SEQ ID NO: 1485

- 5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1485

AAAATGGCGT AATCGGTAAT GGC

23

15

2) INFORMATION FOR SEQ ID NO: 1486

- 20 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1486

CATTGAGCT TGAAATTCCT TTCCTC

26

30

2) INFORMATION FOR SEQ ID NO: 1487

- 35 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

40 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1487

AATCGAAAAT ATGCAGTAGT GTCGAG

26

45

2) INFORMATION FOR SEQ ID NO: 1488

- 50 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1488

AGACTATTGT AGATTGACC GCCA

24

10

2) INFORMATION FOR SEQ ID NO: 1489

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 474 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

20

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Escherichia coli*
(B) STRAIN: VA292
(C) ACCESSION NUMBER: U31119

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1489

30 TTGAAAATTT CATTGATTTT TGCAACGTCA GAAAATGGCG TAATCGGTAA 50
TGGCCCTGAT ATCCCATGGT CAGCAAAAGG TGAGCAGTTA CTCTTTAAAG 100
CGCTCACATA TAATCAGTGG CTCCTTGTTG GAAGGAAAAC ATTTGACTCT 150
ATGGGTGTTT TTCCAAATCG AAAATATGCA GTAGTGTCGA GGAAAGGAAT 200
TTCAAGCTCA AATGAAAATG TATTAGTCTT TCCTTCAATA GAAATCGCTT 250
TGCAAGAACT ATCGAAAATT ACAGATCATT TATATGTCTC TGGTGGCGGT 300
CAAATCTACA ATAGTCTTAT TGAAAAAGCA GATATAATTC ATTTGTCTAC 350
35 TGTTACGTT GAGGTTGAAG GTGATATCAA TTTTCCTAAA ATTCCAGAGA 400
ATTTCAATTT GGTTTTGTAG CAGTTTTTTT TGTCTAATAT AAATTACACA 450
TATCAGATTT GGAAAAAAGG CTAA 474

40

2) INFORMATION FOR SEQ ID NO: 1490

(i) SEQUENCE CHARACTERISTICS:

- 45 (A) LENGTH: 25 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1490

GACCTATGAG AGCTTGCCCG TCAAA

25

2) INFORMATION FOR SEQ ID NO: 1491

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 26 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1491

TCGCCTTCGT ACAGTCGCTT AACAAA

26

15

2) INFORMATION FOR SEQ ID NO: 1492

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 26 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

25 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1492

CATTTTAGCT GCCACCGCCA ATGGTT

26

30

2) INFORMATION FOR SEQ ID NO: 1493

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 25 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

40

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1493

45 GCGTCGCTGA CGTTGTTTAC GAAGA

25

50

2) INFORMATION FOR SEQ ID NO: 1494

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 510 bases
(B) TYPE: Nucleic acid

- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

5

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Escherichia coli*
- (B) STRAIN: BL26A
- (C) ACCESSION NUMBER: U10186

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1494

ATGATCGAGC TTCATGCCAT TTTAGCTGCC ACCGCCAATG GTTGCATTGG 50
GAAGGACAAC GCACTTCCCT GGCCACCACT AAAAGGCGAT CTGGCCAGAT 100
15 TCAAAAAATT GACCATGGGG AAGGTGGTCA TTATGGGGCG CAAGACCTAT 150
GAGAGCTTGC CCGTCAAATT AGAAGGTCGC ACCTGCATCG TTATGACGCG 200
CCAAGCGCTG GAGCTTCCGG GTGTTCTGTA CGCTAACGGC GCTATCTTCG 250
TGAACAACGT CAGCGACGCC ATGCGGTTTC CTCAAGAAGA GAGCGTGGGC 300
GATGTGGCCT ACGTCATTGG TGGCGCTGAG ATATTCAAGC GACTTGCCTT 350
20 GATGATCACG CAGATTGAAT TGACCTTTGT TAAGCGACTG TACGAAGGCG 400
ACACCTACGT TGATCTGGCC GAAATGGTCA AAGACTACGA GCAGAATGGC 450
ATGGAAGAAC ATGACCTTCA CACTTACTTC ACTTACCGTA AAAAGGAGCT 500
TACAGAATGA 510

25

2) INFORMATION FOR SEQ ID NO: 1495

(i) SEQUENCE CHARACTERISTICS:

30

- (A) LENGTH: 24 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1495

40

TCTCTAAACA TGATTGTCGC TGTC 24

2) INFORMATION FOR SEQ ID NO: 1496

45

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1496

CAGTGAGGCA AAAGTTTTTC TACC

24

5

2) INFORMATION FOR SEQ ID NO: 1497

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 25 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1497

CGGACGACTT CATGTGGTAG TCAGT

25

20

2) INFORMATION FOR SEQ ID NO: 1498

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 26 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1498

TTTGTTTTCA GTAATGGTCG GGACCT

26

35

2) INFORMATION FOR SEQ ID NO: 1499

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 534 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

45

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 50 (A) ORGANISM: *Escherichia coli*
(C) ACCESSION NUMBER: X57730

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1499

	ATGGCTTCTC	TAAACATGAT	TGTCGCTGTC	AATAAGACAG	GAGGTATCGG	50
	ATTTGAAAAT	CAGATTCCGT	GGCATGAACC	AGAAGATTTA	AAACACTTCA	100
	AAGCTGTTAC	AATGAACTCA	GTTTTGATTA	TGGGTAGAAA	AACTTTTGCC	150
	TCATGCTCCTA	AAGTGCTGCC	CGGACGACTT	CATGTGGTAG	TCAGTAAAC	200
5	AGTACCACCC	ACCCAGAACA	CTGATCAAGT	TGTGTATGTA	AGTACATACC	250
	AGATCGCAGT	AAGAACTGCA	AGCTTGTTGG	TTGACAAACC	AGAGTATTCT	300
	CAAATTTTGT	TAATTGGTGG	GAAGAGTGCG	TACGAGAACT	TAGCTGCCTA	350
	CGTGGACAAA	CTCTACTTAA	CTAGAGTACA	GCTCAACACA	CAACAAGACA	400
	CTGAACTGGA	TTTATCCCTA	TTCAAGTCAT	GGAAACTCGT	ATCTGAGGTC	450
10	CCGACCATTA	CTGAAAACAA	AACAAAACCT	ATTTTCCAAA	TTTGGATTAA	500
	CCCTAACCT	ATTAGTGAGG	AACCCACATG	TTAG		534

15 2) INFORMATION FOR SEQ ID NO: 1500

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 24 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1500

ATCGGGTTAT TGGCAATGGT CCTA

24

30

2) INFORMATION FOR SEQ ID NO: 1501

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 25 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1501

GCGGTAGTTA GCTTGCGTG AGATT

25

45

2) INFORMATION FOR SEQ ID NO: 1502

(i) SEQUENCE CHARACTERISTICS:

- 50 (A) LENGTH: 22 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1502

5

GCGGGCGGAG CTGAGATATA CA

22

10 2) INFORMATION FOR SEQ ID NO: 1503

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 26 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1503

AACGGAGTGG GTGTACGGAA TTACAG

26

25

2) INFORMATION FOR SEQ ID NO: 1504

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 498 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

35

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Escherichia coli*
(B) STRAIN: TKS84
(C) ACCESSION NUMBER: Z21672

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1504

	ATGAACTCGG AATCAGTACG CATTATCTC GTTGCTGCGA TGGGAGCCAA	50
	TCGGGTATT GGCAATGGTC CTAATATCCC CTGGAAAATT CCGGGTGAGC	100
45	AGAAGATTTT TCGCAGACTC ACTGAGGGAA AAGTCGTTGT CATGGGGCGA	150
	AAGACCTTTG AGTCTATCGG CAAGCCTCTA CCGAACCGTC ACACATTGGT	200
	AATCTCACGC CAAGCTAACT ACCGCGCCAC TGGCTGCGTA GTTGTTTCAA	250
	CGCTGTCGCA CGCTATCGCT TTGGCATCCG AACTCGGCAA TGAACCTAC	300
	GTCGCGGGCG GAGCTGAGAT ATACACTCTG GCACTACCTC ACGCCCACGG	350
50	CGTGTTTCTA TCTGAGGTAC ATCAAACCTT CGAGGGTGAC GCCTTCTTCC	400
	CAATGCTCAA CGAAACAGAA TTCGAGCTTG TCTCAACCGA AACCATTCAA	450
	GCTGTAATTC CGTACACCCA CTCGGTTTAT GCGCGTCGAA ACGGCTAA	498

2) INFORMATION FOR SEQ ID NO: 1505

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 24 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1505

ATTTTTCGCA GGCTCACCGA GAGC

24

15

2) INFORMATION FOR SEQ ID NO: 1506

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 27 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

25 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1506

CGGATGAGAC AACCTCGAAT TCTGCTG

27

30

2) INFORMATION FOR SEQ ID NO: 1507

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 498 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

40

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 45 (A) ORGANISM: *Escherichia coli*
 (B) STRAIN: RA33.2
 (C) ACCESSION NUMBER: Z50802

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1507

50 ATGAACCCGG AATCGGTCCG CATTTATCTG GTCGCTGCCA TGGGTGCCAA 50
 TCGGGTTATT GGCAATGGTC CCGATATCCC CTGGAAAATC CCAGGTGAGC 100
 AGAAGATTTT TCGCAGGCTC ACCGAGAGCA AAGTGGTCGT TATGGGCCGC 150
 AAGACATTTG AGTCCATAGG CAAGCCCTTA CCAAACCGCC ACACAGTGGT 200

	GCTCTCGCGC	CAAGCTGGTT	ATAGCGCTCC	TGGTTGTGCA	GTTGTTTCAA	250
	CGCTGTCACA	CGTATCGCCA	TCGACAGCCG	AACACGGCAA	AGAACTCTAC	300
	GTAGCGCGCG	GAGCCGAGGT	ATATGCGCTG	GCGCTACCGC	ATGCCAACGG	350
	CGTCTTTCTA	TCTGAGGTAC	ATCAAACCTT	TGAGGGTGAC	GCCTTCTTCC	400
5	CAGTGCTTAA	CGCAGCAGAA	TTGAGGTTG	TCTCATCCGA	AACCATTCAA	450
	GGCACAATCA	CGTACACGCA	CTCCGTCTAT	GCGCGTCGTA	ACGGCTAA	498

10 2) INFORMATION FOR SEQ ID NO: 1508

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 27 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1508

AGAATGTATT GGTATTTCCA TCTATCG

27

25

2) INFORMATION FOR SEQ ID NO: 1509

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 26 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1509

CAATGTCGAT TGTTGAAATA TGTAAA

26

40

2) INFORMATION FOR SEQ ID NO: 1510

(i) SEQUENCE CHARACTERISTICS:

- 45 (A) LENGTH: 22 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

50 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1510

TGGAGTGCCA AAGGGGAACA AT

5 2) INFORMATION FOR SEQ ID NO: 1511

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 bases
 (B) TYPE: Nucleic acid
 10 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1511

CAGACACAAT CACATGATCC GTTATCG

27

20

2) INFORMATION FOR SEQ ID NO: 1512

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 474 bases
 25 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

30

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Escherichia coli*
 (B) STRAIN: UI14
 (C) ACCESSION NUMBER: Z83331

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1512

	GTGAAACTAT CACTAATGGC AGCAATTTTCG AAGAATGGAG TTATCGGAAA	50
	TGGCCCAGAT ATTCCATGGA GTGCCAAAGG GGAACAATTA CTCTTCAAAG	100
40	CGATTACCTA TAATCAGTGG CTTTGTGGTAG GCCGAAAGAC TTTTCGAGTCA	150
	ATGGGGGCTT TACCCAACCG AAAATATGCC GTTGTAAGTC GTTCAAGCTT	200
	CACTTCCAGT GATGAGAATG TATTGGTATT TCCATCTATC GATGAAGCGC	250
	TAAATCATCT GAAGACGATA ACGGATCATG TGATTGTGTC TGGTGGTGGT	300
	GAAATATACA AAAGCCTGAT CGATAAAGTT GATACTTTAC ATATTTCAAC	350
45	AATCGACATT GAGCCAGAAG GTGATGTCTA TTTTCCAGAA ATCCCCAGTA	400
	GTTTTAGGCC AGTTTTTAGC CAAGACTTCG TGTCTAACAT AAATTATAGT	450
	TACCAAATCT GGCAAAAGGG TTAA	474

50

2) INFORMATION FOR SEQ ID NO: 1513

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

5

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1513

10 TTCAAGCTCA AATGAAAACG TCC

23

2) INFORMATION FOR SEQ ID NO: 1514

15

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1514

25

GAAATTCTCA GGCATTATAG GGAAT

25

30 2) INFORMATION FOR SEQ ID NO: 1515

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: DNA

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1515

GTGGTCAGTA AAAGGTGAGC AAC

23

45

2) INFORMATION FOR SEQ ID NO: 1516

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

50

PAGE 786

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CTATGTCTCA	AGGCCGTGCA	ACATACTCTA	TGGAATTTGC	TAAATATGCT	50
GAAACTCCAC	GTAACGTGGC	TGAAGGCATC	ATTTCTAAAT	TTCAGTCTGG	100
CGGTAAAAAA	GGTGACGACG	AGTAA			125

5

2) INFORMATION FOR SEQ ID NO: 1519

- 10 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 93 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Double
 - (D) TOPOLOGY: Linear
- 15 (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Acinetobacter lwoffii*
 - 20 (B) STRAIN: CDCF 3697
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1519

TCTTTCGATT	ACTATAAGCC	CAAAC TAATT	CATAGTTAAA	AACCAAGTGC	50
25 TCATGCAGTG	ATCCTGCATG	AGTAGTTTAA	AAAGGAAGAT	CTC	93

2) INFORMATION FOR SEQ ID NO: 1520

- 30 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1106 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Double
 - 35 (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
- 40 (A) ORGANISM: *Acinetobacter lwoffii*
 - (B) STRAIN: CDCF 3697
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1520

45 ATGGCTAAGG	CTAAGTTTGA	ACGTAATAAG	CCACACGTTA	ACGTGGGCAC	50
AATCGGTCAC	GTTGACCATG	GTAACAAC	TTTAACAGCT	GCAATTGCAA	100
CTGTATGTGC	GAAGAAATTC	GGTGGCGAAG	CGAAAGACTA	CGCTGCAATT	150
GACTCTGCAC	CAGAAGAAAA	AGCACGTGGT	ATTACAATTA	ATACTTCACA	200
CGTAGAATAC	GATTCTCCAA	CTCGTCACTA	CGCACACGTA	GACTGCCCCG	250
50 GCCACGCCGA	TTATGTTAAA	AACATGATTA	CTGGTGCTGC	TCAGATGGAC	300
GGCGCGATCC	TTGTATGTGC	TGCGACTGAT	GGTCCAATGC	CACAGACTCG	350
TGAACACATC	CTTCTTTCTC	GTCAGGTTGG	TGTACCTTAC	ATTCTTGTAT	400
TCCTTAACAA	GTGTGACCTT	GTTGATGATG	AAGAACTTCT	TGAGCTAGTG	450

	GAAATGGAAG	TTCGTGAACT	TCTTTCTACT	TATGACTTCC	CAGGTGATGA	500
	CACTCCAGTT	ATCCGTGGTT	CAGCTCTTCT	TGCACTTAAC	GGTGACGCTG	550
	GTCAGTATGG	CGAAGAAGCA	GTTGTTGCGC	TTGTTGACGC	ACTTGACACT	600
	TACATTCCAG	AGCCAGTACG	TGCAATCGAC	CAAGCATTCT	TAATGCCAAT	650
5	CGAAGACGTA	TTCTCTATTT	CTGGTCGTGG	TACAGTAGTA	ACTGGCCGTG	700
	TAGAACTGG	TATTGTGAAA	GTAGGCGAAT	CAGTTGAAAT	CGTTGGTATC	750
	CGTGATACTC	AAGTAACTAC	AGTTACTGGC	GTAGAAATGT	TCCGTAAATT	800
	GCTTGACGAA	GGTCGTGCGG	GCGAGAACTG	TGGTGTTCTT	CTACGTGGTA	850
	CTAAGCGTGA	AGACGTACAA	CGTGGTCAAG	TACTTGCTAA	ACCAGGTGCA	900
10	ATCAAGCCAC	ACACTAAATT	CGATGCAGAA	GTATACGTAC	TTTCTAAAGA	950
	AGAAGGTGGT	CGTCACACTC	CATTCTTTAA	CGGTTACCGT	CCACAGTTCT	1000
	ACTTCCGTAC	AACTGACGTA	ACTGGCGCGA	TCAAATTACA	AGATGGCGTT	1050
	GAAATGGTTA	TGCCTGGTGA	CAACGTAGAA	ATGTCAGTAG	AATTAATCCA	1100
	CCCAAT					1106

15

2) INFORMATION FOR SEQ ID NO: 1521

20 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 100 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

25

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Haemophilus influenzae*
- (B) STRAIN: ATCC 9006

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1521

	ACAAACTCAA	GGTCGTGCAT	CTTACTCAAT	GGAACCGTTA	AAATATGCTG	50
35	AAGCTCCAAC	AAGTGTTCG	GCTGCAGTAA	TTGAAGCGCG	TAAAAAATAA	100

2) INFORMATION FOR SEQ ID NO: 1522

40

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 64 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

45

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Haemophilus influenzae*
- (B) STRAIN: ATCC 9006

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1522

TTTTTGTAAG CCAGCGGTGT AAAATATGAT TGTTTTATAC CGCACTTCTT 50
 AGGAAACATT AGAA 64

5

2) INFORMATION FOR SEQ ID NO: 1523

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 1098 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

15 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Haemophilus influenzae*
 (B) STRAIN: ATCC 9006

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1523

ATGTCTAAAG AAAAATTTGA ACGTACAAAA CCGCACGTAA ACGTGGGTAC 50
 AATCGGCCAC GTTGACCACG GTAAAACAAC TTTAACAGCA GCAATTACAA 100
 25 CCGTATTAGC AAAACACTAC GGTGGTGCAG CGCGTGCATT TGACCAAATC 150
 GATAACGCGC CAGAAGAAAA AGCGCGTGGT ATTACCATCA ACACTTCACA 200
 TGTTGAATAC GATACACCAA CTCGCCACTA TGCACACGTA GACTGTCCAG 250
 GACACGCCGA CTATGTTAAA AACATGATTA CCGGTGCGGC GCAAATGGAT 300
 GGTGCTATTT TAGTAGTAGC AGCAACAGAT GGTCTTATGC CACAAACTCG 350
 30 TGAACATATC TTATTAGGTC GCCAAGTAGG TGTTCCATAC ATCATCGTAT 400
 TCTTAAACAA ATGCGACATG GTAGATGATG AAGAGTTATT AGAATTAGTA 450
 GAAATGGAAG TGCCTGAACT TCTATCTCAA TATGACTTCC CAGGTGACGA 500
 TACACCAATC GTACGTGGTT CAGCATTACA AGCATTGAAC GGCCTAGCAG 550
 AATGGGAAGA AAAAATCCTT GAATTAGCTG GTCACCTAGA TACTTACATC 600
 35 CCAGAACCAG AACGTGCGAT TGACCAACCG TTCCTTCTTC CAATTGAAGA 650
 CGTATTCTCA ATTTGAGGTC GTGGTACAGT AGTAACTGGT CGTGTAGAAC 700
 GTGGTATCAT CCGTACTGGT GATGAAGTAG AAATCGTCGG TATCAAAGAT 750
 ACAGCGAAAA CTACTGTAAC AGGTGTTGAA ATGTTCCGTA AATTACTTGA 800
 CGAAGGTCGT GCAGGTGAAA ACATCGGTGC ATTATTACGT GGTACCAAAC 850
 40 GTGAAGAAAT CGAACGTGGT CAAGTATTAG CGAAACCAGG TTCAATCACA 900
 CCACACACTG ATTTTGAATC AGAAGTATAC GTATTATCAA AAGATGAAGG 950
 TGGTCGTCAT ACTCCATTCT TCAAAGGTTA CCGTCCACAA TTCTATTTCC 1000
 GTACAACAGA CGTAACTGGT ACAATTGAAT TACCAGAAGG CGTGGAATG 1050
 GTAATGCCAG GCGATAACAT CAAGATGACA GTAAGCTTAA TCCACCCA 1098
 45

2) INFORMATION FOR SEQ ID NO: 1524

50 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 77 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

5 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Proteus mirabilis*

(B) STRAIN: ATCC 25933

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1524

10- CAATGGAGTT CTTGAAGTAC AACGAAGCGC CTAGCAACGT CGCTCAGGCT 50
ATTATCGAAG CTCGTAAAGC GAAATAA 77

15

2) INFORMATION FOR SEQ ID NO: 1525

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 67 bases

20 (B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

25

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Proteus mirabilis*

(B) STRAIN: ATCC 25933

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1525

GATCCTTTTCG AGTTCAATTT AGTTTACGCT CCCTCTGTGA GAGGGAGCGA 50
TATTAAGGAA TATAGTC 67

35

2) INFORMATION FOR SEQ ID NO: 1526

(i) SEQUENCE CHARACTERISTICS:

40 (A) LENGTH: 1112 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

45 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Proteus mirabilis*

(B) STRAIN: ATCC 25933

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1526

GTGTCTAAAG AAAAATTTGA ACGTTCAAAA CCGCACGTTA ACGTTGGTAC 50

	TATCGGCCAC	GTTGACCACG	GTAAAACAAC	TCTGACTGCT	GCAATCACTA	100
	CAGTTTTAGC	TAAAACTTAC	GGTGGTGCTG	CTCGTGCATT	CGACCAAATC	150
	GATAATGCAC	CAGAAGAAAA	AGCGCGTGGT	ATCACCATCT	CTACTTCACA	200
	CGTAGAATAC	GATACTCCAA	CTCGCCACTA	CGCACACGTA	GACTGCCCAG	250
5	GTCACGCCGA	CTATGTTAAA	AACATGATCA	CTGGTGCTGC	GCAAATGGAC	300
	GGCGCTATTC	TGGTAGTAGC	AGCAACTGAT	GGTCCAATGC	CACAACTCG	350
	TGAGCACATC	CTGTTAGGTC	GTCAGGTTGG	TGTTCTTAC	ATCATCGTAT	400
	TCCTGAACAA	ATGTGACATG	GTAGATGATG	AAGAGCTGTT	AGAATTAGTT	450
	GAAATGGAAG	TTCGTGAACT	TCTGTCTCAA	TACGATTTCC	CAGGTGATGA	500
10	CACTCCAGTA	ATCCGTGGTT	CAGCGCTGAA	AGCACTGGAA	GGCGAAGCAG	550
	AGTGGGAAGC	AAAAATTGTT	GAATTAGCAG	AAGCACTGGA	TTCTTATATC	600
	CCAGAGCCAG	AGCGTGCAAT	TGACAAACCA	TTCTGTGTTAC	CAATCGAAGA	650
	TGTATTCTCA	ATCTCAGGCC	GTGGTACAGT	AGTTACTGGT	CGTGTAGAGC	700
	GTGGTATCAT	CAAAGTAGGT	GATGAAGTTG	AGATTGTTGG	TATCAAAGAA	750
15	ACCACCAAAA	CAACTTGTA	TGGCGTTGAA	ATGTTCCGTA	AATTACTTGA	800
	CGAAGGTCGT	GCAGGTGAGA	ACGTAGGTGT	TCTGCTGCGT	GGTACAAAAC	850
	GTGAAGAAAT	CGAACGTGGA	CAAGTACTGG	CAAAACCAGG	CTCAATCAAC	900
	CCACACAACA	AATTTGAATC	AGAAGTTTAT	ATTCTGAGCA	AAGATGAAGG	950
	TGGTCGTCAC	ACACCATTCT	TCAAAGGCTA	CCGTCCACAG	TTCTACTTCC	1000
20	GTACAACTGA	CGTAACTGGT	ACTATCGAAT	TACCAGAAGG	CGTAGAAATG	1050
	GTAATGCCAG	GCGACAACGT	GAACATGATC	GTTGAACTGA	TCCACCCAAT	1100
	CGCAATGGAC	GA				1112

25

2) INFORMATION FOR SEQ ID NO: 1527

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 800 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

35

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Campylobacter curvus*
 (B) STRAIN: ATCC 35224

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1527

	ATCAACGAAG	CTATCGAGGT	TTATTTTGAG	GTTGAGGGCA	AGAAAAATAG	50
	ATTGATCCTG	GAGGTCGCGG	CTCACTTGGG	TGATAACCGC	GTCAGAACGA	100
	TCGCTATGGA	TATGAGTGAG	GGGCTTACTC	GCGGGCTTGA	AGCTACCGCT	150
45	CTTGGTGCGC	CTATTAGTGT	GCCGTTGGC	GAGAAGGTTT	TGGGAAGAAT	200
	TTTTAACGTC	GTCGGCGATC	TCATCGACGA	GGGCGAGGGC	GTAAATTTTG	250
	ATAAACATTG	GTCTATCCAC	CGCGATCCGC	CACCATTTGA	AGAACAAAGC	300
	ACGAAAAGTG	AAATTTTGA	AACCGGTATA	AAGGTTGTGG	ATCTTCTTGC	350
	GCCTTACGCA	AAGGGCGGTA	AGGTCGGACT	ATTTGGCGGT	GCAGGTGTGC	400
50	GTAAACGGT	CATCATCATG	GAGCTCATCC	ACAATGTCGC	CTTCAAACAC	450
	AGCGGATACT	CTGTATTTGC	AGGTGTTGGC	GAGAGGACGC	GCGAAGGAAA	500
	CGACCTTTAT	CACGAGATGA	AAGAAAGTAA	CGTTTTGGAT	AAAGTCGCCT	550
	TGTGCTACGG	ACAGATGAAC	GAGCCGCCAG	GGGCGAGAAA	TCGTATCGCA	600

CTGACTGGTC	TAACGATGGC	TGAGTATTTTC	CGCGATGAGA	TGGGACTTGA	650
TGTGCTTATG	TTTATCGACA	ACATCTTCCG	CTTCTCTCAA	TCTGGTGCAG	700
AGATGTCGGC	ACTCCTCGGA	CGTATCCCAT	CAGCCGTTGG	TTACCAGCCG	750
ACGCTGGCAA	GCGAGATGGG	TAAATTTCAA	GAAAGGATCA	CATCGACTAA	800

5

2) INFORMATION FOR SEQ ID NO: 1528

10 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

15

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1528

20 AACTTGAGCG ATTTTCGGAT ACCCTG

26

2) INFORMATION FOR SEQ ID NO: 1529

25

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

30

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1529

35

TTGCCGATGA AATAACCGCC GACT

24

40 2) INFORMATION FOR SEQ ID NO: 1530

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1035 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

45

(ii) MOLECULE TYPE: Genomic DNA

50 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Escherichia coli*
- (C) ACCESSION NUMBER: M11277

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1530

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5  ATGCGATTGG TTTGGAAATG TGGGGCGATT CAGGCATCCC GGTTATCTGA      50
   ATGGCTCAAC TCAACAGCCG GTGCTCATGA ACTTGAGCGA TTTTCGGATA      100
   CCCTGACCTT TTCTGTGTAT GGCTCAGTGC TGATCTGGCT GAAATCATAT      150
   CTCCGCGAAT CAGGAAGAAA ACTGCAGTTA GTCGGAATCG CCTTACCCAA      200
   CACCCTGAAC CCAAGGGACG ACCTAGCGCA ATTGGCCGAA ATTATCCAGC      250
   TCATCGATCA CCTCATGAAA CCGCACGTTG ATATGTTGAC TCACTTGTTG      300
   GCGTCCATTG ATGGCCAGTC GCGGTTATT TCATCGGCAA AATGGGGGGA      350
10  GCTAGAAACG GCTCGGCAGG AGAAAGCTAT CTCAGGGGTA ACCAGATTGA      400
   AGCTCCGCTT GGCGTCGCTT GCGCCCGTCC TGAAAAAACA CGTCAACAGC      450
   GATTTGTTCC GAAAAGCCTC TGATCGAATA GAGTCGATAG AGTATACGTT      500
   GGAAACCTTG CGTATAATGA AAACCTTCTT CGATGGTACC TCTCTTGAGG      550
   GAGATACTTC CGTACGTGAC TCGTATATGG CGGGCGTAGT AGATGGAATG      600
15  GTTCGAGCGA ATCCGGATGT GAAGATAATT CTGCTGGCGC ACAACAATCA      650
   TCTACAAAAA ACTCCAGTCT CCTTTTCAGG CGAGCTTACG GCTGTTCCCA      700
   TGGGGCAGCA CCTCGCAGAG AGGGTGAATT ACCGTGCGAT TGCATTACC      750
   CATCTTGAC CCACCGTGCC GGAAATGCAT TTCCCATCGC CAAAAAGTCC      800
   TCTTGATTTC TCTGTTGTGA CCACGCCTGC CGATGCAATC CGTGAGGATA      850
20  GTATGGAACA GTATGTCATC GACGCCTGTG GTACGGAGAA TTCATGTCTG      900
   ACATTGACAG ATGCCCCCAT GGAAGCAAAG CGAATGCGGT CTCAAAGCGC      950
   CTCTGTAGAA ACGAAATTGA GCGAGGCATT TGATGCCATC GTCTGTGTTA     1000
   CAAGCGCCGG CAAGGACAGC CTGGTTGCCC TATAG                       1035

```

25

2) INFORMATION FOR SEQ ID NO: 1531

```

30  (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 25 bases
      (B) TYPE: Nucleic acid
      (C) STRANDEDNESS: Single
      (D) TOPOLOGY: Linear

```

35 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1531

```

40  TCTTTTGTGTT ACGACATACG CTTTT      25

```

2) INFORMATION FOR SEQ ID NO: 1532

```

45  (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 24 bases
      (B) TYPE: Nucleic acid
      (C) STRANDEDNESS: Single
      (D) TOPOLOGY: Linear

```

50

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1532

AGTGCTTCTT TATCCGCTGT TCTA

24

5

2) INFORMATION FOR SEQ ID NO: 1533

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1533

CAGCGGATAA AGAAGCACTA CACATT

26

20

2) INFORMATION FOR SEQ ID NO: 1534

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

30

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1534

CCTCCTGAAA TAAAGCCCGA CAT

23

35

2) INFORMATION FOR SEQ ID NO: 1535

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1260 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

45

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Escherichia coli*
- (C) ACCESSION NUMBER: A15097

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1535

	ATGAGGTTTCG	AAGAATGGGT	CAAAGATAAG	CATATTCCTT	NCAAACNGAA	50
	TCACCCTGAT	GATAATTACG	ATGATTTTAA	GCCATTAAGA	AANATAATTG	100
	GAGATACCCG	AGTTGTAGCA	TTAGGTGAAA	ATTCTCATTT	CATAAAAGAA	150
	TTCTTTTTGT	TACGACATAC	GCTTTTGCGT	TTTTTTATCG	AAGATCTAGG	200
5	TTTTACTACG	TTTGCTTTTG	AATTTGGTTT	TGCTGAGGGT	CAAATCATCA	250
	ATAACTGGAT	ACATGGACAA	GGAAGTGACG	ATGAAATAGG	CAGATTCTTA	300
	AAACACTTCT	ATTATCCAGA	AGAGCTCAAA	ACCACATTTT	TATGGCTAAG	350
	GGAGTACAAT	AAAGCAGCAA	AAGAAAAAAT	CACATTTCTT	GGCATTGATA	400
	TACCCAGAAA	TGGAGGTTCA	TACTTACCAA	ATATGGAGAT	AGTGCATGAC	450
-10	TTTTTTAGAA	CAGCGGATAA	AGAAGCACTA	CACATTATCG	ATGATGCATT	500
	TAATATTGCA	AAAAAGATTG	ATTACTTCTC	CACATCACAG	GCAGCCTTAA	550
	ATTTACATGA	GCTAACAGAT	TCTGAGAAAT	GCCGTTTAAC	TAGCCAATTA	600
	GCTCGAGTAA	AAGTTCGCCT	TGAAGCTATG	GCTCCAATTC	ACATTGAAAA	650
	ATATGGGATT	GATAAATATG	AGACAATTCT	GCATTATGCC	AACGGTATGA	700
15	TATACTTGA	CTATAACATT	CAAGCTATGT	CGGGCTTTAT	TTCAGGAGGC	750
	GGAATGCAGG	GCGATATGGG	TGCAAAAGAC	AAATACATGG	CAGATTCTGT	800
	GCTGTGGCAT	TTAAAAAACC	CACAAAGTGA	GCAGAAAGTG	ATAGTAGTAG	850
	CACATAATGC	ACATATTCAA	AAAACACCCA	TTCTGTATGA	TGGATTTCTA	900
	AGTTGCCTAC	CAATGGGCCA	AAGACTTAAA	AATGCCATTG	GTGATGATTA	950
20	TATGTCTTTA	GGTATTACTT	CTTATAGTGG	GCATACTGCA	GCCCTCTATC	1000
	CGGAAGTTGA	TACAAAATAT	GGTTTTTCGAG	TTGATAACTT	CCAACTGCAG	1050
	GAACCAAATG	AAGGTTCTGT	CGAGAAAGCT	ATTTCTGGTT	GTGGAGTTAC	1100
	TAATTCTTTT	GTCTTTTTTTA	GAAATATTCC	TGAAGATTTA	CAATCCATCC	1150
	CGAACATGAT	TCGATTTGAN	TCTATTTACA	TGAAAGCAGA	ACTCGAGAAA	1200
25	GCTTTCGATG	GAATATTTCA	AATTGAAAAG	TCATCTGTAT	CTGAGGTCGT	1250
	TTATGAATAA					1260

30 2) INFORMATION FOR SEQ ID NO: 1536

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 bases
 (B) TYPE: Nucleic acid
 35 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1536

AGATGTATTA ACTGGAAAAC AACAA

25

45

2) INFORMATION FOR SEQ ID NO: 1537

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 bases
 50 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1537

5 CTTTGTAATT AGTTTCTGAA AACCA

25

2) INFORMATION FOR SEQ ID NO: 1538

10

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 28 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

15 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1538

20

TTAGAAGATA TAGGATACAA AATAGAAG

28

25 2) INFORMATION FOR SEQ ID NO: 1539

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 bases

(B) TYPE: Nucleic acid

30 (C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1539

GAATGAAAAA GAAGTTGAGC TT

22

40

2) INFORMATION FOR SEQ ID NO: 1540

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 486 bases

45 (B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

50

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Staphylococcus haemolyticus*

(C) ACCESSION NUMBER: M14039

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1540

```

5  ATGAAAAATA ATAATGTAAC AGAAAAAGAA TTATTTTATA TTTTAGATTT      50
   ATTTGAACAC ATGAAAGTAA CTTATTGGTT AGATGGTGGC TGGGGGGTAG      100
   ATGTATTAAC TGGAAAACAA CAAAGAGAAC ACAGAGATAT AGATATAGAT      150
   TTTGACGCTC AACACACTCA AAAAGTTATA CAAAATTAG AAGATATAGG      200
   ATACAAAATA GAAGTTCATT GGATGCCTTC ACGTATGGAA CTTAAGCATG      250
   AAGAATATGG GTATTTAGAT ATTCATCCTA TAAATCTAAA TGATGATGGA      300
10 TCAATTACCC AAGCAAACCC AGAAGGTGGT AATTATGTTT TCCAAATGA      350
   CTGGTTTTCA GAAACTAATT ACAAAGATCG AAAAATACCA TGTATTTCAA      400
   AAGAAGCTCA ACTTCTTTTT CATTCTGGTT ATGATTTAAC AGAAACAGAC      450
   CATTTTGATA TAAAAAATTT AAAATCAATA ACATAA      486

```

15

2) INFORMATION FOR SEQ ID NO: 1541

```

20 (i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 25 bases
    (B) TYPE: Nucleic acid
    (C) STRANDEDNESS: Single
    (D) TOPOLOGY: Linear

```

25 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1541

```

30 TGATAATCTT ATACGTGGGG AATTT      25

```

2) INFORMATION FOR SEQ ID NO: 1542

```

35 (i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 26 bases
    (B) TYPE: Nucleic acid
    (C) STRANDEDNESS: Single
    (D) TOPOLOGY: Linear

```

40

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1542

```

45 ATAATTTTCT AATTGCCCTG TTTCAT      26

```

2) INFORMATION FOR SEQ ID NO: 1543

50

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(i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 26 bases
    (B) TYPE: Nucleic acid

```

(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1543

GGGCAATTAG AAAATTATTT ATCAGA

26

10

2) INFORMATION FOR SEQ ID NO: 1544

(i) SEQUENCE CHARACTERISTICS:

15

(A) LENGTH: 26 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1544

TTTTACTCAT GTTTAGCCAA TTATCA

26

25

2) INFORMATION FOR SEQ ID NO: 1545

(i) SEQUENCE CHARACTERISTICS:

30

(A) LENGTH: 804 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

40

(A) ORGANISM: *Enterococcus faecium*
(C) ACCESSION NUMBER: AF110130

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1545

	ATGTTAAAAC AAAAAGAATT AATTGCAAAC GTTAAGAATC TTAGTGAGTC	50
45	AGATGAACGA ATTACAGCTT GTATGATGTA TGGATCGTTT ACCAAAGGAG	100
	AAGGTGACCA ATACTCTGAT ATAGAGTTCT ATATATTTTT GAAACATAGT	150
	ATAACCTCGA ACTTTGATTC ATCCAAGTGG TTGTTTGACG TAGCTCCGTA	200
	CTTGATGCTT TATAAAAATG AGTACGGAAC AGAGGTAGTT ATTTTGTGATA	250
	ATCTTATACG TGGGGAATTT CATTTCTTTT CTGAAAAAGA TATGAACATA	300
50	ATCCCCTCGT TTAAAGATTC AGGTTATATT CCTGATACGA AGGCTATGCT	350
	TATTTACGAT GAAACAGGGC AATTAGAAAA TTATTTATCA GAGATAAGTG	400
	GTGCAAGACC AAATAGACTT ACTGAAGAAA ATGCTAATTT TTTGTTGTGT	450
	AATTTCTCTA ATCTATGGTT GATGGGAATC AACGTTCTAA AAAGAGGAGA	500

ATATGCTCGT TCATTAGAAC TCTTATCACA ACTTCAAAAA AATACACTAC 550
 AACTTATACG TATGGCAGAA AAAAATGCTG ATAATTGGCT AAACATGAGT 600
 AAAAACCTTG AAAAAGAAAT TAGCCTTGAA AATTATAAAA AATTTGCAAA 650
 GACCACTGCT CGATTAGATA AGGTAGAATT ATTTGAAGCC TATAAAAATT 700
 5 CTTTGCTATT AGTTATGGAT TTGCAAAGTC ACCTTATTGA ACAATACAAC 750
 TTAAAAGTTA CACATGACAT TTTAGAAAGA TTGTTGAATT ACATTAGTGA 800
 ATAG 804

10

2) INFORMATION FOR SEQ ID NO: 1546

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 22 bases
 - 15 (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1546

CAAGAAGGAA TGGCTGTACT AC

22

25

2) INFORMATION FOR SEQ ID NO: 1547

- (i) SEQUENCE CHARACTERISTICS:
- 30 (A) LENGTH: 27 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1547

TAATTCCCAA ATAACCCTAA TAATAGA

27

40

2) INFORMATION FOR SEQ ID NO: 1548

- (i) SEQUENCE CHARACTERISTICS:
- 45 (A) LENGTH: 1218 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Double
 - (D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pyogenes*
 (C) ACCESSION NUMBER: U70055

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1548

```

5   ATGGAAAAAT ACAACAATTG GAAACTTAAG TTTTATACAA TATGGGCAGG      50
   GCAAGCAGTA TCATTAATCA CTAGTGCCAT CTTGCAAATG GCGATTATTT      100
   TTTACCTTAC AGAAAAAACT GGATCCGCGA TGGTCTTGTC TATGGCTTCA      150
   CTATTAGGTT TTTTACCCTA TGCGGTCTTT GGACCTGCAA TTGGTGTGCT      200
10  AGTGGATCGT CATGATAGGA AGAAGATAAT GATTGGTGCT GATTTAATTA      250
   TCGCAGCAGC TGGTTCGGTG CTTACTATTG TTGCATTCTA TATGGAGCTA      300
   CCTGTCTGGA TGGTTATGAT AGTATTGTTT ATCCGTAGCA TTGGAACAGC      350
   TTTTCACACC CCGGCTCTCA ATGCGGTAC GCCACTTTTA GTACCAGAAG      400
   AACAGCTTAC GAAATGTGCA GGCTATAGTC AGTCTTTGCA GTCTATAAGC      450
15  TATATTGTTA GTCCGGCGGT TGCAGCACTC TTATACTCCG TTTGGGAACT      500
   AAATGCTATT ATTGCCATCG ATGTATTGGG TGCTGTGATT GCATCTATTA      550
   CGGTAGCAAT TGTACGTATT CCTAAGCTGG GTGATCGCGT GCAAAGTTTG      600
   GACCCAAATT TCATAAGAGA AATGCAAGAA GGAATGGCTG TACTACGGCA      650
   AAATAAAGGA TTATTTGCTT TATTACTCGT TGGAACATTA TATATGTTTG      700
20  TTTATATGCC AATTAATGCA CTATTCCCTT TAATTAGCAT GGATTACTTT      750
   AATGGAACAC CTGTGCATAT TTCTATTACG GAAATTTCTT TTGCATCTGG      800
   AATGTTGATA GGGGGTCTAT TATTAGGGTT ATTTGGGAAT TACCAAAGC      850
   GAATCTTATT AATAACGGCA TCCATTTTTA TGATGGGGAT AAGCTTAACC      900
   ATTTCAGGAT TACTTCCCCA AAGTGGATTT TTCATTTTGT TAGTCTGCTG      950
25  TGCAATAATG GGGCTTTCTG TTCCGTTTTA CAGCGGTGTG CAAACAGCTC     1000
   TTTTTCAGGA GAAAATTAAG CCTGAATATT TAGGACGTGT ATTTTCTTTA     1050
   ACTGGAAGTA TCATGTCTCT TGCTATGCCA ATTGGATTAA TTCTTTCTGC     1100
   ACTCTTTGCT GATAGAATCG GTGTAAATCA TTGGTTTTTA CTATCAGGTA     1150
   CTTTAATTAT TTGCATTGCA ATAGTTTGCC CAATGATAAA TGAGATTAGA     1200
30  AAATTAGATT TAAAATAA                                     1218
  
```

2) INFORMATION FOR SEQ ID NO: 1549

35

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 26 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

40

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1549

45

GCTTATTATT AGGAAGATTA GGGGGC

26

50 2) INFORMATION FOR SEQ ID NO: 1550

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 bases

800

- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

5 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1550

TAGCAAGTGA CATGATACTT CCGA

24

10

2) INFORMATION FOR SEQ ID NO: 1551

15 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1218 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
- (C) ACCESSION NUMBER: U83667

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1551

	ATGGAAAAAT	ACAACAATTG	GAAACGAAAA	TTTTATGCAA	TATGGGCAGG	50
30	GCAAGCAGTA	TCATTAATCA	CTAGTGCCAT	CCTGCAAATG	GCGATTATTT	100
	TTTACCTTAC	AGAAAAACA	GGATCTGCGA	TGGTCTTGTC	TATGGCTTCA	150
	TTAGTAGGTT	TTTTACCCTA	TGCGATTTTG	GGACCTGCCA	TTGGTGTGCT	200
	AGTGGATCGT	CATGATAGGA	AGAAGATAAT	GATTGGTGCC	GATTTAATTA	250
	TCGCAGCAGC	TGGTGCAGTG	CTTGCTATTG	TTGCATTCTG	TATGGAGCTA	300
35	CCTGTCTGGA	TGATTATGAT	AGTATTGTTT	ATCCGTAGCA	TTGGAACAGC	350
	TTTTCATACC	CCAGCACTCA	ATGCGGTTAC	ACCACTTTTA	GTACCAGAAG	400
	AACAGCTAAC	GAAATGCGCA	GGCTATAGTC	AGTCTTTGCA	GTCTATAAGC	450
	TATATTGTTA	GTCCGGCAGT	TGCAGCACTC	TTATACTCCG	TTTGGGATTT	500
	AAATGCTATT	ATTGCCATCG	ACGTATTGGG	TGCTGTGATT	GCATCTATTA	550
40	CGGTAGCAAT	TGTACGTATA	CCTAAGCTGG	GTAATCAAGT	GCAAAGTTTA	600
	GAACCAAATT	TCATAAGGGA	GATGAAAGAA	GGAGTTGTGG	TTCTGAGACA	650
	AAACAAAGGA	TTGTTTGCCT	TATTACTCTT	AGGAACACTA	TATACTTTTG	700
	TTTATATGCC	AATCAATGCA	CTATTTCTTT	TAATAAGCAT	GGAACACTTT	750
	AATGGAACGC	CTGTGCATAT	TTCTATTACG	GAAATTTTCT	TTGCATTTGG	800
45	GATGCTAGCA	GGAGGCTTAT	TATTAGGAAG	ATTAGGGGGC	TTCGAAAAGC	850
	ATGTATTACT	AATAACAAGT	TCATTTTTTA	TAATGGGGAC	CAGTTTAGCC	900
	GTTTCGGGAA	TACTTCCTCC	AAATGGATTT	GTAATATTCG	TAGTTTGCTG	950
	TGCAATAATG	GGGCTTTCGG	TGCCATTTTA	TAGCGGTGTG	CAAACAGCTC	1000
	TTTTTCAGGA	GAAAATTAAG	CCTGAATATT	TAGGACGTGT	ATTTTCTTTG	1050
50	ATCGGAAGTA	TCATGTCACT	TGCTATGCCA	ATTGGGTAA	TTCTTTCTGG	1100
	ATTCTTTGCT	GATAAAATCG	GTGTAAATCA	TTGGTTTTTA	CTATCAGGTA	1150
	TTTTAATTAT	TGGCATTGCT	ATAGTTTGCC	AAATGATAAC	TGAGGTTAGA	1200
	AAATTAGATT	TAAAATAA				1218

2) INFORMATION FOR SEQ ID NO: 1552

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1552

GGCAAGCAGT ATCATTAATC ACTA

24

2) INFORMATION FOR SEQ ID NO: 1553

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1553

CAATGCTACG GATAACAAT ACTATC

26

2) INFORMATION FOR SEQ ID NO: 1554

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 27 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1554

AGAAAATTAA GCCTGAATAT TTAGGAC

27

2) INFORMATION FOR SEQ ID NO: 1555

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 bases
(B) TYPE: Nucleic acid

- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1555

TAGTAAAAAC CAATGATTTA CACCG

25

10

2) INFORMATION FOR SEQ ID NO: 1556

(i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 25 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1556

ACTGTACGCA CTTGCAGCCC GACAT

25

25

2) INFORMATION FOR SEQ ID NO: 1557

(i) SEQUENCE CHARACTERISTICS:

30

- (A) LENGTH: 24 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1557

GAACGGCAGG CGATTCTTGA GCAT

24

40

2) INFORMATION FOR SEQ ID NO: 1558

45

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1558

GTGGTGGTGC ATGGCGATCT CT

22

5

2) INFORMATION FOR SEQ ID NO: 1559

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 24 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

15 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1559

GCCGCAGCGA GGTACTCTTC GTTA

24

20

2) INFORMATION FOR SEQ ID NO: 1560

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 906 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

30

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Escherichia coli*
 35 (C) ACCESSION NUMBER: D16251

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1560

	ATGACCGTAG TCACGACCGC CGATACCTCC CAACTGTACG CACTTGCAGC	50
40	CCGACATGGG CTCAAGCTCC ATGGCCCGCT GACTGTCAAT GAGCTTGGGC	100
	TCGACTATAG GATCGTGATC GCCACCGTCG ACGATGGACG TCGGTGGGTG	150
	CTGCGCATCC CGCGCCGAGC CGAGGTAAGC GCGAAGGTCG AACCAGAGGC	200
	GCGGGTGCTG GCAATGCTCA AGAATCGCCT GCCGTTTCGCG GTGCCGGACT	250
	GGCGCGTGCG CAACGCCGAG CTCGTTGCCT ATCCCATGCT CGAAGACTCG	300
45	ACTGCGATGG TCATCCAGCC TGGTTCGTCC ACGCCCGACT GGGTCGTGCC	350
	GCAGGACTCG GAGGTCTTCG CGGAGAGCTT CGCGACCGCG CTCGCCGCCC	400
	TGCATGCCGT CCCCATTTCC GCCGCCGTGG ATGCGGGGAT GCTCATCCGT	450
	ACACCGACGC AGGCCCGTCA GAAGGTGGCC GACGACGTTG ACCGCGTCCG	500
	ACGCGAGTTC GTGGTGAACG ACAAGCGCCT CCACCGGTGG CAGCGCTGGC	550
50	TCGACGACGA TTCGTCGTGG CCAGATTTCT CCGTGGTGGT GCATGGCGAT	600
	CTCTACGTGG GCCATGTGCT CATCGACAAC ACGGAGCGCG TCAGCGGGAT	650
	GATCGACTGG AGCGAGGCCG GCGTTGATGA CCCTGCCATC GACATGGCCG	700
	CGCACCTTAT GGTCTTTGGT GAAGAGGGGC TCGCGAAGCT CCTCCTCACG	750

TATGAAGCGG	CCGGTGGCCG	GGTGTGGCCG	CGGCTCGCCC	ACCACATCGC	800
GGAGCGCCTT	GCGTTCGGGG	CGGTCACCTA	CGCACTCTTC	GCCCTCGACT	850
CGGGTAACGA	AGAGTACCTC	GCTGCGGCCA	AGGCGCAGCT	CGCCGCAGCG	900
GAATGA					906

5

2) INFORMATION FOR SEQ ID NO: 1561

10 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1048 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

15

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Candida albicans*
- (B) STRAIN: ATCC 18804

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1561

	GATCATGGTA	AAACTACATT	GACTGCTGCT	ATCACCAAAG	TTTTAGCCGA	50
25	ACAAGGTGGT	GCCAACTTCT	TGGATTAYGG	TTCTATTGAT	AGAGCTCCAG	100
	AAGAAAGAGC	TAGAGGTATC	ACTATTTCCT	CTGCCCACGT	TGAATACGAA	150
	ACCAAGAACA	GACACTATGC	CCACGTTGAT	TGTCCAGGAC	ACGCTGATTA	200
	TATCAAAAAT	ATGATTACTG	GTGCCGCTCA	AATGGATGGT	GCTATCATTG	250
	TTGTTGCTGC	CACTGATGGT	CAAAATGCCTC	AAACCAGAGA	ACATTTGTTA	300
30	TTGGCCAGAC	AAGTTGGTGT	TCAAGACTTG	GTTGTGTTTG	TCAACAAAGT	350
	CGATACTATT	GATGACCCTG	AAATGTTGGA	ATTAGTCGAA	ATGGAAATGA	400
	GAGAATTGTT	ATCCACCTAC	GGTTTGTATG	GTGACAACAC	TCCAGTTATT	450
	ATGGGATCTG	CTTTAATGGC	TTTGGAAGAC	AAGAAACCAG	AAATTGGTAA	500
	GGAAGCTATC	TTGAAATTGT	TAGATGCTGT	CGATGAACAC	ATTCCAACCTC	550
35	CATCAAGAGA	CTTGGAACAA	CCATTTTGTG	TACCAGTTGA	AGACGTGTTC	600
	TCCATCTCCG	GTAGAGGAAC	TGTTGTCACT	GGTAGAGTTG	AAAGAGGTGT	650
	TTTGAAGAAG	GGTGAAGAAA	TCGAAATTGT	TGGTGGTTTT	GACAAACCTT	700
	ACAAGACTAC	TGTTACCGGT	ATTGAAATGT	TCAAAAAAGA	ATTAGACTCT	750
	GCTATGGCTG	GTGACAACCTG	TGGTGTTTTG	TTAAGAGGTG	TTAAAAGAGA	800
40	TGAAATCAAG	AGAGGTATGG	TTTTGGCCAA	ACCAGGTACT	GCCACTTCTC	850
	ACAAGAAGTT	CTTGCTTCC	TTGTATATTT	TGACTTCCGA	AGAAGGTGGY	900
	CGTTCCACTC	CATTTGGTGA	AGGTTACAAG	CCTCAATGCT	TCTTCAGAAC	950
	TAACGATGTC	ACTACCACAT	TTTCATTCCC	AGAAGGAGAA	GGTGTTGACC	1000
45	ATTCTCAAAT	GATCATGCCA	GGTGACAACA	TTGAAATGGT	TGGTGAAT	1048

2) INFORMATION FOR SEQ ID NO: 1562

50 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1074 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double

805

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

5 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Candida dubliniensis*

(B) STRAIN: NCPF 3949

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1562

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10  TGATCACGGT AAAACCACAT TAACTGCTGC CATTACCAAA GTATTAGCTG      50
    AACAAGGTGG TGCCAAC TTT TTGGATTACG GTTCCATTGA TAGAGCTCCA      100
    GAAGAAAGAG CCAGAGGTAT CACTATTTCC ACTGCCCACG TTGAATACGA      150
    AACCAAGAAC AGACACTATG CCCACGTTGA TTGTCCAGGA CACGCTGATT      200
15  ATATCAAAAA CATGATTACT GGTGCTGCTC AAATGGATGG TGCTATCATT      250
    GTTGTGTGCTG CTACTGACGG TCAAATGCCA CAAACCAGAG AACATTTATT      300
    GTTGGCAAGA CAAGTTGGTG TTCAAGACTT GGTGTCTTT GTCAACAAAG      350
    TTGATACTAT TGATGACCCT GAGATGTTGG AATTAGTCGA AATGGAAATG      400
    AGAGAATTGT TGTCCACCTA CGGTTTTGAT GGTGACAACA CTCCTGTTAT      450
20  TATGGGATCT GCTTTAATGG CCTTGAAGG CAAAAACCA GAAATTGGTA      500
    AGGAAGCTAT TTTGAGATTG TTAGATGCTG TCGATGAACA CATTCCAAC T      550
    CCATCAAGAG ACTTGAACA ACCATTTTTG TTGCCAGTTG AAGACGTGTT      600
    CTCCATCTCT GGTAGAGGAA CTGTTGTCAC CGGTAGAGTT GAAAGAGGTG      650
    TCTTGAAGAA GGGTGAAGAA ATCGAAATTG TTGGTGGTTT TGACAAACCA      700
25  TACAAGACCA CTGTTACTGG TATTGAAATG TTCAAAAAGG AATTAGATTC      750
    TGCTATAGCT GGTGACAACT GTGGTGT TTT GTTGTGAGAGGT GTTAAAAGAG      800
    ATGAAATCAA GAGAGGTATG GTTTTGGCCA AGCCAGGTAC TGCTACTTCT      850
    CACAAGAAAT TTTTAGCATC TTTGTATATT TTGACTTCAG AAGAAGGTGG      900
    TCGTTCCACT CCATTTGGAG AAGGTTACAA GCCTCAATGT TTCTTCAGAA      950
30  CTAATGACGT CACTACCACA TTTTCATTCC CAGAAGGAGA AGGTGTTGAC      1000
    CACTCCCAA TGGTCATGCC AGGTGATAAC ATTGAAATGG TTGGTGAATT      1050
    GATCAAATCA TGTCCATTGG AAGT                                     1074

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35

2) INFORMATION FOR SEQ ID NO: 1563

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1033 bases

40 (B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

45

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Candida famata*

(B) STRAIN: ATCC 62894

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1563

```

GATCACGGGA AGACTACTTT GACCGCTGCC ATCACCAAAG TTTTAGCCGA      50
AAAAGGTGGT GCTAACTTCT TGGACTACGG TTCTATCGAT AAAGCTCCAG      100

```

AAGAAAGAGC CAGAGGTATT ACTATTTCTG CTGCCCATGT TGAATACGAA 150
 ACTGACAAGA GACACTATGC CCATGTTGAT TGTCCAGGTC ACGCAGATTA 200
 TATCAAGAAT ATGATTACTG GTGCTGCTCA AATGGATGGT GCCATTATTG 250
 TTGTTGCTGC TTCCGATGGT CAAATGCCTC AAACCAGAGA ACATTTGTTA 300
 5 TTGGCCAGAC AAGTTGGTGT TCAACACTTG GTTGTTTTCG TCAACAAGGT 350
 CGACACCATT GACGATCCAG AAATGTTGGA ATTGGTTGAA ATGGAAATGA 400
 GAGATTTGTT AACTACTTAC GGTTTTGATG GTGATAACAC CCCAGTTATC 450
 ATGGGATCTG CTTTGTGTGC TTTGGAATCC AGAGAACCAG AAATTGGTCA 500
 AAAAGCCATT GAAAAATTGT TAGATGCCGT CGATGAATAC ATTCCAACCC 550
 10 CAGTCAGAGA CTTGGAACAA CCATTCTTGA TGCCAGTTGA AGAAGTTTTC 600
 TCCATTTCCG GTAGAGGTAC CGTTGTTGCT GGTAGAGTCG AAAGAGGTAC 650
 CTTGAAGAAG GGTGAAGAAA TCGAAATTGT TGGTGGTTTC GACAAGCCAT 700
 TCAAGGCCAC TGTTACTGGT ATTGAAATGT TCAAGAAGGA ATTGGACTCC 750
 GCTCTTGCTG GTGACAACCTG TGGTATCTTG TTGAGAGGTG TCAAGAGAGA 800
 15 CGAAGTTAAG AGAGGTATGG TCTTGACCAA GCCAAACACC GTCACTTCCC 850
 ACAAGAAGAT CTTGGCCTCG TTGTATATCT TGACCAAGGA AGAAGGTGGT 900
 AGACACTCTC CATTTGGAGC CAACTACAAG CCCCAATTGT TCATGAGAAC 950
 CACCGATGTT ACCGGTACCA TGACCTTCCC AGAAGGTGCC GACCAATCTG 1000
 CCATGGTCAT GCCAGGTGAC AACGTTGAAA TGC 1033
 20

2) INFORMATION FOR SEQ ID NO: 1564

25 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1056 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

30

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Candida glabrata*
 35 (B) STRAIN: ATCC 66032

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1564

GATCACGGTA AGACTACATT GACAGCTGCT ATCACCAAGA CATTGGCCAA 50
 40 GAACGGTGGT GCTGATTTCT TGGACTACTC TTCCATTGAC AAAGCTCCAG 100
 AGGAGAGAGC CCGTGGTATC ACTATCTCTA CTGCCCATGT CGAGTACGAG 150
 ACCGCCAAGA GACATTACTC CCACGTCGAC TGTCCAGGTC ACGCCGACTA 200
 CATCAAGAAC ATGATTACTG GTGCTGCCCCA AATGGACGGT GCTATCATCG 250
 TTGTCGCCGC CACCGATGGT CAAATGCCAC AAAC TAGAGA GCATTTGCTG 300
 45 TTGGCCAGAC AAGTCGGTGT TCAACGTATC GTTGTCTTTG TCAACAAGGT 350
 GGACACCATC GATGACCCTG AAATGTTGGA ATTAGTGGA ATGGAAATGA 400
 GAGAATTGTT GAACGAATAC GGTTTTGACG GTGACAATGC CCCTATCATT 450
 ATGGGTTCG CTTTGTGTGC CCTAGAAGGT CGTCAACCTG AAATTGGTGA 500
 GCAAGCTATC ATGAAACTAT TGGACGCTGT TGATGAATAC ATTCCAACCC 550
 50 CAGAAAGAGA CTTGAACAAG CCATTCTTGA TGCTGTGTTGA AGACATCTTC 600
 TCCATCTCTG GTAGAGGTAC CGTCGTCCT GACGTCGTCG AAAGAGGTAA 650
 CTTGAAGAAG GGTGAAGAAG TTGAAATTGT TGGTCACAAC ACTACCCCAT 700
 TGAAGACCAC CGTTACTGGT ATCGAAATGT TCAGAAAGGA ATTGGACCAA 750

GCTATGGCTG GTGACAACGC CGGTATCCTA TTGAGAGGTA TCAGAAGAGA 800
 CCAATTGAAG AGAGGTATGG TCATGGCCAA GCCAGGTACC GTCAAGGCTC 850
 ACACCAAGAT TTTGGCTTCT TTGTACATCT TGTCTAAGGA AGAAGGTGGT 900
 AGACATTCTG GTTTCGGTGA AACTACAGA CCTCAGATGT TTATCAGAAC 950
 5 CGCAGATGTC ACTGTTGTGA TGAAGTTCCC AGAATCTGTG GAAGACCACT 1000
 CTATGCAAGT TATGCCAGGT GACAACGTCG AAATGGTCTG TGAAGTAGTC 1050
 CACCCA 1056

10

2) INFORMATION FOR SEQ ID NO: 1565

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1061 bases
 15 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- 20 (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Candida guilliermondii*
 (B) STRAIN: ATCC 6260

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1565

GATCATGGTA AGACCACTTT GACCGCTGCT ATCACCAAGG TTTTGTCCGA 50
 AAAAGGAGGT GCTAATTTCT TGGATTACGG CTCCATCGAC AGAGCTCCAG 100
 AAGAGAGAGC CAGAGGTATC ACCATTTCCA CTGCCCATGT TGAGTACCAA 150
 30 ACTGATAAGA GACATTATGC CCACGTTGAC TGTCCAGGTC ACGCCGATTA 200
 CATTAGAAT ATGATTACTG GTGCCGCCCA GATGGACGGT GCCATTATTG 250
 TTGTTGCTGC CACTGACGGT CAAATGCCTC AGACCAGAGA GCACTTGTTG 300
 TTGGCCAGAC AAGTTGGTGT GCAACACTTG GTAGTTTTTG TGAACAAGGT 350
 GGACACCAAT GACGATCCCG AGATGTTGGA ATTGGTCGAG ATGGAAATGA 400
 35 GAGAATTGTT GAGTCAGTAC GGTTCGATG GTGACAACAC CCCAGTTATC 450
 ATGGGATCTG CTTTGTGTGC TTTGGAAAGT AAGCAGCCAG AAATTGGTGT 500
 GCAAGCCATT GAAAAATTGT TGGACGCTGT CGATGAGCAC ATTCCTACTC 550
 CTACCCGTGA CTTGGAACAG CCATTCTTGT TGCCTGTTGA AGATGTGTTC 600
 TCCATTTCTG GTAGAGGAAC TGTGGTTACT GGTAGAGTCG AAAGAGGTTC 650
 40 GTTGAAGAAG GGTGAGGAAA TCGAGATTGT TGGTGACTTT GACAAGCCAT 700
 TCAAGACCAC TGTGACTGGA ATTGAAATGT TCAAGAAGGA ATTGGATGCT 750
 GCTATGGCTG GTGACAATGC TGGTATCTTG TTGAGAGGTG TCAAGAGAGA 800
 CGATGTCAAG AGAGGTATGG TTTTGGCCAA GCCTTCCACC GTCATTCTC 850
 ACAAGAAGGT GTTGGCTTCC TTGTACATCT TGAGTAAGGA AGAAGGTGGC 900
 45 CGTCACTCTC CTTTTGGTGA GAACTACAAG CCTCAATTGT TCATCAGAAC 950
 TACTGACGTT ACCGGTACTT TAAGATTCCC AGCCGGCGAG GGTGTGACAC 1000
 ACTCGCAAAT GGTATGCCA GGTGACAATG TTGAGATGGA AATTGAGCTT 1050
 GTGAGAAAGA C 1061

50

2) INFORMATION FOR SEQ ID NO: 1566

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1073 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Candida haemulonii*
 (B) STRAIN: ATCC 22991

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1566

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15  GATCACGGTA AGACTACCTT GACTGCTGCT ATCACCAAGG TTTTGGCTTC      50
    TAAGGGTGGT GCTAGCTTCT TGGACTATGG TTCCATTGAC AGAGCCCCAG      100
    AGGAGAGAGC TAGAGGTATT ACTATTTCTA CTGCCCACGT TGAGTACCAA      150
    ACCGAAAAGA GACACTACGC CCACGTCGAC TGTCCAGGTC ACGCTGATTA      200
    CATTAGAAT  ATGATTACTG GTGCCGCCCA GATGGACGGT GCTATCATTG      250
20  TTGTTGCTGC TTCTGATGGT CAGATGCCTC AGACCAGAGA GCACCTTTTG      300
    TTGGCCAGAC AGGTTGGTGT TCAGAACTTG GTTGTTTTCG TTAACAAGGT      350
    TGACACCATT GACGACCCTG AAATGTTGGA ATTGGTTGAG ATGGAAATGA      400
    GAGAATTGTT GACTACTTAC GGTTTTGACG GTGATGAGAC TCCTGTTATC      450
    ATGGGTTCTG CTTTGTGCGC TTTGGAAGAG AAGCAACCAG AGATTGGTGA      500
25  GCAGGCTATC ATGAAGTTGT TGGACGCTGT CGATGAGTAC ATTCCAACCC      550
    CACAGCGTGA CTTGGAGCAG CCATTCTTGA TGCCTGTTGA GGATGTTTTTC      600
    TCCATTTCTG GTAGAGGTAC TGTCGTTACT GGTAGAGTTG AGAGAGGTTT      650
    TTTGAAGAAG GGTGAGGAAA TCGAGATTGT CGGTGACTTC GCCAAGACTT      700
    TCAAGGCTAC CGTTACTGGT ATTGAGATGT TCAAGAAGGA ATTGGATGCT      750
30  GCTATGGCTG GTGACAACGC CGGTATCTTG TTGAGAGGTG TCAAGAGAGA      800
    TGAGATCTCC CGTGGTGATG TCTTGGCCAA GCCAGGTAAT GTTACTCCAC      850
    ACAAGAAGAT CTTGGCTTCT TTGTACGTTT TGACCAAGGA AGAAGGTGGT      900
    CGTCACAACC CATTCGCTGA GAACTACAAG CCACAGTTGT TCCTCAGAAC      950
    CACCAACGTC ACTGGTACCA TGAGATTCCC AGAAGGTGAA GATGTTGACC     1000
35  ACTCTGCCAT GGTAAACCCA GGTGACAACG TTGAGATGGA AATCGAGTTG     1050
    GGTAGAAAGG CCCCACTTGA GTT                                     1073
  
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40 2) INFORMATION FOR SEQ ID NO: 1567

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1062 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Candida kefyr*
 (B) STRAIN: ATCC 28838

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1567

	CATGGTAAGA	CCACTTTGAC	TGCTGCCATC	ACCAAGACTC	TAGCTGAACG	50
	TGGTGGTGCT	GACTTTTGG	ACTACTCTTC	TATTGACAAG	GCTCCAGAAG	100
5	AAAGAGCYAG	AGGTATCACT	ATTTCTACTG	CTCATGTTGA	ATACGAGACT	150
	GAAAAGAGAC	ATTACTCCCA	CGTTGACTGT	CCAGGTCACG	CTGATTACAT	200
	CAAGAACATG	ATTACTGGTG	CTGCTCAAAT	GGACGGTGCT	ATTATTGTTG	250
	TTGCTGCTAC	TGATGGTCAA	ATGCCTCAAA	CCAGAGAGCA	TTTGTTGTTG	300
	GCCAGACAAG	TTGGTGTTCA	ACACATTGTT	GTTTTCGTTA	ACAAGGTTGA	350
10	CACCATCGAT	GATCCAGAAA	TGTTGGAATT	GGTTGAAATG	GAAATGAGAG	400
	AATTRTTGAC	TCAATATGGC	TTTGACGGTG	ACAACACTCC	AGTGATCATG	450
	GGTTCTGCTT	TGTGTGCCTT	GGAAGGTAAG	CAACCAGAAA	TTGGTGAGCA	500
	AGCCATCATG	AAGTTGTTGG	ACGCTGTTGA	CGAATACATC	CCAACCCAG	550
	CCCGTGACTT	GGAAAAVCCA	TTCTTGATGC	CTGTTGAAGA	TATCTTCTCC	600
15	ATTTCCGGTA	GAGGTACTGT	CGTCACTGGT	AGAGTTGAAC	GTGGTAACTT	650
	GAAGAAGGGT	GAAGAAATCG	AAATTGTTGG	TCACAACACC	ACTCCTTTCA	700
	AGACTACTGT	TACTGGTATT	GAAATGTTCA	GAAAGGAATT	GGACCAAGCC	750
	ATGGCTGGTG	ACAACGCTGG	TGTCCTTTTG	AGAGGTGTCA	GAAGAGACCA	800
	ATTGAAGAGA	GGTATGGTTT	TGGCTAAGCC	AGGTACTGTT	AAGGCCCACA	850
20	CCAAGTTCTT	GGCTTCCTTG	TACATTTTGA	CCAAGGAAGA	AGGTGGTAGA	900
	CACTCCGGTT	TCGGTGAAAA	CTACAGACCA	CAAACTCTACG	TCAGAACTGC	950
	TGACGTTACC	GTDGTCTTGA	AGTTCCCAGA	ATCTGTTGAA	GACCATTCCA	1000
	TGCAAGTCAT	GCCAGGTGAC	AATGTGCGAA	TGGAGTGTGA	ATTGGTTCAC	1050
	CCAACTCCAT	TG				1062

25

2) INFORMATION FOR SEQ ID NO: 1568

30 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1062 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Candida lusitanae*
- (B) STRAIN: ATCC 66035

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1568

	CGGAAAGACC	ACCTTGACCG	CCGCCATTAC	CAAGGTTTTG	GCTGACAAGG	50
45	GTGGCGCCAA	CTTCTTGAC	TACGGTGCCA	TTGACAAGGC	TCCTGAAGAA	100
	AGAGCACGTG	GTATCACCAT	TTCCACTGCC	CACGTTGAAT	ACGAGACCGA	150
	CAACAGACAC	TACGCCCACG	TTGACTGTCC	AGGTCACGCC	GATTACATCA	200
	AGAACATGAT	CACGGGTGCC	GCTCAAATGG	ACGGTGCCAT	TATTGTTGTT	250
	GCAGCCACCG	ACGGCCAAAT	GCCTCAAACC	AGAGAGCACT	TGTTGTTGGC	300
50	CAGACAAGTT	GGTGTGCAAC	ACTTGGTTGT	TTTCGTGAAC	AAGGTTGATA	350
	CCATCGACGA	CCCAGAAATG	TTGGAATTGG	TTGAAATGGA	AATGAGAGAA	400
	TTGTTGACTC	AATACGGATT	TGACGGCGAT	GAAACCCCTG	TTGTTATGGG	450
	CTCTGCTCTT	TGCGCTTTGG	AAGGTAGAGA	ACCAGAGATT	GGTGAGCAAG	500

	CCATCACCAA	GTTGTTGGAG	GCTGTTGACG	AGTACATCCC	AACCCACAA	550	
	CGTGA	CTTGG	CTTGCCT	GTTGAAGATG	TTTTCTCCAT	600	
	TTCTG	GGTAGA	GGTACTGTTG	TCACTGGTAG	AGTGGAGAGA	GGTTCCTTGA	650
	AGAAGGGTGA	GGAGATCGAG	ATTGTTGGTG	ACTTTGACAA	GCCTTTCAAG	700	
5	ACTACTGTTA	CTGGTATTGA	GATGTTCAAG	AAGGAATTGG	ACGCTGCTAT	750	
	GGCTGGTGAC	AATGCTGGTA	TCTTGTGAG	AGGTGTCAAG	AGAGAACAAG	800	
	TTTCCCGTGG	TATGGTTTTG	GCCAAGCCAG	GCACTGTGAC	CTCGCACAAG	850	
	AAGGTTTTTG	CTTCTTTGTA	CATTTTGTCT	AAGGAAGAAG	GTGGTCGTCA	900	
	CTCTCCATTT	GGCGAGAACT	ACAAGCCTCA	ATTGTCCTT	AGA	ACTACCG	950
10	ATGTCACTGG	TACTTTGAGA	TTCCAGCAG	GTGAGGACGT	TGACCACTCC	1000	
	GCTATGGTTT	CTCCAGGTGA	CAATGTCGAG	ATGGAAATCG	AGTTGGTCAG	1050	
	AAAGACTCCT	CT				1062	

15

2) INFORMATION FOR SEQ ID NO: 1569

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 990 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

25

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Candida sphaerica*
 (B) STRAIN: ATCC 2504

(ii) MOLECULE TYPE: DNA

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1569

	TCACCAAGAC	TTTGGCTGAA	CGTGGTGGTG	CTGATTCTT	GGACTACTCT	50	
35	TCCATTGACA	AGGCTCCAGA	AGAAAGAGCR	AGAGGTATCA	CTATTTCTAC	100	
	TGCACATGTT	GAATATGAAA	CTGACAAGAG	ACATTACTCT	CACGTCGACT	150	
	GTCCAGGTCA	TGCTGATTAC	ATCAAGAATA	TGATTACTGG	TGCTGCCCAA	200	
	ATGGATGGTG	CTATCATTGT	TGTTGCTGCT	ACAGATGGTC	AAATGCCTCA	250	
	AACCAGAGAA	CATTTGTTGT	TGGCTAGACA	AGTTGGTGTT	CAACAYATCG	300	
40	TTGTTTTTCGT	TAACAAGGTT	GACACTATCG	ATGACCCTGA	AATGTTAGAA	350	
	TTGGTTGAAA	TGGAAATGAG	AGAATTATTG	ACCCAATACG	GTTTCGATGG	400	
	TGACAACACT	CCAGTCATCA	TGGGTTCTGC	TTTGTGTGCT	TTAGAAGGTA	450	
	AGCAACCAGA	AATTGGTGAA	CAAGCAATCA	TGAAGTTATT	GGACGCTGTT	500	
	GACGAATACA	TCCCAACTCC	AGCTCGTGAT	TTGGAAAAGC	CTTTCTTGAT	550	
45	GCCTGTTGAA	GATATCTTCT	CCATCTCCGG	TAGAGGTACC	GTCGTA	ACTG	600
	GTAGAGTTGA	ACGTGGTAAC	TTGA	AKAAGG	GTRAAGAAAT	CGAAATCGTT	650
	GGTCACAACA	CCACTCCATT	CAAGACCACT	GTTACTGGTA	TTGAAATGTT	700	
	CAGAAAGGAA	TTGGACCAAG	CTATGGCTGG	TGATAACGCT	GGTGTCTGTG	750	
	TGAGAGGTGT	CAGAAGAGAC	CAATTAAAGA	GAGGTATGGT	CTTGGCCAAG	800	
50	CCAGGTACTG	TCAAGGCTCA	CACCRAATTC	TTGGCCTCTT	TGTATATCTT	850	
	GACCAAGGAA	GAAGGTGGTA	GACATTCCGG	TTTCGGTGAA	AATTACAGAC	900	
	CTCAAATCTA	CGTTAGAACT	GCTGATGTCA	CCGTTGTTTT	GAAGTTCCCA	950	
	GAAGCTGTTG	AAGATCACTC	TATGCAAGTC	ATGCCAGGTG		990	

2) INFORMATION FOR SEQ ID NO: 1570

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 1184 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

- - - - (ii) MOLECULE TYPE: Genomic DNA

10

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Candida tropicalis*
 (B) STRAIN: ATCC 750

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1570

	GATCATGGTA	AAACCACTTT	GACTGCTGCC	ATTACTAAAG	TCTTGGCTGA	50
	TAAAGGTCAA	GCTAACTTCT	TAGATTACGG	TTCTATTGAT	AGAGCTCCAG	100
	AAGAAAGAGC	CAGAGGTATC	ACCATCTCTA	CTGCCCACGT	TGAATATGAA	150
20	ACCGAAAAAA	GACATTACGC	CCATGTTGAG	TATGTATACT	TTTTTTTGT	200
	GTGTAATTGT	TTTAAAGATT	TTCTTTAAAG	CTGAAGAAGT	CAAATCAGTT	250
	CTTTGATAAC	TTCTATTAAA	AAAAGGGAAA	AATTAACAAG	ATATACTAAC	300
	ACTATAACAG	TTGTCCTGGA	CATCAAGATT	ATATCAAGAA	TATGATTACC	350
	GGTGCCGCTC	AAATGGATGG	TGCTATTATT	GTTGTTGCTG	CCACTGATGG	400
25	TCAAATGCCA	CAAACCAGAG	AACATTTGTT	GTTGGCTAGA	CAAGTCGGTG	450
	TTCAAGATTT	GGTTGTCTTT	GTTAACAAAG	TCGACACTAT	TGATGACCCA	500
	GAAATGTTGG	AATTGGTTGA	AATGGAAATG	AGAGAATTAT	TGACTACTTA	550
	CGGTTTTGAT	GGTGATAACA	CTCCTGTTAT	CATGGGTTCT	GCTTTGATGG	600
	CCTTGCAAGG	TAAACAACCA	GAAATTGGTG	AACAAGCTAT	CATGAAATTG	650
30	ATGGACGCTA	TTGATGAACA	CATTCCAACC	CCAACCAGAG	ACTTGGAAAC	700
	ATCTTTCTTG	ATGCCAGTTG	AAGATGTTTT	CTCCATTTCT	GGTAGAGGTA	750
	CTGTTGTTAC	TGGTAGAGTC	GAAAGAGGTG	TCTTAAAGAA	GGGTGAAGAA	800
	ATTGAAATTG	TTGGTGGTTT	CGAAAAACCA	TTCAAGACCA	CTGTTACTGG	850
	TATTGAAATG	TTCAAGAAAG	AATTAGATGC	TGCTATGGCT	GGTGACAAC	900
35	GTGGTGTCTT	GTTGAGAGGT	GTCAAGAGAG	ACGAAATCAA	GAGAGGTATG	950
	GTTTTGGCTA	AACCAGGTAC	TGCTACTTCC	CACAAGAAAT	TCTTGGCTTC	1000
	CATGTATATC	TTAACTGCTG	AAGAAGGTGG	TCGTTCCACT	CCATTCGGTG	1050
	AAGGTTACAA	GCCACAATGT	TTCTTCAGAA	CTAACGATGT	TACCACTTCC	1100
	TTCTCTTTCC	CAGAAGGTGA	AGGTGTTGAC	CACTCCCAA	TGGTTATGCC	1150
40	AGGTGACAAC	ATTGAAATGG	TCGGTGAATT	GATT		1184

2) INFORMATION FOR SEQ ID NO: 1571

45

(i) SEQUENCE CHARACTERISTICS:

- 50 (A) LENGTH: 1071 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Candida viswanathii*
 (B) STRAIN: ATCC 28269

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1571

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CGATCACGGT AAGACCACCT TGACCGCCGC CATCACCAAG GTCTTGGCCG      50
ACAAGGGTCA GGCTAACTTC TTGGACTACG GATCCATTGA CAGAGCCCCCT      100
GAAGAAAGAG CAAGAGGTAT CACTATCTCC ACTGCCCACG TTGAATACGA      150
10 GACTGATAAG AGACACTATG CCCACGTTGA TTGCCCCGGC CATCAAGATT      200
ATATCAAGAA TATGATCACT GGTGCTGCCC AAATGGACGG TGCTATCATT      250
GTTGTTGCTG CTA CTGACGG TCAGATGCCA CAAACCAGAG AACACTTGTT      300
GTTGGCTAGA CAAGTTGGTG TCCAAGACTT GGTGTGTTTC GTTAACAAGG      350
TTGACACTAT CGATGACCCA GAAATGTTGG AATTGGTTGA AATGGAAATG      400
15 AGAGAATTAT TATCTTCTTA YGGCTTTGAC GGTGACAACA CCCAGTTGT      450
CATGGGTTC GCTTTGATGG CTTTGCAAGG TAAGCAACCA GAAATTGGTG      500
AACAAGCTAT TATTAAGTTG ATGGACGCTA TTGATGAACA CATYCCAACC      550
CCAACCAGAG ACTTGGAACA ACCATTCTTG TTGCCAGTTG AAGATGTCTT      600
TTCTATTTCC GGTAGAGGTA CCGTCGTCAC TGGTAGAGTC GAAAGAGGTG      650
20 TCTTGAAGAA GGGTGAAGAA ATTGAAATTG TCGGTAACCT TGAAAAGCCA      700
TTCAAGACCA CCGTTACTGG TATTGAAATG TTCAAGAAGG AATTGGATGC      750
TGCTATGGCT GGTGACAAC GTGGTGTCTT GTTGAGAGGT GTCAAGAGAG      800
ACGAAATCAG CAGAGGTATG GTTTTGGCCA AGCCAGGTAC CGTCACTTCC      850
CACAAGAAGT TCTTGGCCTC CATGTACATC TTGACTGGTG AAGAAGGTGG      900
25 TCGTCGTACC CCATTCGGTG AAGGTTACAA GCCACAATGT TTCTTCAGAA      950
CCAATGACAT CACCACCACT TTCACTTTCC CAGAAGGTGA AGGTGTCGAC      1000
CACTCCCAAA TGGTTATGCC AGGTGACAAC ATCGAAATGG TTGGTGAATT      1050
GTACAAGGCT TGTCTTGGA A                                1071

```

30

2) INFORMATION FOR SEQ ID NO: 1572

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 817 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

40 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Alcaligenes faecalis* subsp. *faecalis*
 (B) STRAIN: ATCC 8750

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1572

```

TATCTTGGTT WGCTCGGCCG CTGACGGCCC AATGCCTCAG ACTCGCGAGC      50
ACATCCTGCT GAGCCGTCAG GTTGGCGTTC CTTACATCAT CGTGTTCTTG      100
50 AACAAGGCCG ACATGTTGA TGACGAAGAG CTGATCGAAC TGGTTGAAAT      150
GGAAGTTCGC GAGCTGTTGT CCAAGTACGA CTTCCCTGGC GACGACACCC      200
CGATCATCAA GGGTTCGGCC AAAGTGGCTC TGGAAGGCCA CGAAGGCCCA      250
CTGGGCAGCC AAGCCGTTCT GGCTCTGGCC GAAGCGCTGG ACAACTACAT      300

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	TCCTACGCCT	GAGCGTGCCG	TTGACGGTAC	GTTCCCTGATG	CCTGTTGAAG	350
	ACGTGTTCTC	GATCTCCGGC	CGTGGTACGG	TTGTGACCGG	TCGTATTGAG	400
	CGCGGCATCA	TCAAGGTCGG	CGAAGAAATC	GAAATCGTGG	GTATCAAAGA	450
	CACGGTCAAG	ACCATTTGTA	CCGGCGTTGA	AATGTTCCGC	AAACTGCTGG	500
5	ACCAGGGCGA	AGCTGGCGAT	AACGTCGGTC	TGCTGCTGCG	TGGTACCAAG	550
	CGTGAAGACG	TGGAACGTGG	TCAAGTTCTG	GCCAAGCCAG	GCTCGATCAA	600
	GCCACACACT	GACTTCGACG	CCGAGGTGTA	CATTCTGTCC	AAAGAAGAAG	650
	GTGGTCGTCA	CACTCCTTTC	TTCAAGGGCT	ACCGTCCTCA	GTTCTACTTC	700
	CGTACAAC TG	ACGTGACCGG	CACCATCGAG	CTGCCAGAAG	ACAAGGAAAT	750
10	GGTTCTGCCA	GGCGACAACA	TTTCGATGAA	AGTGTCCCTG	ATCGCTCCTA	800
	TCGCCATGGA	AGAAGGT				817

15 2) INFORMATION FOR SEQ ID NO: 1573

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 796 bases
 (B) TYPE: Nucleic acid
 20 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

25 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Prevotella buccalis*
 (B) STRAIN: ATCC 35310

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1573

30	TATCCTTGTA	GTTGCTGCTA	CTGATGGTCC	TATGCCACAG	ACACGTGAGC	50
	ACGTGCTTTT	GGCTCGTCAG	GTAAACGTTC	CTCGTTTGGT	TGTGTTTCATG	100
	AACAAGTGTG	ACTTGGTAGA	AGACGAAGAG	ATGCTTGAAC	TCGTTGAAAT	150
	GGAGTTGCGC	GAAC TTCTTG	AGCAATACGA	ATTCTGAAGAG	GATACTCCAA	200
35	TCGTTTCGTGG	TTCTGCACTG	GGTGCAATTGA	ATGGTGTTGA	CAAGTGGGTT	250
	GACAGCGTGA	TGACGTTGAT	GGACACTGTT	GACGAGTGGA	TTCAAGAGCC	300
	AGAGCGTGAC	CTTGACAAAC	CTTTCTTGAT	GCCAGTAGAG	GACGTGTTCT	350
	CTATCACAGG	TCGTGGTACC	GTTGTAAACAG	GACGTATTGA	GACTGGTAAG	400
	GTAAAGGTTG	GCGACGAGAT	TCAGTTGCTC	GGTCTTGGTG	AGGACAAGAA	450
40	GTCTGTTGTA	ACAGGCGTTG	AAATGTTCCG	TAAGATTCTT	TCTGAAGGTG	500
	AAGCAGGTGA	TAACGTAGGA	CTTTTGCTCC	GCGGTATCGA	TAAGGATGAA	550
	GTAAAGCGTG	GTATGGTTGT	TGTACACCCA	GGTGCCATCA	CTCCTCACGA	600
	TCACTTCAAG	GCTTCCATCT	ATGTATTGAA	GAAGGAAGAG	GGTGGACGTC	650
	ATACTCCATT	CGGAAACAAG	TATCGTCCTC	AGTTCTATCT	CCGTACAATG	700
45	GACTGTACAG	GTGAGATCAC	TTTGCCAGAA	GGCGTAGAGA	TGGTGATGCC	750
	TGGTGACAAC	G TAGAGATTG	AGGTTACCTT	GATTTACAAG	GTTGCC	796

50 2) INFORMATION FOR SEQ ID NO: 1574

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 820 bases

- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

5 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Succinivibrio dextrinosolvens*
- (B) STRAIN: ATCC 19716

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1574

	GCTATTCTAG	TAGTAGCAGC	AACTGATGGT	CCTATGCCAC	AGACCCGTGA	50
	GCACATCCTA	TTAGCACGTC	AGGTAGGCGT	ACCATACATC	ATCGTATTCC	100
15	TAAACAAGTG	CGATATGGTT	GACGACGAGG	AATTATTAGA	GTTAGTTGAG	150
	ATGGACGTAC	GTGATCTATT	AAATCAGTAC	CAGTTCCCAG	GCGACGACAC	200
	TCCAATCATC	CGTGGTTCAG	CACTAGGTGC	ATTAAACGGC	GAAGAGAAGT	250
	GGAAAGAGGC	AATCTATCAG	TTAGCAGACA	CTCTAGATTG	ATACATTCCA	300
	GAGCCAAAGC	GTGATATCGA	TGATCCATTG	CTATTACCAA	TCGAAGATAT	350
20	CTTCTCAATC	TCAGGTCGTG	GTACTGTAGT	AACCGGCCGT	GTAAGAGCGTG	400
	GTATTGTACA	CGTAGGTGAC	GAAGTTGAAA	TCGTTGGTAT	TCGTCCAACC	450
	ACCAAGACCA	CTGTAAGTGG	CGTTGAAATG	TTCCGTAAGT	TACTAGACGA	500
	AGGTCGTGCA	GGTGATAACG	TTGGTGTCTT	ACTACGTGGT	ACCAAGCGTG	550
	ATGAGGTTGA	GCGTGGTCAG	GTTCTAGCTG	CTCCAGGCAC	AATCACTCCA	600
25	CACACCAAGT	TCACTGGTCA	GGTTTACGTA	CTAAGCAAGG	ATGAAGGTGG	650
	TCGTCACTAC	CCATTCTTCA	AGGGCTACCG	TCCACAGTTC	TTCTTCCGTA	700
	CAACCGATAT	TACCGGTTCT	ATCGATCTGA	AAGAGGGCGT	AGAGATGGTA	750
	ATGCCAGGTG	ATAACACCGA	CATGACCGTA	ACCCTAATCC	ACCCAGTAGC	800
30	TATGGCTGAA	GGCGAGAGAT				820

2) INFORMATION FOR SEQ ID NO: 1575

35 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 803 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

40

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Tetragenococcus halophilus*
- (B) STRAIN: ATCC 33315

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1575

	GGTAGTGTCT	GCAGCTGACG	GCCCAATGCC	ACAAACTCGT	GAACATATCC	50
50	TATTGTCACG	TAACGTTGGT	GTACCATACA	TCGTTGTATT	CTTAAACAAA	100
	ATGGATATGG	TTGACGATGA	AGAATTACTT	GAATTAGTTG	AAATGGAAGT	150
	ACGTGATCTA	TTAACTGAAT	ACGACTTCCC	AGGTGATGAT	ACTCCTGTTA	200
	TTTCTGGTTC	AGCTTTGAAA	GCTTTAGAAG	GCGACGAAGA	ATATGAACAA	250

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AAAGTCTTAG ACTTAATGGC AGCTGTAGAT GATTTTCATCC CAACTCCTGA      300
ACGTGACCAT GACAAACCGT TCATGATGCC GATTGAAGAT GTTTTCTCAA      350
TCACTGGTCG TGGAAGTGT GCTACAGGTC GTGTTGAACG TGGAAGTATT      400
AAAGTCGGTG ATGAAGTTGA TATCATCGGT ATTCATGAAA ATGTTAAAAA      450
5  GACAACTGTT ACGGGTGTAG AAATGTTCCG TAAATTGTTG GATTACGCTG      500
AAGCTGGCGA TAACATCGGT ACATTATTGC GTGGTGTTTC TCGTGATGAT      550
ATCGAACGTG GTCAAGTGT GGCTAAACCA GGCACAATCA CACCACATAC      600
AAAATTCTCA GCTGAAGTTT ATGTATTAAC AAAAGAAGAA GGCGGACGTC      650
ATACTCCATT CTTCTCAAAC TATCGCCAC AATTTTACTT CCGTACAACT      700
10 GACATCACTG GTGTCATTGA ATTGCCAGAA GGTACTGAAA TGGTTATGCC      750
AGGTGATAAC GTAGCAATGG AAGTTGAATT AATTCACCCT GTTGCTATTG      800
AAA                                                                803

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15

2) INFORMATION FOR SEQ ID NO: 1576

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 805 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

25

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Campylobacter jejuni* subsp. *jejuni*
 (B) STRAIN: ATCC 33292

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1576

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TTAATGAAGC AATTGTTGTA AATTTTGAAA GCGAAGGAAA AAAACATAAA      50
CTTGTTTTAG AAGTAGCAGC TCATTTAGGA GATAATAGAG TTAGAAGTAT      100
TGCTATGGAT ATGACAGATG GTTTGGTAAG GGGCTTAAAA GCTGAGGCTT      150
35 TAGGTGCTCC TATTAGTGTT CCTGTTGGTG AGAAAGTTTT AGGAAGAATT      200
TTCAATGTGA CTGGAGATTT GATCGATGAA GGTGAAGAAA TTTCTTTTGA      250
TAAAAAATGG GCAATTCATA GAGATCCGCC AGCTTTTGAA GATCAAAGCA      300
CAAAAAGTGA GATTTTTGAA ACAGGGATTA AAGTTGTAGA TTTGCTTGCT      350
CCTTATGCAA AAGGTGGTAA AGTAGGTCTT TTTGGTGGTG CAGGTGTTGG      400
40 TAAACTGTT ATTATTATGG AGCTTATTCA CAATGTTGCA TTTAAGCATA      450
GCGGCTATTC TGTATTTGCA GGTGTGGGTG AGAGAACTCG TGAAGGAAAT      500
GACCTTTATA ATGAAATGAA AGAAAGTAAT GTTTTAGACA AAGTTGCTCT      550
ATGTTATGGA CAAATGAATG AACCACCAGG AGCAAGAAAT CGTATTGCTT      600
TAACAGGTTT AACAATGGCT GAGTATTTTA GAGATGAAAT GGGTCTTGAT      650
45 GTGCTTATGT TTATTGATAA TATCTTTAGA TTTTACAAT CAGGTCTCTGA      700
AATGTCAGCA CTTTLAGGAA GAATTCCATC AGCTGTGGGT TATCAACCAA      750
CCCTAGCAAG TGAAATGGGT AAATTCCAAG AAAGAATTAC TTCAACTAAA      800
AAAGG                                                                805

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50

2) INFORMATION FOR SEQ ID NO: 1577

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 809 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Campylobacter rectus*
 (B) STRAIN: ATCC 33238

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1577

```

15  ATTTACCCAA GATCAACGAA GCCGTCGAAG TAAATTTTCGA GGTGAGGGC      50
    AAGCAAAACA GACTTGTGTT AGAGGTTGCC GCACACCTTG GCGATAACCG      100
    CGTAAGAACG ATCGCTATGG ATATGAGCGA AGGCTTAACC AGAGGCCTTG      150
    AGGCTACGGC TCTTGGCGCG CCTATTAGCG TTCCGGTCGG CGAAAAAGTT      200
    TTGGGAAGGA TTTTAAACGT CGTCGGCGAT CTGATCGACG AGGGTGAAGG      250
20  CATAGAATTT GATAAAAAAT GGTCTATCCA CCGCGATCCT CCGCCGTTTG      300
    AAGAGCAAAG CACGAAGAGT GAAATTTTTG AAACGGGTAT AAAAGTGGTC      350
    GATCTTCTAG CCCCTTATGC AAAAGGCGGT AAGGTCGGAT TATTCGGCGG      400
    TGCCGGCGTC GGTAAGACGG TTATTATCAT GGAGCTTATC CACAACGTTG      450
    CATTTAAGCA TAGCGGTTAT TCCGTGTTTG CCGGCGTGGG CGAGCGAACC      500
25  CGCGAAGGAA ACGACCTTTA TCACGAGATG AAAGAGAGTA ACGTTTTGGA      550
    CAAAGTCGCC TTGTGCTACG GCCAGATGAA CGAGCCGCCG GGAGCAAGAA      600
    ACCGCATCGC TCTAACAGGC CTAACGATGG CTGAATACTT CCGCGACGAG      650
    ATGGGACTTG ACGTTTTGAT GTTTATAGAC AACATCTTCC GTTTCTCTCA      700
    GTCTGGCGCT GAGATGTCGG CGCTTCTTGG ACGTATCCCG TCAGCCGTTG      750
30  GTTATCAGCC GACTTTGGCG AGCGAAATGG GCAAATTCCA AGAGAGAATT      800
    ACATCAACC                                     809
  
```

2) INFORMATION FOR SEQ ID NO: 1578

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1671 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus casseliflavus*
 (B) STRAIN: ATCC 25788

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1578

```

50  AATCGAAGTG CAACGTTTAT TGCGTGTACT TGATGGTGCT GTAAGTGTGT      50
    TGGACTCACA ATCAGGTGTA GAACCTCAA CAGAAACAGT TTGGCGTCAA      100
    GCGACAGATT ACCGCGTACC GCGTGTGTGA TTCTGTAACA AAATGGACAA      150
  
```

	AATTGGTGCA	GACTTCTTAT	ACTCTGTATC	AACTTTACAT	GATCGTTTAC	200
	AAGCAAATGC	TCACCCAATC	CAATTACCAA	TTGGTGCGGA	AGATGACTTT	250
	ACTGGTATTA	TCGACTTAGT	AAAAATGAAA	GCTGAAATCT	ACACAAATGA	300
	CTTAGGAAC	GAAATCCAAG	AGACTGAAAT	TCCTGAAGAA	TACGTAGAAT	350
5	TAGCTGAAGA	ATGGCGCGAA	AAATTAATTG	AAGCTGTTGC	TGATACTGAT	400
	GAAGAACTAA	TGATGAAATT	CTTGGAAGGT	GAAGAAATCA	CTGAAGAAGA	450
	ATTGAAAGCT	GGTATTCGTC	AAGCAACATT	GACTGTTGAC	TTTTTCCCTG	500
	TTCTTTGCGG	ATCTGCCTTT	AAAAACAAAG	GGGTTCAATT	GATGTTGGAT	550
	GCAGTCATCG	ACTACTTGCC	TTCACCACTT	GATGTTCCCTG	CGATTAAAGG	600
10	GATCAATCCT	AAAACAGACG	AAGAACTGA	TCGTCCGGCT	GACGATGAAG	650
	CACCATTTGC	TTCATTAGCA	TTTAAAGTAA	TGACTGACCC	ATTTCGTARGT	700
	CGTTTGACAT	TCTTYCGTGT	GTATTTCARGT	ATCTTGAAC	CTGGATCATA	750
	CGTATTGAAT	GCTTCAAAAG	GCAAACGCGA	ACGTATCGGT	CGGATCCTAC	800
	AAATGCACGC	CAACACTCGT	GCTGAAATCC	AAACAGTATA	CTCAGGCGAT	850
15	ATCGCCGCTG	CTGTTGGTTT	GAAAGACACA	ACAACGGGG	ATCCACTATG	900
	TGATGAAAAA	TCCCCAGTAA	TCCTTGAATC	AATCGAATTC	CCAGAACCAG	950
	TTATCGAAGT	CGCTGTTGAG	CTTAAATCAA	AAGCTGACCA	AGATAAAATG	1000
	GGGGTTGCTT	TACAAAAACT	TGCTGAAGAA	GATCCATCAT	TCCGTGTGGA	1050
	AMCAAACGCT	GAAACAGGCG	AAACTGTTAT	CGCTGGTATG	GGAGAACTTC	1100
20	ACTTGGACGT	CTTAGTTGAC	CGTATGCGTC	GCGAATTTAA	AGTTGAAGCA	1150
	AACGTAGGTG	CGCCTCAAGT	TTCTTATCGT	GAAACATTCC	GTGCAGCAAC	1200
	ACAAGCGGAA	GGTAAATTTG	TACGTCAGTC	TGGTGGTAAA	GGTCAATACG	1250
	GTCACGTATG	GGTCGAATTT	ACACCAAACG	AAGAAGGTAA	AGGCTTCGAA	1300
	TTCGAAAACG	CGATTGTGCG	TGGTGTGGTT	CCTCGTGAAT	ACATCCCAGC	1350
25	AGTTGAAAAA	GGACTTGAAG	AATCAATGGC	GAACGGTGTC	TTAGCCGGTT	1400
	ACCCATTAGT	AGACATCAAA	GCAAAACTTT	ATGATGGTTC	ATACCATGAT	1450
	GTCGATTCAA	GTGAAACTGC	CTTCCGTGTT	GCAGCTTCTA	TGGCTTTACG	1500
	TGCTGCAGCG	AAGAAAGCAA	ACCCAGTAAT	TCTTGAACCA	ATGATGAAAG	1550
	TAGTTATCAC	TGTACCAGAA	GATTACTTAG	GTGATGTTAT	GGGTCACGTA	1600
30	ACTGCTCGTC	GTGGACGCGT	AGAAGGAATG	GAAGCACWCG	GTAAC TCACA	1650
	AATCGTGAAC	GCAATCGTGC	C			1671

35 2) INFORMATION FOR SEQ ID NO: 1579

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1662 bases
 (B) TYPE: Nucleic acid
 40 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

45 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus gallinarum*
 (B) STRAIN: ATCC 49573

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1579

50

GAAGTACAAC	GTTCACTACG	GGTTCTTGAC	GGWGCTGTAA	CAGTATTGGA	50
CTCACAATCT	GGTGTAGAAC	CACAACTGA	AACAGTTTGG	CGTCAAGCGA	100
CAGATTACCG	CGTACCACGT	ATCGTATTCT	GTAACAAAAT	GGATAAAATC	150

	GGTGCAGACT	TCTTATACTC	TGTATCTACT	TTACATGATC	GCTTGCAAGC	200
	AAATGCTCAT	CCAATCCAAT	TACCAATTGG	TGCGGAAGAT	GACTTTACTG	250
	GTATCATCGA	TCTAGTAAAA	ATGAAAGCTG	AGATCTATAC	AAACGATTTA	300
	GGAACAGAGA	TTCAAGAAAC	TGAAATTCCT	GAAGAGTACA	AAGAATTAGC	350
5	TGAAGAATGG	CGCGAAAAAT	TAGTTGAAGC	TGTTGCAGAT	ACTGACGAAG	400
	AGCTAATGAT	GAAATTCTTG	GAAGGTGAAG	AAATCACTGA	AGAAGAATTG	450
	AAAGCTGGTA	TCCGTCAAGC	GACATTGACT	GTTGAATTTT	TCCCAGTTCT	500
	TTGTGGTTCA	GCCTTCAAAA	ACAAAGGGGT	TCAATTGATG	TTGGATGCAG	550
	TCATCGACTA	CCTTCCTTCA	CCACTTGATG	TTCCTGCAAT	CAAAGGGATC	600
10	AATCCTAAAA	CTGACGAAGA	AACTGATCGT	CCTGCTGACG	ATGAAGCGCC	650
	TTTTGCTTCA	CTAGCATTTA	AAGTAATGAC	TGACCCATTC	GTAGGTCGTT	700
	TGACATTCTT	CCGTGTGTAT	TCAGGTGTCT	TGAACTCTGG	ATCATATGTC	750
	TTGAATGCTT	CAAAAGACAA	ACGCGAACGT	ATCGGTCGTA	TTCTGCAAAT	800
	GCACGCGAAC	ACTTGTGCAG	AAATCCAAAC	AGTTTATTCA	GGCGATATCG	850
15	CTGCAGCTGT	TGGTTTGAAA	GATTCCACAA	CAGGGGATAC	ATTGTGTGCG	900
	AAAAATCACC	CAGTAATCCT	TGAATCAATC	GAATTCCCAG	AMCCAGTTAT	950
	CGAAGTAGCT	GTTGAACYTA	AATCAAAAAGC	TGACCAAGAT	AAAATGGGTG	1000
	TGGCTTTACA	AAAACCTGCT	GAAGAAGATC	CTTCATTCCG	TGTAGAAMCA	1050
	AACGCTGAAA	CTGGCGAAAC	TGTTATCGCA	GGGATGGGTG	AACTTCACTT	1100
20	GGACGTCCCTT	GTTGACCGTA	TGCGTCGCGA	ATTTAAAGTT	GAAGCAAACG	1150
	TTGGTGCGCC	TCAAGTTTCT	TACCGCGAAA	CATTCCGTGC	TTCTACGCAA	1200
	GCCGAAGGTA	AATTTGTACG	TCAGTCTGGT	GGTAAAGGTC	AATACGGTCA	1250
	CGTATGGATC	GAATTTACAC	CAAACGAAGA	AGGTAAAGGC	TTCGAATTTCG	1300
	AAAACGCAAT	TGTCGGTGGT	GTGGTTCCAC	GTGAATACAT	CCCAGCAGTT	1350
25	GAAAAAGGAC	TTGAAGACTC	AATGGCTAAC	GGTGTCTAG	CTGGTTATCC	1400
	ATTGGTTGAC	ATCAAAGCCA	AGCTTTACGA	TGGTTCATAC	CATGATGTGC	1450
	ATTCAAGTGA	AACAGCCTTC	CGTGTGGCAG	CTTCAATGGC	TTTACGTGCT	1500
	GCAGCGAAGA	AAGCTAATCC	AGTGATTCTT	GAACCAATGA	TGAAAGTTGT	1550
	TATCACTGTT	CCTGAAGATT	ACTTAGGTGA	TATTATGGGA	CACGTAAGTG	1600
30	CTCGTCGTGG	ACGTGTTGAA	GGTATGGAAG	CGCATGGTAA	CTCACAAATC	1650
	GTTAACGCGA	TT				1662

35 2) INFORMATION FOR SEQ ID NO: 1580

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 1669 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

45 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus mitis*
 (B) STRAIN: ATCC 49456

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1580

50	CAATCGAAGT	ACAACGTTCT	CTTCGTGTAT	TGGATGGTGC	TGTTACCGTT	50
	CTTGACTCAC	AATCAGGTGT	TGAGCCTCAA	ACTGAAACAG	TTTGGCGTCA	100
	AGCAACTGAG	TATGGAGTTC	CACGTATCGT	ATTTGCCAAC	AAAATGGACA	150

	AAATCGGTGC	TGACTTCCTT	TACTCTGTAA	GCACACTTCA	CGATCGTCTT	200
	CAAGCAAATG	CACACCCAAT	CCAATTGCCA	ATCGGTTCTG	AAGATGACTT	250
	CCGTGGTATC	ATCGACTTGA	TCAAGATGAA	AGCTGAAATC	TATACTAACG	300
	ACCTTGGTAC	AGATATCCTT	GAAGAAGACA	TCCCAGCTGA	ATACCTTGAC	350
5	CAAGCTCAAG	AATACCGTGA	AAAATTGATC	GAAGCAGTTG	CTGAAACTGA	400
	CGAAGAATTG	ATGATGAAAT	ACCTCGAAGG	TGAAGAAATC	ACTAACGAAG	450
	AATTGAAAGC	TGGTATCCGT	AAAGCGACTA	TCAACGTTGA	ATTCTTCCCA	500
	GTATTGTGTG	GCTCTGCCTT	CAAGAACAAA	GGTGTTCAT	TGATGCTTGA	550
	TGCGGTTATT	GACTACCTTC	CAAGCCCACT	TGACATCCCA	GCGATCAAAG	600
10	GTATCAACCC	AGATWCAGAT	GAAGAAGAAA	CTCGTCCAGC	ATCTGATGAA	650
	GAGCCATTTG	CAGCTCTTGC	CTTCAAGATC	ATGACAGACC	CATTCGTAAG	700
	TCGTTTGACA	TTCTTCCGTG	TTTACTCARG	TGKTCTTCAA	TCAGGTTCAT	750
	ACGTATTGAA	CACCTCTAAA	GGKAAACGTG	AGCGTATCGG	ACGTATCCTT	800
	CAAATGCACG	CCAACAGCCG	TCAAGAAATT	GACACTGGTT	ACTCAAGAGA	850
15	TATCGCTGCT	GCCGTTGGTT	TGAAAGATAC	TCCAACGGT	GACTCATTGC	900
	CAGATGAAAA	AGCTAAAATC	ATTCTTGAGT	CAATCAACGT	TCCAGAMCCA	950
	GTTATCCAAT	TGATGGTTGA	GCCAAAATCT	AAAGCTGACC	AAGCCAAGAT	1000
	GGGTATCGCC	CTTCAAAAAT	TGGCTGAAGA	AGATCCAACA	TTCCGCGTTG	1050
	AAMCAAACGT	TGAAACTGGT	GAAMCAGTTA	TCTCTGGTAT	GGGTGAGCTT	1100
20	CACCTTGACG	TCCTTGTTGA	CCGTATGCGT	CGTGAGTTCA	AAGTTGAAGC	1150
	AAACGTAGGT	GCTCCTCAAG	TATCTTACCG	TGAAACATTC	CGCGCTTCTA	1200
	CTCAAGCACG	TGGATTCTTC	AAACGTCAGT	CTGGTGGTAA	AGGTCAATTC	1250
	GGTGATGTAT	GGATTGAATT	TACTCCAAAC	GAAGAAGGTA	AAGGATTCTGA	1300
	ATTCGAAAAC	GCAATCGTCG	GTGGTGTGGT	TCCTCGTGAA	TTTATCCAG	1350
25	CGGTTGAAAA	AGGTTTGGTA	GAATCTATGG	CTAACGGTGT	ACTTGCAGGT	1400
	TACCCAATGG	TTGACGTTAA	AGCTAAGCTT	TACGATGGTT	CATACCACGA	1450
	TGTCGACTCA	TCTGAAACTG	CCTTCAAGAT	TGCGGCTTCA	CTTGCTCTTA	1500
	AAGAAGCTGC	TAAATCAGCA	CAACCAGCTA	TCCTTGAGCC	AATGATGCTT	1550
	GTAACAATCA	CTGTTCCAGA	AGAAAACCTT	GGTGATGTTA	TGGGTCACGT	1600
30	AACTGCTCGT	CGTGGACGTG	TAGATGGTAT	GGAAGCACWC	GGTAACAGCC	1650
	AAATCGTTTCG	TGCTTACGT				1669

35 2) INFORMATION FOR SEQ ID NO: 1581

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 26 bases
 - (B) TYPE: Nucleic acid
 - 40 (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1581

AATTGGGGAC TACACCTATT ATGATG

26

50

2) INFORMATION FOR SEQ ID NO: 1582

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

5

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1582

10- GGCAAATCAG TCAGTTCAGG AGT- 23

2) INFORMATION FOR SEQ ID NO: 1583

15

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1583

25

CGATTGGCAA CAATACACTC CTG 23

30 2) INFORMATION FOR SEQ ID NO: 1584

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1584

40

TCACCTATTT TTACGCCTGG TAGGAC 26

45

2) INFORMATION FOR SEQ ID NO: 1585

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 645 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Enterococcus faecium*

5 (C) ACCESSION NUMBER: AF139725

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1585

```
10 ATGACTATAC CTGACGCAAA TGCAATCTAT CCTAACTCAG CCATCAAAGA      50
GGTTGTCTTT ATCAAGAACG TGATCAAAAG TCCCAATATT GAAATTGGGG      100
ACTACACCTA TTATGATGAC CCAGTAAATC CCACCGATTT TGAGAAACAC      150
GTTACCCATC ACTATGAATT TCTAGGCGAC AAATTAATCA TCGGTAAATT      200
TTGTTCTATC GCCAGTGGCA TTGAATTTAT CATGAACGGT GCCAACCACG      250
TAATGAAAGG TATTTGACT TATCCATTTA ATATTTTAGG TGGCGATTGG      300
15 CAACAATACA CTCCTGAACT GACTGATTG CCGTTGAAAG GTGATACTGT      350
AGTCGGAAAT GACGTGTGGT TTGGGCAAAA TGTGACCGTC CTACCAGGCG      400
TAAAAATAGG TGACGGTGCC ATTATCGGAG CAAATAGTGT TGTAACAAAA      450
GACGTCGCTC CATATACAAT TGTCGGTGGC AATCCAATTC AACTCATCGG      500
ACCAAGATTT GAACCGGAAG TTATTCAAGC ATTAGAAAAT CTGGCATGGT      550
20 GGAATAAAGA TATTGAATGG ATAACGCTA ATGTTTCCTAA ACTAATGCAA      600
ACAACACCCA CACTTGAATT GATAAACAGT TTAATGGAAA AATAA          645
```

25 2) INFORMATION FOR SEQ ID NO: 1586

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 26 bases

(B) TYPE: Nucleic acid

30 (C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1586

```
ATTCCCACAA TCTTTTTTAT CAATAA      26
```

40

2) INFORMATION FOR SEQ ID NO: 1587

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 bases

45 (B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1587

```
CATTGTTTCTG ATTCGGTAAA GTTC      24
```

2) INFORMATION FOR SEQ ID NO: 1588

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 25 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1588

GTTTTTGAAG TTAAATAGTG TTCTT

25

15

2) INFORMATION FOR SEQ ID NO: 1589

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 21 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

25 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1589

CTTCCATTTG TACTTTCCCT A

21

30

2) INFORMATION FOR SEQ ID NO: 1590

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 1920 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

40

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 45 (A) ORGANISM: Cloning vector pFW16
 (C) ACCESSION NUMBER: U50983

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1590

50 ATGAAAATTA TTAATATTGG AGTTTTAGCT CATGTTGATG CAGGAAAAAC 50
 TACCTTAACA GAAAGCTTAT TATATAACAG TGGAGCGATT ACAGAATTAG 100
 GAAGCGTGGA CAAAGGTACA ACGAGGACGG ATAATACGCT TTTAGAACGT 150
 CAGAGAGGAA TTACAATTCA GACAGGAATA ACCTCTTTTC AGTGGGAAAA 200
 TACGAAGGTG AACATCATAG ACACGCCAGG ACATATGGAT TTCTTAGCAG 250

	AAGTATATCG	TTCATTATCA	GTTTTAGATG	GGGCAATTCT	ACTGATTTCT	300
	GCAAAAGATG	GCGTACAAGC	ACAAACTCGT	ATATTATTTT	ATGCACTTAG	350
	GAAAATGGGG	ATTCCCACAA	TCTTTTTTAT	CAATAAGATT	GACCAAAATG	400
	GAATTGATTT	ATCAACGGTT	TATCAGGATA	TTAAAGAGAA	ACTTTCTGCC	450
5	GAAATTGTAA	TCAAACAGAA	GGTAGAACTG	TATCCTAATG	TGTGTGTGAC	500
	GAACCTTTACC	GAATCTGAAC	AATGGGATAC	GGTAATAGAG	GGAAACGATG	550
	ACCTTTTAGA	GAAATATATG	TCCGGTAAAT	CATTAGAAGC	ATTGGAACCTC	600
	GAACAAGAGG	AAAGCATAAG	ATTTTCAGAAT	TGTTCTCTGT	TCCCTCTTTA	650
	TCATGGAAGT	GCAAAAAGTA	ATATAGGGAT	TGATAACCTT	ATAGAAGTTA	700
10	TTACTAATAA	ATTTTATTCA	TCAACACATC	GAGGTCCGTC	TGAACTTTGC	750
	GGAAATGTTT	TCAAATTTGA	ATATACAAAA	AAAAGACAAC	GTCTTGCATA	800
	TATACGCCCT	TATAGTGGAG	TACTACATTT	ACGAGATTCG	GTTAGAGTAT	850
	CAGAAAAGGA	AAAAATAAAA	GTTACAGAAA	TGTATACTTC	AATAAATGGT	900
	GAATTATGTA	AGATTGATAG	AGCTTATTCT	GGAGAAATTG	TTATTTTGCA	950
15	AAATGAGTTT	TTGAAGTTAA	ATAGTGTTCT	TGGAGATACA	AAACTATTGC	1000
	CACAGAGAAA	AAAGATTGAA	AATCCGCACC	CTCTACTACA	AACAACCTGT	1050
	GAACCGAGTA	AACCTGAACA	GAGAGAAATG	TTGCTTGATG	CCCTTTTGGA	1100
	AATCTCAGAT	AGTGATCCGC	TTCTACGATA	TTACGTGGAT	TCTACGACAC	1150
	ATGAAATTAT	ACTTTCTTTC	TTAGGGAAAG	TACAAATGGA	AGTGATTAGT	1200
20	GCACTGTTGC	AAGAAAAGTA	TCATGTGGAG	ATAGAAATAA	CAGAGCCTAC	1250
	AGTCATTTAT	ATGGAGAGAC	CGTTAAAAAA	TGCAGAATAT	ACCATTACACA	1300
	TCGAAGTGCC	GCCAAATCCT	TTCTGGGCTT	CCATTGGTCT	ATCTGTATCA	1350
	CCGCTTCCGT	TGGGAAGTGG	AATGCAGTAT	GAGAGCTCGG	TTTCTCTTGG	1400
	ATACTTAAAT	CAATCATTTT	AAAATGCAGT	TATGGAAGGG	ATACGCTATG	1450
25	GTTGTGAACA	AGGATTGTAT	GGTTGGAATG	TGACGGACTG	TAAAATCTGT	1500
	TTTAAGTATG	GCTTATACTA	TAGCCCTGTT	AGTACCCAG	CAGATTTTTCG	1550
	GATGCTTGCT	CCTATTGTAT	TGGAACAAGT	CTTAAAAAAA	GCTGGAACAG	1600
	AATTGTTAGA	GCCATATCTT	AGTTTTTAAA	TTTATGCGCC	ACAGGAATAT	1650
	CTTTCACGAG	CATACAACGA	TGCTCCTAAA	TATTGTGCGA	ACATCGTAGA	1700
30	CACTCAATTG	AAAAATAATG	AGGTCATTCT	TAGTGGAGAA	ATCCCTGCTC	1750
	GGTGTATTCA	AGAATATCGT	AGTGATTTAA	CTTTCTTTAC	AAATGGACGT	1800
	AGTGTGTTG	TAACAGAGTT	AAAAGGGTAC	CATGTTACTA	CCGGTGAACC	1850
	TGTTTGCCAG	CCCCGTCGTC	CAAATAGTCG	GATAGATAAA	GTACGATATA	1900
	TGTTCAATAA	AATAACTTAG				1920
35						

2) INFORMATION FOR SEQ ID NO: 1591

40 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

45

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1591

50 ATGAGGTAAT AGAACGGATT

20

2) INFORMATION FOR SEQ ID NO: 1592

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 bases
(B) TYPE: Nucleic acid
5 (C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

- 10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1592

CAGTATTTCA GTAAGCGTAA A

21

15

2) INFORMATION FOR SEQ ID NO: 1593

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 36 bases
20 (B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

25

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1593

CCGAGCGATT TACCGGATAC TTGGCTGCIC GCTCGG

36

30

2) INFORMATION FOR SEQ ID NO: 1594

- (i) SEQUENCE CHARACTERISTICS:
35 (A) LENGTH: 1032 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

40 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus faecium*
(B) STRAIN: N97-330
45 (C) ACCESSION NUMBER: AF175293

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1594

ATGTTTAGAA TTAAAGTTGC AGTTCTGTTT GGGGGCTGTT CAGAGGAACA 50
50 TAATGTTTCG ATAAAATCTG CGATGGAGAT TGCCGCAAAC ATAGATACAA 100
AAAAGTATCA GCCTTATTAT ATTGGAATCA CAAAATCCGG CGTTTGGAAG 150
ATGTGTGAAA AACCTTGTTT GGAGTGGGAA CAATATGCGG GGGATCCGGT 200
TGTTTTTTCA CCGGACAGAA GTACGCATGG TCTGCTGATA CAAAAGACA 250

CTGGGTATGA AATCCAGCCT GTGGATGTGG GATTACCGAT GATTCATGGC 300
 AAGTTTGGCG AGGATGGCTC CATACAAGGC TTGCTTGAAT TGTCAGGCAT 350
 TCCGTATGTG GGATGCGATA TTCAAAGCTC CGTGACCTGC ATGGATAAGG 400
 CGCTTGCATA TACCGTTGTG AAAAATGCGG GTATCGCTGT GCCTGGGTTC 450
 5 CGGATCCTTC AGGAGGGGGA TCGCCTGGAA ACAGAGGATT TCGTATATCC 500
 CGTTTTTGTA AAGCCTGCCC GTTCCGGCTC ATCCTTTGGC GTAAACAAGG 550
 TATGCAAGGC AGAAGAAGT CAGGCAGCAA TCGAAGATGC AAGAAAATAT 600
 GACAGCAAGA TTTTGATTGA AGAGGCCGTT ACCGGGAGTG AGGTAGGCTG 650
 CGCCATACTG GGAAACGGAA ATGATCTCAT GGCTGGCGAG GTGGATCAGA 700
 10 TTGAGCTGAG ACACGGCTTT TTTAAGATTC ATCAGGAAGC ACAGCCGGAG 750
 AAAGGATCTG AAAATGCAGT CATCCGAGTT CCAGCCGCCT TACCGGATGA 800
 GGTAATAGAA CGGATTCAGA AAACAGCAAT GAAGATTTAC CGGATACTTG 850
 GCTGCAGAGG ATTGCCCCGC ATTGACCTGT TTTTGCGGGA GGACGGCTGC 900
 ATTGTGTTGA ATGAAGTGAA TACCATGCCG GGTTTTACTT CCTACAGCCG 950
 15 TTATCCCCGC ATGATGACAG CAGCCGGTTT TACGCTTACT GAAATACTGG 1000
 ATCGCTTGAT TGAACCTTCA CTTAGGAGGT AA 1032

20 2) INFORMATION FOR SEQ ID NO: 1595

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 bases
 (B) TYPE: Nucleic acid
 25 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1595

AAATAATGCT CCATCAATTT GCTGA

25

35

2) INFORMATION FOR SEQ ID NO: 1596

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases
 40 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1596

ATAGTCGAAA AAGCCATCCA CAAG

24

50

2) INFORMATION FOR SEQ ID NO: 1597

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

5

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1597

10

GATGAATTTC CGAAAATACA TGGA

24

15 2) INFORMATION FOR SEQ ID NO: 1598

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: DNA

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1598

CAGCCAATTT CTACCCCTTT CAC

23

30

2) INFORMATION FOR SEQ ID NO: 1599

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 604 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: Genomic DNA

40

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus faecalis*
 (B) STRAIN: BM4405
 (C) ACCESSION NUMBER: AF136925

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1599

CAGGGAGTAT	TTGAGTTATT	AGATATTCCA	TATGTAGGTT	GTGGTATCGG	50
AGCTGCAGCA	ATTTCCATGA	ATAAAATAAT	GCTCCATCAA	TTTGCTGAAA	100
50 TAGTTGGTGT	AAAAAGCACT	CCTAGTATGA	TTATAGAAAA	GGGACAAGAC	150
CTACAAAAAG	TCGATGAATT	TGCGAAAATA	CATGGATTTC	CTTTATATAT	200
CAAACCGAAT	GAGGCAGGCT	CATCAAAAGG	AATTAGCAAG	GTAGAACAAA	250
AAAGTGATTT	ATATAAAGCA	ATAGACGAAG	CTTCAAAATA	TGATAGCCGT	300

ATTTTAATTC AAAAGGAAGT GAAAGGGGTA GAAATTGGCT GTGGGATTTT 350
 AGGGAATGAA CAATTGCTCG TTGGAGAATG TGATCAAATT AGTCTTGTGG 400
 ATGGCTTTTT CGACTATGAA GAGAAATACA ATTTAGTAAC AGCAGAAATT 450
 TTGTTACCAG CTAAACTATC AATAGACAAA AAAGAAGACA TCCAGATAAA 500
 5 AGCAAAAAAA CTATACAGAC TATTAGGGTG CAAAGGATTA GCGAGAATCG 550
 ACTTTTTCTT AACGGATGAC GGAGAAATTT TATTAAATGA GATCAACACC 600
 CTCC 604

10

2) INFORMATION FOR SEQ ID NO: 1600

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 805 bases
 15 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

20

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Campylobacter jejuni* subsp. *doylei*
 (B) STRAIN: ATCC 49349

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1600

ACCTCAAATT AATGAAGCAA TTGTTGTAA TTTTGAAAGC GAAGGAAAAA 50
 AACATAAACT TGTTTTAGAA GTAGCAGCTC ATTTAGGAGA TAATAGAGTT 100
 AGAACTATTG CTATGGATAT GACAGATGGT TTGGTAAGGG GCTTAAAAGC 150
 30 TGAGGCTTTA GGTGCTCCTA TTAGTGTTCC TGTGGTGAG AAAGTTTTAG 200
 GAAGAATTTT CAATGTTACT GGAGATTGTA TCGATGAAGG TGAAGAAATT 250
 CCTTTTGATA AAAAATGGGC AATTCATAGA GATCCGCCAG CTTTGAAGA 300
 TCAAAGCACA AAAAGTGAGA TTTTGTAAAC AGGGATTAAA GTTGTAGATT 350
 TACTTGCTCC TTATGCAAAA GGTGGTAAAG TAGGTCTTTT TGGTGGTGCA 400
 35 GGTGTTGGTA AACTGTTAT TATTATGGAG CTTATTCACT ATGTTGCATT 450
 TAAGCATAGC GGCTATTCTG TATTTCAGG TGTGGGTGAG AGAACTCGTG 500
 AAGGAAATGA CCTTTATAAT GAAATGAAAG AAAGTAATGT TTTAGACAAA 550
 GTTGCTCTAT GTTATGGACA AATGAATGAA CCACCAGGAG CAAGAAATCG 600
 TATTGCTTTA ACAGGTTTAA CAATGGCTGA GTATTTTAGA GATGAAATGG 650
 40 GTCTTGATGT GCTTATGTTT ATTGATAATA TCTTTAGATT TTCACAATCA 700
 GGTCTGAAA TGTCAGCACT TTTAGGAAGA ATTCCATCAG CTGTGGGTTA 750
 TCAACCAACC CTAGCAAGTG AAATGGGTAA ATTCCAAGAA AGAATTACTT 800
 CAACT 805

45

2) INFORMATION FOR SEQ ID NO: 1601

(i) SEQUENCE CHARACTERISTICS:

- 50 (A) LENGTH: 826 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 5 (A) ORGANISM: *Enterococcus sulfureus*
(B) STRAIN: ATCC 49903

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1601

```

10 CTCCTTACCA GATATCAACA-ATGCGCTGGT TGTATATAAA AATGATGCCA - 50
   ATAAACAAA AGTTGTTTTA GAAGCAGCGT TAGAATTAGG TGACGGAATC 100
   ATTCGTGCGA TTGCAATGGA ATCGACTGAT GGATTGCAAC GTGGGATGGA 150
   AGTTGTCGAT ATGGGAGAAT CTATTTCTGT ACCAGTTGGA ACAGAAACTT 200
   TAGGACGTGT GTTTAATGTA TTAGGAGATA CGATTGACTT AGAAGCTCCT 250
15 TTTCTTAAAG ATGCACCGCG TAGTGGAATC CATAAAAAG CCCCTAATTT 300
   TGATGAATTA AGTACAAGCA CAGAAATTCT AGAAACAGGG ATCAAAGTCA 350
   TCGATCTATT AGCCCCCTTAT TTAAGAGGTG GTAAAGTTGG ATTGTTTGGG 400
   GGAGCCGGTG TAGGAAAAAC GGTATTGATT CAAGAGTTGA TTCACAATAT 450
   CGCACAAGAA CACGGTGGGA TTTCCGTCTT TACTGGTGTT GGTGAGCGTA 500
20 CACGTGAAGG AAACGATTG TATTATGAAA TGAAAGATTC AGGAGTCATT 550
   GAAAAACAG CGATGGTGTT TGGACAAATG AATGAGCCAC CTGGTGCACG 600
   GATGCGTGTA GCCTTGACTG GATTAACGAT TGCTGAATAT TTCCGTGATG 650
   TTGAAGGACA GGATGTACTG TTGTTTATCG ACAATATCTT CCGTTTTACA 700
   CAAGCTGGTT CTGAAGTGTG TGCCTTGTTA GGTCGTATGC CATCAGCTGT 750
25 GGGATATCAA CCAACATTAG CTACCGAAAT GGGGCAATTG CAAGAGCGGA 800
   TCACGTCAAC GAAAAAGGA TCGATC 826

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30 2) INFORMATION FOR SEQ ID NO: 1602

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 833 bases
(B) TYPE: Nucleic acid
35 (C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

40 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus solitarius*
(B) STRAIN: ATCC 49428

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1602

```

45 TGATACTTTA CCAGATATTA ATAATGCATT AGTAGTATAT AAAAAGGACG 50
   AGGACAAGAC ACGCGTTGTC TTAGAAGCCA CCTTGGAAC TGGAGATGGC 100
   ATGATTCGTG CAATCTCTAT GGGATCGACT GATGGCTTGC AACGGGGAAT 150
   GGAAGTTGTG GACACACAAG CACCTATTTC TGTTCCAGTA GGAATGAAA 200
50 CCTTAGGACG TGTTTTTAAT GTCTTAGGAG AAACGATTGA TAAACAGGCA 250
   CCGTTTCCTG AAGATGCCAA AAAAAGTGGT ATTCATAAAA AAGCACCCGC 300
   TTTTGATGAA TTAAGTACCA GTTCTGAAAT ATTGGAAACC GGGATTAAAG 350
   TAATCGATTT GCTAGCTCCT TATTTACGAG GTGGTAAAGT TGGATTATTT 400

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GGCGGTGCTG GCGTGGGTAA AACGGTATTA ATTCAAGAAT TAATTCATAA      450
CGTTGCCCAA GAACATGGGG GAATTTCTGT TTTTACGGGT GTCGGAGAGC      500
GTACTCGTGA AGGAAATGAC CTATATTATG AAATGCAGGA TTCAGGCGTT      550
ATTGAAAAAA CGGCTATGGT ATTTGGACAA ATGAACGAAC CCCCTGGTGC      600
5  ACGTATGCGT GTAGCGTTAA CTGGTTTGAC ACTTGCTGAG TACTTCCGTG      650
ATGTACAAGG TCAAGACGTA TTATTATTTA TAGATAATAT TTTCCGCTTT      700
ACTCAAGCAG GAACAGAAGT ATCTGCTTTA TTAGGACGGA TGCCGTCTGC      750
CGTTGGTTAC CAACCAACTC TAGCAACGGA AATGGGACAG TTGCAAGAAC      800
GAATCACATC GACAGATAAA GGATCAATTA CCT                          833
10

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2) INFORMATION FOR SEQ ID NO: 1603

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15  (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 806 bases
      (B) TYPE: Nucleic acid
      (C) STRANDEDNESS: Double
      (D) TOPOLOGY: Linear
20
      (ii) MOLECULE TYPE: Genomic DNA

      (vi) ORIGINAL SOURCE:
          (A) ORGANISM: Campylobacter sputorum subsp. sputorum
25  (B) STRAIN: ATCC 35980

```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1603

```

ATCAGCCTAA AATTAACGAA GCAATAGAAG TTAATTATGA ATTAGATGGT      50
30  AAAAAAATAA GACTTATTCT TGAAGTAGCT GGACATCTTG GCGATAATAG      100
AGCAAGAACC ATTGCTATGG ATATGAGTGA TGGTTTACAA AGAGGATTAG      150
AAGTTACGGC TCTTGGTGCT CCTATAACAG TTCCTGTTGG AGATAAAGTT      200
TTAGGTAGAA TGTTTAATGT TGTAGGTGAC TTAATAGATG AAGGTGAAGT      250
AACAGATTTT GATAAAAGAT GGGCTATCCA TAGAGATCCT CCTTCGTTTG      300
35  AAGATCAAAG TACAAAAAGT GAAATTTTGG AAACAGGTAT AAAAGTAGTT      350
GATCTTCTTG CACCTTATGC AAAAGGTGGT AAAGTTGGCT TATTTGGTGG      400
TGCTGGCGTT GGAAAAACAG TTATCATAAT GGAGCTTATA CATAATGTTG      450
CATTTAAACA CAGCGGTAT TCAATTTTGG CCGGTGTTGG AGAGAGAACA      500
AGAGAGGGAA ATGATCTTTA TAATGAGATG AAAGAGTCTG GTGTTTTGGA      550
40  TAAAGTTGCC TTATGTTATG GACAAATGAA TGAACCACCA GGAGCAAGAA      600
ACCGTATAGC ATTAACAGGT CTTACAATGG CTGAATATTT CCGTGATGAA      650
ATGGGGCTTG ATGTGTTGAT GTTTATAGAT AATATTTTGA GATTTTCTCA      700
ATCAGGTTCT GAAATGTCAG CGCTGCTTGG TAGAATTCCA TCTGCTGTTG      750
GTTATCAACC AACATTAGCA AGTGAGATGG GAAAACTTCA AGAAAGAATT      800
45  ACTTCC                          806

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2) INFORMATION FOR SEQ ID NO: 1604

```

50  (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 738 bases
      (B) TYPE: Nucleic acid

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(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

5

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Enterococcus pseudoavium*

(B) STRAIN: ATCC 49372

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1604

	GGTGTATCC	GCACAATCGC	TATGGAATCT	ACAGATGGAT	TGCAACGGGG	50
	GATGGAAGTT	GTCGATACCG	GCAAACCAAT	CTCTGTTCTT	GATAGGTAAAG	100
	AAACATTAGG	TCGTGTGTTT	AACGTATTAG	GTGAAACGAT	CGACAAAGAA	150
15	GCACCTTTTC	CAGAAGATGT	AGAAAAGAGC	GGTATTACAC	AAAAGGCCCC	200
	CGCTTTTGAA	GACCTTAGCA	CCAGTAATGA	GATTTTAGAA	ACTGGGATCA	250
	AGGTTATCGA	CTTATTAGCC	CCTTACTTAA	AAGGTGGTAA	AGTTGGACTA	300
	TTCGGTGGTG	CCGGTGTGTT	TAAAACCGTC	TTAATTCAAG	AACTGATTCA	350
	TAATATCGCC	CAAGAACACG	GTGGGATTTT	TGTCTTTACC	GGGGTTGGGG	400
20	AACGGACTCG	TGAAGGGAAC	GACCTTTATT	ATGAAATGAA	AGAATCCGGC	450
	GTTATTGAAA	AAACAGCGAT	GGTCTTCGGA	CAAATGAATG	AGCCACCAGG	500
	TGCGCGGATG	CGCGTTGCCT	TGACTGGTTT	GACATTAGCT	GAATATTTCC	550
	GTGATGAAGA	AGGTCAAGAT	GTGTTGCTAT	TTATCGATAA	CATTTTCCGC	600
	TTCACACAAG	CCGGATCAGA	AGTTTCGGCG	CTATTAGGTC	GGATGCCATC	650
25	TGCCGTTGGT	TATCAACCAA	CCTTGGCAAC	AGAAATGGGT	CAATTACAAG	700
	AACGAATCAC	TTCAACGAAA	AAAGGCTCAA	TTACATCG		738

30 2) INFORMATION FOR SEQ ID NO: 1605

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 bases

(B) TYPE: Nucleic acid

35 (C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1605

ATYATYGAAR TITAYGCICC

20

45

2) INFORMATION FOR SEQ ID NO: 1606

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 bases

50 (B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1606

5 CCRAACATIA YICCIAC TTT TTC

23

2) INFORMATION FOR SEQ ID NO: 1607

10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 336 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

15

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

20

- (A) ORGANISM: *Klebsiella ornithinolytica*
- (B) STRAIN: ATCC 31898

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1607

25	CTGGATTATG CGATGTCGGT CATTGTTGGC CGTGCGCTGC CGGATGTCCG	50
	AGATGGCCTG AAACCGGTAC ACCGTCGCGT ACTTTACGCC ATGAACGTAT	100
	TGGGCAATGA CTGGAACAAA GCCTATAAAA AATCCGCCCG TGTCGTTGGT	150
	GACGTAATCG GTAAATACCA CCCTCATGGT GATACGCCCG TTTATGACAC	200
	CATTGTACGT ATGGCACAGC CATTCTCCTT GCGTTATATG CTGGTCGATG	250
30	GCCAGGGTAA CTTCCGTTCT GTCGATGGCG ACTCCGCCCG AGCGATGCGT	300
	TATACGGAAA TCCGTATGTC GAAAATCGCC CACGAG	336

35 2) INFORMATION FOR SEQ ID NO: 1608

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 341 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

40

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

45

- (A) ORGANISM: *Klebsiella oxytoca*
- (B) STRAIN: ATCC 13182

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1608

50

CTATCTGGAT TATGCGATGT CGGTCATTGT TGGCCGTGCG CTGCCGGATG	50
TCCGAGATGG CCTGAAGCCG GTACACCGTC GCGTACTATA CGCCATGAAC	100
GTATTGGGCA ATGACTGGAA CAAAGCCTAT AAAAAATCTG CCCGTGTCGT	150

GGGTGACGTC ATCGGTAAAT ACCACCCTCA TGGTGATACT GCCGTATACG 200
 ACACCATTGT ACGTATGGCG CAGCCATTCT CCCTGCGTTA CATGCTGGTA 250
 GATGGCCAGG GTAACCTTGG TTCGGTCGAC GGCGACTCCG CCGCAGCGAT 300
 GCGTTATACG GAAATCCGTA TGTCGAAGAT CGCCCATGAA C 341

5

2) INFORMATION FOR SEQ ID NO: 1609

- 10 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 22 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

15

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1609

20 GCCCTGATCC AAATAGCATA TA

22

2) INFORMATION FOR SEQ ID NO: 1610

25

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 23 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

30

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1610

35

CCTGGCATAA CAGTAACATT CTG

23

40 2) INFORMATION FOR SEQ ID NO: 1611

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 22 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

45

(ii) MOLECULE TYPE: DNA

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1611

TGGGAAAAAG CAACTCCATC TC

22

2) INFORMATION FOR SEQ ID NO: 1612

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 23 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1612

ACAACTGAAT TCGCAGCAAC AAT

23

15

2) INFORMATION FOR SEQ ID NO: 1613

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 639 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus aureus*
 (C) ACCESSION NUMBER: U19459

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1613

	ATGAAATATG GCCCTGATCC AAATAGCATA TATCCACATG AAGAAATAAA	50
	AAGTGTGTTGT TTTATTAAAA ATACAATTAC CAATCCAAAT ATTATAGTTG	100
35	GAGATTATAC TTACTATTCC GATGTTAACG GAGCTGAAAA ATTTGAAGAA	150
	CATGTGACAC ATCATTATGA ATTTAGGGGT GATAAACTTG TAATTGGCAA	200
	GTTTTGTGCA ATAGCTGAAG GTATAGAATT TATTATGAAT GGAGCAAACC	250
	ATAGAATGAA TTCAATAACA ACTTATCCTT TTAATATAAT GGGAAATGGT	300
	TGGGAAAAAG CAACTCCATC TCTTGAAGAT TTACCATTTA AGGGAGATAC	350
40	TGTTGTTGGA AATGATGTGT GGATTGGTCA GAATGTTACT GTTATGCCAG	400
	GAATTCAAAT AGGAGATGGA GCAATTGTTG CTGCGAATTC AGTTGTTACA	450
	AAAGATGTAC CACCATATCG TATTATTGGT GGAAATCCGA GTAGAATTAT	500
	AAAGAAAAGG TTTGAAGATG AATTGATAGA TTATTTATTG CAAATAAAAT	550
	GGTGGGATTG GTCAGCACAA AAAATATTTT CTAATCTTGA AACACTTTGT	600
45	AGCTCTGATT TAGAGAAAAT AAAATCTATT CGAGATTAG	639

2) INFORMATION FOR SEQ ID NO: 1614

50

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
 (B) TYPE: Nucleic acid

- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1614

CCAATCCAGA AGAAATATAC CC

22

10

2) INFORMATION FOR SEQ ID NO: 1615

(i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 24 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1615

ATTAGTTTAT CCCCAATCAA TTCA

24

25

2) INFORMATION FOR SEQ ID NO: 1616

(i) SEQUENCE CHARACTERISTICS:

30

- (A) LENGTH: 26 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1616

ATAATGAATG GGGCTAATCA TCGTAT

26

40

2) INFORMATION FOR SEQ ID NO: 1617

(i) SEQUENCE CHARACTERISTICS:

45

- (A) LENGTH: 24 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1617

GCCAACAACT GAATAAGGAT CAAC

24

5

2) INFORMATION FOR SEQ ID NO: 1618

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 639 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

15 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus cohnii*
 (C) ACCESSION NUMBER: AF015628

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1618

	ATGAAATGGC	AAAATCAGCA	AGGCCCCAAT	CCAGAAGAAA	TATACCCTAT	50
	AGAAGGTAAT	AAACATGTTC	AATTTATTAA	ACCATCTATA	ACAAAGCCCA	100
25	ATATTTTAGT	TGGGGAATAT	TCATATTACG	ATAGTAAAGA	TGGTGAATCT	150
	TTTGAAAGCC	AAGTTCTTTA	TCACTATGAA	TTGATTGGGG	ATAAACTAAT	200
	ATTAGGGAAG	TTTTGTTCTA	TTGGACCCGG	AACGACATTT	ATAATGAATG	250
	GGGCTAATCA	TCGTATGGAT	GGTTCAACAT	TTCCATTCAA	TCTTTTCGGA	300
	AATGGTTGGG	AGAAGCATAC	CCCTACATTG	GAAGACCTTC	CTTATAAGGG	350
30	TAACACGGAA	ATTGGGAACG	ATGTTTGGAT	TGGACGAGAT	GTGACAATTA	400
	TGCCCCGGTGT	AAAAATAGGA	AACGGGGCTA	TTATTGCAGC	AAAATCGGTT	450
	GTGACAAAGA	ACGTTGATCC	TTATTCAAGT	GTTGGCGGTA	ATCCTTCACG	500
	ATTAATTAAG	ATAAGGTTT	CCAAGGAAAA	AATCGCAGCA	TTACTAAAAG	550
	TAAGGTGGTG	GGACCTAGAG	ATAGAGACGA	TAAATGAAAA	TATTGATTGC	600
35	ATCCTGAATG	GTGATATAAA	AAAGGTTAAA	AGAAGTTAG		639

2) INFORMATION FOR SEQ ID NO: 1619

40

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 45 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1619

50

AAGGCAAAAT AAAAGGAGCA AAGC

24

2) INFORMATION FOR SEQ ID NO: 1620

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 23 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1620

TGTACCCGAG ACATCTTCAC CAC

23

15

2) INFORMATION FOR SEQ ID NO: 1621

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 26 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

25 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1621

AATTGAAGGA CGGGTATTGT GGAAAG

26

30

2) INFORMATION FOR SEQ ID NO: 1622

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 26 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

40

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1622

45 CGATTTTGAC AGATGGCGAT AATGAA

26

2) INFORMATION FOR SEQ ID NO: 1623

50

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1569 bases
(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

5

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Staphylococcus aureus*

(C) ACCESSION NUMBER: M90056

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1623

	ATGAAAATAA	TGTTAGAGGG	ACTTAATATA	AAACATTATG	TTCAAGATCG	50
	TTTATTGTTG	AACATAAATC	GCCTAAAGAT	TTATCAGAAT	GATCGTATTG	100
	GTTTAATTGG	TAAAAATGGA	AGTGGAAAAA	CAACGTTACT	TCACATATTA	150
15	TATAAAAAAA	TTGTGCCTGA	AGAAGGTATT	GTAAAACAAT	TTTCACATTG	200
	TGAACTTATT	CCTCAATTGA	AGCTCATAGA	ATCAACTAAA	AGTGGTGGTG	250
	AAGTAACACG	AAACTATATT	CGGCAAGCGC	TTGATAAAAA	TCCAGAAGCTG	300
	CTATTAGCAG	ATGAACCAAC	AACTAACTTA	GATAATAACT	ATATAGAAAA	350
	ATTAGAACAG	GATTTAAAAA	ATTGGCATGG	AGCATTATTT	ATAGTTTCAC	400
20	ATGATCGCGC	TTTTTTAGAT	AACTTGTGTA	CTACTATATG	GGAAATTGAC	450
	GAGGGAAGAA	TAAGTGAATA	TAAGGGGAAT	TATAGTAACT	ATGTTGAACA	500
	AAAAGAATTA	GAAAGACATC	GAGAAGAATT	AGAATATGAA	AAATATGAAA	550
	AAGAAAAGAA	ACGATTGGAA	AAAGCTATAA	ATATAAAAGA	ACAGAAAGCT	600
	CAACGAGCAA	CTAAAAAACC	GAAAAACTTA	AGTTTATCTG	AAGGCAAAAT	650
25	AAAAGGAGCA	AAGCCATACT	TTGCAGGTAA	GCAAAAAGAAG	TTACGAAAAA	700
	CTGTAAAATC	TCTAGAAACC	AGACTAGAAA	AACTTGAAAG	CGTCGAAAAG	750
	AGAAACGAAC	TTCCTCCACT	TAAAATGGAT	TTAGTGAAGT	TAGAAAGTGT	800
	AAAAAATAGA	ACTATAATAC	GTGGTGAAGA	TGTCTCGGGT	ACAATTGAAG	850
	GACGGGTATT	GTGGAAAGCA	AAAAGTTTTA	GTATTCGCGG	AGGAGACAAG	900
30	ATGGCAATTA	TCGGATCTAA	TGGTACAGGA	AAGACAACGT	TTATTAAAAA	950
	AATTGTGCAT	GGGAATCCTG	GTATTTTCATT	ATCGCCATCT	GTCAAAATCG	1000
	GTTATTTTAT	CCAAAAAATA	GATACATTAG	AATTAGATAA	GAGCATTTTA	1050
	GAAAATGTTC	AATCTTCTTC	ACAACAAAAT	GAAACTCTTA	TTCGAACTAT	1100
	TCTAGCTAGA	ATGCATTTT	TTAGAGATGA	TGTTTATAAA	CCAATAAGTG	1150
35	TCTTAAGTGG	TGGAGAGCGA	GTAAAGTAG	CACTAACTAA	AGTATTCTTA	1200
	AGTGAAGTTA	ATACGTTGGT	ACTAGATGAA	CCAACAACT	TTCTTGATAT	1250
	GGAAGCTATA	GAGGCGTTTG	AATCTTTGTT	AAAGGAATAT	AATGGCAGTA	1300
	TAATCTTTGT	ATCTCACGAT	CGTAAATTTA	TCGAAAAAGT	AGCCACTCGA	1350
	ATAATGACAA	TTGATAATAA	AGAAATAAAA	ATATTTGATG	GCACATATGA	1400
40	ACAATTTAAA	CAAGCTGAAA	AGCCAACAAG	GAATATTAAA	GAAGATAAAA	1450
	AACTTTTACT	TGAGACAAAA	ATTACAGAAG	TACTCAGTCG	ATTGAGTATT	1500
	GAACCTTCGG	AAGAATTAGA	ACAAGAGTTT	CAAAACTTAA	TAAATGAAAA	1550
	AAGAAATTTG	GATAAATAA				1569

45

2) INFORMATION FOR SEQ ID NO: 1624

(i) SEQUENCE CHARACTERISTICS:

50

(A) LENGTH: 26 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1624

5

TTCTTTAATG CTCGTAGATG AACCTA

26

10 2) INFORMATION FOR SEQ ID NO: 1625

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 25 bases

(B) TYPE: Nucleic acid

15 (C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1625

TTTTCGTATT CTTCTTGTTG CTTTC

25

25

2) INFORMATION FOR SEQ ID NO: 1626

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 26 bases

30 (B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1626

AGGAATGATT AAGCCCCCTT CAAAAA

26

40

2) INFORMATION FOR SEQ ID NO: 1627

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 26 bases

45 (B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

50 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1627

TTACATTGCG ACCATGAAAT TGCTCT

26

2) INFORMATION FOR SEQ ID NO: 1628

5

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1658 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

10

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus aureus*
(C) ACCESSION NUMBER: U82085

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1628

20	ATGCTTAAAA	TCGACATGAA	GAATGTAAAA	AAATATTATG	CAGATAAATT	50
	AATTTTAAAT	ATAAAAGAAC	TAAAGATTTA	TAGTGGGGAT	AAAAATAGGTA	100
	TTGTAGGTAA	GAATGGAGTT	GGCAAAACAA	CACCTTTTAA	AATAATAAAA	150
	GGACTAATAG	AGATTGACGA	AGGAAATATA	ATTATAAGTG	AAAAACAAC	200
	TATTAAATAT	ATCTCTCAAT	TAGAAGAACC	ACATAGTAAG	ATAATTGATG	250
25	GAAAATATGC	TTCAATATTT	CAAGTTGAAA	ATAAGTGGAA	TGACAATATG	300
	AGTGGTGGTG	AAAAAACTAG	ATTTAAACTA	GCAGAGGGAT	TTCAAGATCA	350
	ATGTTCTTTA	ATGCTCGTAG	ATGAACCTAC	AAGTAATTTA	GATATCGAAG	400
	GAATAGAGTT	GATAACAAAT	ACTTTTAAAG	AGTACCGTGA	TACTTTTTTG	450
	GTAGTATCTC	ATGATAGAAT	TTTTTTAGAT	CAAGTTTGTA	CAAAAATTTT	500
30	TGAAATTGAA	AATGGATATA	TTAGAGAATT	CATCGGTAAT	TATACAAACT	550
	ATATAGAGCA	AAAAGAAATG	CTTCTACGAA	AGCAACAAGA	AGAATACGAA	600
	AAGTATAATT	CTAAAAGAAA	GCAATTGGAG	CAAGCTATAA	AGCTAAAAGA	650
	GAATAAGGCG	CAAGGAATGA	TTAAGCCCCC	TTCAAAAACA	ATGGGAACAT	700
	CTGAATCTAG	AATATGGAAA	ATGCAACATG	CTACTAAACA	AAAAAAGATG	750
35	CATAGAAATA	CGAAATCGTT	GGAAACACGA	ATAGATAAAT	TAAATCATGT	800
	AGAAAAAATA	AAAGAGCTTC	CTTCTATTAA	AATGGATTTA	CCTAATAGAG	850
	AGCAATTTCA	TGGTCGCAAT	GTAATTAGTT	TAAAAAACTT	ATCTATAAAA	900
	TTTAATAATC	AATTTCTTTG	GAGAGATGCT	TCATTTGTCA	TTAAAGGTGG	950
	AGAAAAGGTT	GCTATAATTG	GTAACAATGG	TGTAGGAAAA	ACAACATTGT	1000
40	TGAAGCTGAT	TCTAGAAAAA	GTAGAATCAG	TAATAATATC	ACCATCAGTT	1050
	AAAATTGGAT	ACGTCAGTCA	AAACTTAGAT	GTTCTACAAT	CTCATAAATC	1100
	TATCTTAGAA	AATGTTATGT	CTACCTCCAT	TCAAGATGAA	ACAATAGCAA	1150
	GAATTGTTCT	AGCAAGATTA	CATTTTTTATC	GCAATGATGT	TCATAAAGAA	1200
	ATAAATGTTT	TGAGTGGTGG	AGAACAAATA	AAGGTTGCTT	TTGCCAAGCT	1250
45	ATTTGTTAGC	GATTGTAATA	CATTAAATCT	TGATGAACCA	ACAAACTATT	1300
	TGGATATCGA	TGCTGTTGAG	GCATTAGAAG	AATTGTTAAT	TACCTATGAA	1350
	GGTGTGTGT	TATTTGCTTC	CCATGATAAA	AAATTTATAC	AAAACCTAGC	1400
	TGAACAATTG	TTAATAATAG	AAAATAATAA	AGTGAAAAAA	TTCGAAGGAA	1450
	CATATATAGA	ATATTTAAAA	ATTAAAGATA	AACCAAAATT	AAATACAAAT	1500
50	GAAAAAGAAC	TCAAAGAAAA	AAAGATGATA	CTAGAAATGC	AAATTTTCATC	1550
	ATTATTAAGT	AAAATCTCAA	TGGAAGAAAA	TGAAGAAAAA	AACAAAGAAT	1600
	TAGATGAAAA	GTACAAATTG	AAATTAAAAG	AATTGAAAAG	CCTAAATAAA	1650
	AATATTTA					1658

2) INFORMATION FOR SEQ ID NO: 1629

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 26 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1629

AAGGGGAAAG TTTGGATTAC ACAACA

26

15

2) INFORMATION FOR SEQ ID NO: 1630

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 24 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1630

GAACCACAGG GCATTATCAG AACC

24

30

2) INFORMATION FOR SEQ ID NO: 1631

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 21 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

40

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1631

45 CGACGATGCT TTATGGTTTG T

21

2) INFORMATION FOR SEQ ID NO: 1632

50

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 bases
(B) TYPE: Nucleic acid

- (C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1632

GTTAATTTGC CTATCTTGTC ACACTC

26

10

2) INFORMATION FOR SEQ ID NO: 1633

(i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 900 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

20

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus aureus*
(C) ACCESSION NUMBER: M36022

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1633

ATGGAATTTA AATTACAAGA ATTAAATCTT ACTAACCAAG ATACAGGACC 50
ATATGGTATA ACCGTTTCAG ATAAGGGGAA AGTTTGGATT ACACAACATA 100
AAGCAAATAT GATAAGTTGC ATCAATTTAG ATGGAAAAAT TACAGAGTAC 150
30 CCACTACCGA CACCAGATGC AAAAGTCATG TGTTTAACTA TATCCTCAGA 200
TGGGGAAGTT TGGTTTACTG AGAATGCAGC AAACAAAATA GGGAGGATTA 250
CAAAAAAAGG GATTATTAAG GAATATACAT TGCCTAACCC AGATTCAGCA 300
CCCTACGGTA TTACAGAAGG ACCAAATGGA GATATATGGT TTACAGAAAT 350
GAATGGCAAC CGTATTGGAC GTATTACGGA CGACGGTAAA ATTCGTGAAT 400
35 ACGAGCTGCC TAATAAAGGA TCTTACCCTT CTTTTATCAC TTTGGGTTCT 450
GATAATGCCC TGTGGTTCAC AGAAAAATCAA AATAATGCTA TTGGTAGAAT 500
TACAGAAAGT GGGGATATTA CAGAGTTTAA AATTCCTACA CCTGCATCAG 550
GACCAGTTGG TATTACAAAG GGAACGACG ATGCTTTATG GTTTGTGGAA 600
ATTATCGGTA ATAAGATAGG GCGAATAACT CCTCTGGGGG AAATTACCGA 650
40 ATTCAAAATT CCAACGCCAA ACGCTCGACC TCATGCAATT ACTGCTGGAG 700
CAGGAATTGA TTTATGGTTT ACTGAATGGG GGGCTAATAA AATAGGAAGG 750
CTGACAAGCA ATAATATAAT TGAGGAATAC CCAATTCAA TCAAAAGTGG 800
TGAACCACAT GGCATTTGTT TCGATGGTGA AACAATTTGG TTTGCAATGG 850
AGTGTGACAA GATAGGCAAA TTAACCTCTCA TTAAGGATAA TATGGAGTGA 900
45

2) INFORMATION FOR SEQ ID NO: 1634

50

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1634

TTAACTTGTC TATTCCCGAT TCAGG

25

10

2) INFORMATION FOR SEQ ID NO: 1635

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 23 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1635

GCTGTGGCAA TGGATATTCT GTA

23

25

2) INFORMATION FOR SEQ ID NO: 1636

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 24 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

35 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1636

TTCCTACCCC TGATGCTAAA GTGA

24

40

2) INFORMATION FOR SEQ ID NO: 1637

(i) SEQUENCE CHARACTERISTICS:

- 45 (A) LENGTH: 23 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1637

CAAAGTGCGT TATCCGAACC TAA

23

5

2) INFORMATION FOR SEQ ID NO: 1638

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 527 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

15

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Aspergillus fumigatus*
 (B) STRAIN: WSA-172

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1638

GGTGGGGAAG ACTGTCTTCA TCCAGGAATT GATTGTGAGT CGTTCCACAT 50
 GCTCACCTAG TTTTCGCTCG ATCTTTTCAC TAACGCAAAC CATGTAGAAC 100
 AACATTGCCA AGGCCCACGG TGGTTACTCC GTCTTCACTG GTGTTGGTGA 150
 25 GCGTACTCGT GAGGGTAACG ATCTGTACCA CGAAATGCAG GAGACTGGTG 200
 TCATTACAGCT CGAGGGTGAA TCCAAGGTCG CACTGGTGTT CGGACAGATG 250
 AACGAGCCCC CCGGTGCCCC TGCCCGTGTC GCCCTTACCG GTCTGACCAT 300
 TGCCGAGTAC TTCCGTGACG AGGAGGGTCA GGACGTGCTG CTCTTCATTG 350
 ACAACATTTT CCGTTTCACC CAGGCCGGTT CTGAGGTGTC TGCCCTTCTC 400
 30 GGTCGTATCC CCTCTGCCGT CGGTTACCAG CCCACCCTGG CCGTCGACAT 450
 GGGTGGTATG CAGGAGCGTA TCACCACCAC CAAGAAGGGT TCTATTACCT 500
 CCGTCCARGC CGTCTACGTC CCCGCGA 527

35

2) INFORMATION FOR SEQ ID NO: 1639

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 452 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

45

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Aspergillus fumigatus*
 (B) STRAIN: ATCC 64746

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1639

ACTGTCTTGA TTCAAGAACT TATTAACAAC ATTGCTAAAG CCCATGGTGG 50
 TTACTCTATT TTCTGTGGTG TTGGTGAACG TACTCGTGAA GGTAACGATT 100

TATACCACGA AATGATGGAA ACTGGTGTCA TTAAACTTGA AGGTGACTCC 150
 AAGTGTGCTC TTGTATTCGG TCAAATGAAC GAACCTCCTG GTGCTCGTGC 200
 CCGTGTTGCT TTAAGTGGTT TAACCATGTC TGAATACTTC CGTGATGAAG 250
 AAGGTCAAGA TGTGTTACTT TTCATTGATA ACATTTTCCG TTTCAC TCAA 300
 5 GCTGGTTCTG AAGTATCTGC CCTTTTAGGT CGTATTCCAT CTGCTGTAGG 350
 TTACCAACCC ACTTTATCTA CTGATATGGG TGGTATGCAA GAACGTATTA 400
 CTACTACCAA GAATGGTTCC ATTACCTCTG TACARGCCGT CTACGTCCCC 450
 GC 452

10

2) INFORMATION FOR SEQ ID NO: 1640

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 783 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

20 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacillus mycoides*
 (B) STRAIN: ATCC 6462
 25 (C) ACCESSION NUMBER:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1640

ACGCCCTTAC GGTAACACAA AGCAACGAAA ACGGAAGCAT GAACTTAACA 50
 30 TTTGAAGTTG CACTTCATTT AGGTGATGAT ACAGTTCGTA CAGTTGCGAT 100
 GTCTTCCACA GATGGACTTG TTCGTGGCAC AGAAGTAGAA GATACTGGTA 150
 AAGCAATCTC TGTACCAGTT GGTGATGCAA CACTTGGTCG TGTATTCAAC 200
 GTATTAGGTG ATGCAATTGA CTTAGATGGT GAACTTCCTG CGGATGTACA 250
 CCGTGATCCA ATTCACCGTC AAGCACCTGC ATTCTGAAGAA TTATCTACTA 300
 35 AAGTAGAAAT TCTTGAAACT GGTATTAAAG TAGTAGACTT ACTTGCTCCT 350
 TACATTAAGG GTGGTAAGAT CGGCCTATTC GGTGGTGCCG GCGTAGGTAA 400
 AACAGTATTA ATTCAAGAAT TAATTAACAA CATCGCACAA GAGCACGGTG 450
 GTATCTCTGT ATTCGCTGGT GTAGGTGAGC GTACTCGTGA GGGTAATGAC 500
 TTATACCATG AAATGAGCGA TTCTGGCGTA ATCAAGAAAA CTGCGATGGT 550
 40 ATTCGGACAA ATGAATGAGC CACCTGGAGC ACGTCAACGT GTTGCAATTAA 600
 CAGGTTTAAC AATGGCTGAG CATTTCCGTG ATGAGCAAGG ACAAGACGTA 650
 CTTCTGTTCA TCGATAACAT CTTCCGTTTC ACGCAAGCGG GTTCTGAAGT 700
 ATCTGCCCTT CTTGGTCGTA TGCCATCTGC GGTAGGTTAC CAACCAACAC 750
 TTGCAACAGA AATGGGTCAA TTACAAGAGC GTA 783

45

2) INFORMATION FOR SEQ ID NO: 1641

50 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 823 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

5 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Bacillus mycoides*

(B) STRAIN: NRRL NRS-319

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1641

10
 ATCTACAACG CCCTTACGGT AAAACAAAGC AACGAAAACG GAGCAAGCAT 50
 TAACTTAACA TTTGAAGTTG CACTTCATTT AGGTGATGAC ACAGTTCGTA 100
 CAGTTGCAAT GTCTTCCACA GATGGACTTG TTCGTGGCAC AGAAGTAGAA 150
 GATACTGGTA AAGCAATCTC TGTACCAGTT GGTGATGCAA CACTTGGTCG 200
 15 TGTATTCAAC GTATTAGGTG ATGCAATTGA CTTAGATGGT GATGTTCTCTG 250
 CGGATGTACG TCGTGATCCA ATTCACCGTC AAGCACCTGC ATTCGAAGAA 300
 CTATCTACTA AAGTAGAAAT TCTTGAAACT GGTATTAAAG TAGTAGACTT 350
 ACTTGCTCCT TACATTAAGG GTGGTAAGAT CGGTCTATTC GGTGGTGCCG 400
 GTGTAGGTAA AACAGTATTA ATTCAGGAAT TAATTAACAA CATCGCACAA 450
 20 GAACACGGTG GTATCTCTGT ATTCGCTGGT GTAGGTGAGC GTACTCGTGA 500
 GGGTAACGAC TTATACCATG AAATGAGCGA TTCTGGCGTA ATTAAGAAAA 550
 CTGCGATGGT ATTCGACAA ATGAATGAGC CACCTGGAGC ACGTCAACGT 600
 GTTGCAATTAA CAGGTTTAAC AATGGCTGAA CATTTCCGTG ATGAGCAAGG 650
 ACAAGACGTA CTATTGTTCA TCGATAACAT CTTCCGTTTC ACGCAAGCAG 700
 25 GTTCTGAAGT ATCTGCCCTT CTTGGTCGTA TGCCATCTGC GGTAGGTTAC 750
 CAACCAACAC TTGCAACAGA AATGGGTCAA TTACAAGAGC GTATTACATC 800
 TACAAATAAA GGATCTATCA CGT 823

30

2) INFORMATION FOR SEQ ID NO: 1642

(i) SEQUENCE CHARACTERISTICS:

35 (A) LENGTH: 829 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

40

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Bacillus mycoides*

(B) STRAIN: NRRL BD-15

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1642

50 GATGGCGGAA AGCTACCAGA AATCTACAAC GCCCTTACGG TAAAACAAAG 50
 CAACGAAAAC GGAGCAAACA TTAAGTTAAC ATTTGAAGTT GCACTTCATT 100
 TAGGTGATGA TACAGTTCGT ACAGTTGCGA TGTCTTCCAC AGATGGACTT 150
 GTTCGTGGCA CAGAAGTAGA AGATACTGGT AAAGCAATCT CTGTACCAGT 200
 TGGTGATGTA AACTTGGTC GTGTATTCAA CGTATTAGGT GATGCAATTG 250
 ACTTAGATGG TGAAGTTCCT GCGGATGTAC GTCGTGATCC AATTCACCGT 300
 CAAGCACCTG CATTCGAAGA ATTATCTACT AAAGTAGAAA TTCTTGAAAC 350

	TGGTATTAAA	GTAGTAGACT	TACTTGCTCC	TTACATTAAG	GGTGGTAAGA	400
	TTGGTCTATT	CGGTGGTGCC	GGTGTAGGTA	AAACAGTATT	AATTCAGGAA	450
	TTAATTAACA	ACATCGCACA	AGAACACGGT	GGTATCTCTG	TATTCGCCGG	500
	TGTAGGTGAG	CGTACTCGTG	AAGGTAACGA	CTTATAACCAC	GAAATGAGCG	550
5	ATTCTGGCGT	AATTAAGAAA	ACTGCGATGG	TATTCGGACA	AATGAACGAG	600
	CCACCTGGAG	CACGTCAACG	TGTTGCATTA	ACAGGTTTAA	CAATGGCTGA	650
	GCATTTCCGT	GATGAGCAAG	GACAAGACGT	ACTACTGTTC	ATCGATAACA	700
	TCTTCCGTTT	CACGCAAGCA	GGTTCTGAAG	TATCTGCCCT	TCTTGGTCGT	750
	ATGCCATCTG	CGGTAGGTTA	CCAGCCAACA	CTTGCAACAG	AAATGGGTCA	800
10	ATTACAAGAG	CGTATTACAT	CTACAAATA			829

2) INFORMATION FOR SEQ ID NO: 1643

15

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 823 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

25

- (A) ORGANISM: *Bacillus pseudomycoides*
- (B) STRAIN: NRRL BD-10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1643

30	AATCTACAAT	GCCCTTACGG	TAAAACAAAG	CAACGAAAAC	GGAGCAAGCA	50
	TTAACTTAAC	ATTTGAAGTT	GCACTTCATT	TAGGTGATGA	CACAGTTCGT	100
	ACAGTTGCGA	TGTCTTCCAC	AGATGGACTT	GTTCGTGGCA	CAGAAGTAGA	150
	AGATACTGGT	AAACCAATCT	CTGTACCGGT	TGGTGATGCA	ACACTTGGTC	200
	GTGTATTTAA	CGTATTAGGT	GATGCAATTG	ACTTAGATGG	TGAAGTTCCT	250
35	GCGGATGTAC	GCCGTGATCC	AATTCACCGT	CAAGCACCTG	CGTTCGAAGA	300
	GTTATCTACG	AAAGTAGAAA	TTCTTGAAAC	TGGTATTAAA	GTAGTAGACT	350
	TACTTGCTCC	TTACATTAAG	GGTGGTAAAA	TCGGTCTATT	CGGTGGTGCC	400
	GGTGTAGGTA	AAACAGTATT	AATCCAGGAA	TTAATTAACA	ACATCGCACA	450
	AGAGCACGGT	GGTATTTCTG	TATTCGCTGG	TGTAGGTGAG	CGTACTCGTG	500
40	AAGGTAATGA	CTTATAACCAC	GAAATGAGCG	ATTCTGGCGT	AATCAAGAAA	550
	ACAGCGATGG	TATTCGGACA	AATGAACGAG	CCACCTGGTG	CACGTCAACG	600
	TGTTGCATTA	ACAGGATTAA	CAATGGCTGA	ACATTTCCGT	GATGAGCAAG	650
	GACAAGACGT	ACTATTGTTC	ATCGATAACA	TCTTCCGTTT	CACGCAAGCG	700
	GGTTCTGAAG	TATCTGCCCT	TCTTGGTCGT	ATGCCATCTG	CGGTAGGTTA	750
45	CCAACCAACT	CTTGCAACAG	AAATGGGTCA	ATTACAAGAG	CGTATTACAT	800
	CTACAAATAA	AGGATCTATC	ACG			823

50 2) INFORMATION FOR SEQ ID NO: 1644

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 708 bases

- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

5 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacillus pseudomycoides*
- (B) STRAIN: NRRL B-617

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1644

	GGAAAGCTAC	CTGAAATCTA	CAATGCCCTT	AGAATTAAAC	AAGACGCAGT	50
	TAACTTAACT	TTAGAAGTTG	CAC TTCACTT	AGGTGATGAT	ACAGTTCGTA	100
15	CAGTTGCGAT	GTCTTCCACA	GACGGACTTG	TTCGTGGTAC	TGCAGTAGAA	150
	GATACTGGCA	AAGCGATTTT	TGTTCCAGTT	GGTGATGCAA	CAC TTGGTCG	200
	TGTATTTAAC	GTATTAGGTG	ATGCAATTGA	CTTAGATGGT	GAGGTTCAG	250
	CAGATGTACG	CCGTGATCCA	ATTCACCGTC	AAGCACCTGC	ATTCGAAGAG	300
	TTATCTACAA	AAGTAGAAAT	TCTTGAAACT	GGTATTAAAG	TAGTAGACTT	350
20	ACTTGCTCCT	TACATTAAAG	GTGGTAAAAT	CGGTCTATTC	GGTGGTGCCG	400
	GTGTAGGTAA	AACAGTATTA	ATTCAGGAAT	TAATTAACAA	CATCGCACAA	450
	GAGCACGGTG	GTATCTCTGT	ATTCGCTGGT	G TAGGTGAGC	G TACTCGTGA	500
	AGGTAACGAC	TTATAACCATG	AAATGAGCGA	TTCTGGCGTA	ATCAAGAAAA	550
	CTGCGATGGT	ATTCGGACAA	ATGAACGAGC	CACCTGGTGC	ACGTCAACGT	600
25	GTTGCATTAA	CAGGTTTAAC	AATGGCTGAA	CATTTCCGTG	ATGAGCAAGG	650
	ACAAGACGTA	CTATTGTTCA	TCGATAACAT	CTTCCGTTTC	ACGCAAGCGG	700
	GTTCTGAA					708

30

2) INFORMATION FOR SEQ ID NO: 1645

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 778 bases
- 35 (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

40

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Budvicia aquatica*
- (B) STRAIN: ATCC 35567

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1645

	GTACGATGCG	CTTGAAGTTC	AAAACGATGT	CAAAC TAGTG	CTGGAAGTTC	50
	AACAGCAGCT	CGGTGGTGGT	GTCGTTCTGT	GTATCGCTAT	GGGTACCTCA	100
	GATGGCCTAA	GCCGCGGTCT	GAAAGTACTT	GATTTAGAAC	ACCCTATCGA	150
50	AGTTCCTGTC	GGTGTGGCAA	CTCTGGGCCG	TATTATGAAC	GTGCTTGGTG	200
	AGCCTATCGA	TATGAAGGGT	GACATTGGTG	AAGAAGAGCG	TTGGGCTATC	250
	CATCGCGCTG	CACCAAGCTA	CGAAGATTTA	TCCAGTGCTA	ACGAACTGCT	300
	GGAAACGGGC	ATCAAGGTTA	TCGACCTGAT	TTGTCCGTTT	GCCAAAGGCG	350

	GTAAAGTTGG	TCTGTTTGGT	GGTGCCGGCG	TAGGTAAAAC	GGTAAACATG	400
	ATGGAGCTGA	TTCGTAATAT	TGCGACTGAG	CACTCAGGTT	ACTCTGTATT	450
	TGCCGGCGTT	GGTGAGCGTA	CTCGTGAGGG	TAATGACTTC	TACCACGAAA	500
	TGACAGAATC	TAACGTATTA	GACAAAGTAT	CTCTGGTTTA	TGGCCAAATG	550
5	AATGAGCCAC	CGGGAAACCG	TCTGCGCGTT	GCGTTAACCG	GCCTGACCAT	600
	GGCGGAAAAA	TTCCGTGATG	AAGGCCGTGA	CGTTCTGCTG	TTTATCGATA	650
	ACATTTATCG	TTATACCTTA	GCCGGTACAG	AAGTATCAGC	ACTGTTAGGT	700
	CGTATGCCAT	CAGCGGTAGG	TTACCAACCA	ACGCTGGCGG	AAGAGATGGG	750
	TACACTGCAA	GAACGTATCA	CYTCAACC			778

10

2) INFORMATION FOR SEQ ID NO: 1646

15 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 806 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Buttiauxella agrestis*
 25 (B) STRAIN: ATCC 33320

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1646

	GATGCCGTAC	CAAAAGTGTA	CGACGCTCTT	GAGGTTACAA	ATGGTAAAGA	50
30	CCGTCTGGTG	CTGGAAGTTC	AGCAACAGTT	AGGTGGTGGC	GTAGTGCGTA	100
	CTATCGCCAT	GGGTACTTCT	GATGGTTTGC	GTCGTGGTCT	GGAAGTTTCT	150
	AACCTCGATC	ACCCAATTGA	AGTGCCAGTA	GGTAAAGCAA	CTCTGGGCGG	200
	TATCATGAAC	GTCCTGGGCG	AGCCTATCGA	CATGAAAGGC	GATATCGGCG	250
	AAGAAGAGCG	TTGGGCGATT	CACCGTGCTG	CTCCTAGCTA	CGAAGAAGTG	300
35	TCTAGCTCCC	AGGATCTGCT	GGAAACCGGC	ATCAAAGTAA	TGGACCTGAT	350
	TTGCCCCTTC	GCTAAGGGTG	GTAAAGTCGG	TCTGTTCCGT	GGTGCGGGTG	400
	TGGGTAAAAC	TGTAAACATG	ATGGAGCTGA	TCCGTAACAT	CGCGATCGAG	450
	CACTCCGGTT	ACTCAGTGTT	TGCAGGCGTG	GGGGAACGTA	CTCGTGAGGG	500
	TAACGACTTC	TACCATGAAA	TGACCGATTC	CAACGTTCTG	GACAAAGTAT	550
40	CACTGGTTTA	TGGCCAGATG	AACGAGCCAC	CAGGTAACCG	TCTGCGCGTT	600
	GCGTTGACCG	GTCTGACCAT	GGCTGAGAAG	TTCCGTGACG	AAGGTCGTGA	650
	CGTTCTGCTG	TTCGTTGATA	ACATTTACCG	TTATACCCTG	GCCGGTACAG	700
	AAGTATCTGC	GCTGCTGGGT	CGTATGCCAT	CTGCGGTAGG	TTACCAGCCA	750
	ACTCTGGCAG	AAGAGATGGG	TGTTTTGCAG	GAGCGTATTA	CCTCCACCAA	800
45	AACTGG					806

2) INFORMATION FOR SEQ ID NO: 1647

50

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1122 bases
 (B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

5

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Candida norvegica*
(B) STRAIN: ATCC 36586

-10- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1647

	GAAACCGTTG	TTGACACTGG	TTCCCCAATC	ACCGTCCCAG	TTGGTCGTGA	50
	AACCTTGGGT	CGTATCATTA	ACGTTATCGG	TGAACCAATC	GATGAACGTG	100
	GTCCAATCAA	CACCAAGCAA	AGAAACCCAA	TCCATGCTGA	TCCTCCTTCA	150
15	TTTGCTGAAC	AATCCACTTC	TGCTGAAGTT	TTAGAAACCG	GTATTAAAGT	200
	TGTCGATTTA	TTGGCTCCTT	ATGCCAGAGG	TGGTAAAATT	GGTTTATTCG	250
	GTGGTGCCGG	TGTCGGTAAA	ACCGTCTTTA	TCCAAGAATT	GATTAACAAC	300
	ATTGCTAAAG	CTCATGGTGG	TTTCTCAGTC	TTCACCGGTG	TCGGTGAAAG	350
	AACCAGAGAA	GGTAACGATT	TATACCGTGA	AATGAAAGAA	ACCGGTGTCA	400
20	TTAACTTGA	AGGTGACTCT	AAAGTCGCTT	TAGTCTTCGG	TCAAATGAAC	450
	GAACCTCCAG	GTGCTAGAGC	CCGTGTTGCC	TTAACCGGTC	TAACCATTCG	500
	TGAATACTTC	AGAGATGAAG	AAGGTCAAGA	TGTCTTGTTA	TTCGTTGATA	550
	ACATTTTCAG	ATTCAACCAA	GCTGGTTCAG	AAGTCTCTGC	CTTATTAGGT	600
	CGTATTCCAT	CTGCTGTCGG	TTATCAACCA	ACCTTGGCCA	CTGATATGGG	650
25	TTTGTTGCAA	GAACGTATCA	CCACCACCAG	AAAAGGTTCC	GTCACTTCTG	700
	TCCAAGCTGT	TTATGTCCCA	GCTGATGATT	TGACTGATCC	TGCCCCAGCC	750
	ACCACTTTTCG	CGCATTTGGA	TGCTACTACT	GTCTTGCTCTC	GTGGTATCTC	800
	AGAATTGGGT	ATCTACCCAG	CTGTGATCC	ATTGGATTCC	AAATCAAGAT	850
	TATTAGATGC	CGCTGTTGTT	GGTCAAGAAC	ATTACGATGT	TGCTACTCAA	900
30	GTTCAACAAA	CTTTACAAGC	CTACAAATCT	TTACAAGATA	TTATCGCTAT	950
	TTTAGGTATG	GATGAATTAT	CAGAACAAGA	TAAATTGACC	GTTGAAAGAG	1000
	CTAGAAAGAT	CCAACGTTTC	TTATCTCAAC	CATTTGCTGT	CGCTGAAGTT	1050
	TTCCTGGTA	TTCCAGGTAG	ATTAGTTAGA	TTGAAAGAAA	CCGTTGCTTC	1100
	ATTCAGAGAC	GTTTTAGCTG	GT			1122

35

2) INFORMATION FOR SEQ ID NO: 1648

40 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 813 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

45

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*
(B) STRAIN: ATCC 700677

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1648

TACGTCTCTT ACCCTGACGA TGATTTGCAA GTCGCATCTA CGGTCGTAGA 50
 TGTTTCAAAT GGTAAGTCA TCGCCCAACT TGGAGCTCGT CACCAAGCAA 100
 GTAACGTTTC ATTTGGTACC AACCAAGCTG TGGAAACCAA TCGTGA CTGG 150
 GGATCAACTA TGAAACCAAT CACAGACTAT GCTCCTGCCT TGGAGTACGG 200
 5 TGTCTACGAT TCAACTGCTA CTATCGTTCA CGATGAGCCC TATAACTACC 250
 CTGGGACAGA TATCCCTCTC TATAACTGGG ATCGAGCATA TTTCGGTAAT 300
 ATTACTCTGC AATATGCCCT TCAACAATCT CGTAACGTAC CTGCCGTTGA 350
 AACACTAAAC AAGGTCGGTC TAGATAAGGC TAAAACCTTC CTTAATGGTC 400
 TTGGTATCGA CTATCCAAGC ATGCATTATG CAAACGCCAT TTCAAGTAAT 450
 10 ACAACTGAAT CCAACAAAAA ATATGGTGCA AGTAGTGAAA AAATAGCTAC 500
 CGCCTATGCC GCATTGCGAA ATGGTGGTAT TTACCACAAA CCAATGTACA 550
 TCAATAAAGT TGTCTTTAGC GATGGTAGCG AAAAAGAATT TTCTGACCCCT 600
 GGCACAAGAG CCATGAAAGA AACGACTGCT TACATGATGA CAGAAATGAT 650
 GAAAACAGTC TGGACGTACG GAACTGGTTCG TGGTGCCTAC CTGCCTTGGC 700
 15 TTCCTCAAGC TGGTAAAACA GGTACCTCTA ACTATACTGA CGAAGAAATT 750
 GAAAAGTATA TCAAGAACAC TGGTTACGTA GCTCCAGATG AAATGTTTGT 800
 GGGTTATACC CGT 813

20

2) INFORMATION FOR SEQ ID NO: 1649

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 813 bases
 25 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

30

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Campylobacter lari*
 (B) STRAIN: ATCC 43675

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1649

ATTAATGAAG CTATTGTTGT TAATTATGAA TTAGAAGGAA AAGAATGCAA 50
 GCTAGTTCTT GAAGTAGCTG CACATTTAGG CGATAATAAA GTAAGAACCA 100
 TCGCTATGGA TATGACAGAT GGTCTTGTTA GAGGTTTAAC AGCCGTCGCA 150
 40 ACTGGAAATC CAATTAGTGT TCCAGTAGGC GAAAAAGTTC TTGGAAGAAT 200
 TTTTAATGTA ACGGGTGATT TGATTGATGA GGGCGAAGAA ATCAATTTTG 250
 ATAAGCACTG GTCAATTCAT AGAGATCCAC CTCCATTTGA AGAACAAAGT 300
 ACAAAAAGCG AAATCTTTGA AACAGGTATA AAGGTTGTTG ATTTGCTAGC 350
 TCCTTATGCT AAAGGTGGAA AAGTTGGTCT TTTTGGTGGT GCAGGTGTTG 400
 45 GTAAAACCGT TATTATTATG GAATTAATTC ACAATGTTGC ATTTAAACAT 450
 AGCGGATATT CTGTTTTTGC AGGTGTTGGC GAAAGAACTC GTGAGGGTAA 500
 TGACCTTTAC AATGAAATGA AAGAAAGTAA TGTATTAGAT AAAGTTGCAT 550
 TGTGTTATGG TCAAATGAAT GAACCACCAG GGGCAAGAAA TCGTATAGCT 600
 TTAACAGGTC TTAATATGGC TGAGTATTTT AGAGATGAAA TGGGACTTGA 650
 50 TGTTTTAATG ATTATTGATA ATATTTTCAG ATTTTCTCAA TCAGGCTCAG 700
 AAATGTCAGC ACTTTTAGGA AGAATTCCTT CAGCTGTTGG TTATCAACCA 750
 ACCTTAGCTA GTGAAATGGG TAAGTTCCAA GAAAGAATTA CTTCAACCAA 800
 GAAAGGATCT ATT 813

2) INFORMATION FOR SEQ ID NO: 1650

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 570 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Coccidioides immitis*
 (B) STRAIN: WSA-222
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1650

```

GGTGGGGAAG ACTGTGTTCA TTCAGGAATT GATTGTAAGT TCTGTTATCA      50
ACTAAAGCCG ACAGCGGTTG CTGATATGCT CTAGAACAAC ATTGCTAAGG     100
CTCACGGTGG TTA CTCCGTG TTA CTGGTG TCGGTGAGCG TACCCGTGAG     150
20 GGTAACGATT TGTACCATGA AATGCAAGAG ACCCGTGTCA TTCAACTCGA     200
CGGAGAGTCC AAGGTCGCTC TTGTCTTCGG TCAAATGAAC GAGCCCCCTG     250
GTGCCCCTGC CCGTGTTGCC CTTACCGGTT TGACCATTCG TGAATACTTC     300
CGTGACGAGG AAGGCCAAGA CGGTAGGCTT CATGCTTCTA TCGCTAGGGG     350
CGTGTGATAC AGGAGGCTAA TCGCTTTTCT AGTGCTTCTC TTTATTGACA     400
25 ACATTTTCCG TTCACTCAA GCTGGTTCTG AAGTGTCTGC CTTGCTCGGT     450
CGTATTCTCT CCGCTGTCGG TTACCAACCT ACTCTCGCCG TCGACATGGG     500
TGTTATGCAG GAACGTATCA CCACCACCAC CAAGGGATCC ATTACTTCAG     550
TGCARGCCGT CTACGTCCCC                                     570

```

30

2) INFORMATION FOR SEQ ID NO: 1651

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 560 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Emmonsia parva*
 (B) STRAIN: ATCC 10784
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1651

```

TGTCTTCATC CAGGAGTTAA TTGTACGTTT TTTGTCTGCC TACTATAATA      50
GACGAAGAAA TATTTTGATT TATTTTCTA ATAATTCAA TAGAACAACA     100
50 TTGCCAAAGC CCACGGTGGT TACTCTGTCT TCACTGGTGT TGGCGAGCGG     150
ACCCGTGAAG GAAACGATCT GTACCACGAA ATGCAGGAGA CCCGTGTCAT     200
CCAGCTCGAT GGCAGTCCA AGGTCGCCCT CGTCTTCGGT CAAATGAACG     250
AACCCCCCGG AGCCCGTGCC CGTGTTGCCC TCACTGGTCT GACCGTTGCT     300

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	GAATACTTCC	GTGACGAGGA	AGGTCAAGAT	GGTGCGTATA	TATATATTCC	350
	CCAGTAATTT	GACTCGAAGC	TCCACTCACA	CATATATTAG	TGCTCCTCTT	400
	CATCGACAAC	ATTTTCCGCT	TCACCCAGGC	AGGTTCGGAA	GTGTCCGCCC	450
	TGCTCGGCCG	TATCCCCTCC	GCCGTCGGTT	ACCAGCCCAC	CCTCGCTGTC	500
5	GACATGGGTA	TGATGCAGGA	ACGTATCACC	ACCACCACCA	AGGGCTCCAT	550
	CACCTCCGTG					560

10 2) INFORMATION FOR SEQ ID NO: 1652

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 780 bases
 (B) TYPE: Nucleic acid
 15 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

20 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Erwinia amylovora*
 (B) STRAIN: ATCC 14976

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1652

25	CCACAAGTGT	ACAGCGCCCT	TGAGGTAA	AATGGTGATG	CTCGTCTGGT	50
	GCTGGAAGTT	CAGCAGCAGC	TGGGCGGTGG	CGTGGTTCGT	ACCATCGCCA	100
	TGGGTTCTTC	AGACGGCCTT	AAGCGTGGTC	TGGAAGCCGT	TGACCTTCAG	150
	CACCCAATTG	AAGTACCGGT	AGGTACTGCC	ACACTTGGCC	GTATCATGAA	200
30	CGTGCTGGGT	GAGCCGATCG	ATATGAAAGG	CGACATTGGC	GAAGAAGAGC	250
	GCTGGGCGAT	TCACCGCTCT	GCACCTTCTT	ACGAAGATCA	GTCGAACTCT	300
	CAGGATCTGC	TGGAAACCGG	CATCAAGGTG	ATTGACCTGA	TGTGTCCGTT	350
	CGCCAAGGGC	GGTAAAGTCG	GCTTGTTTCG	TGGTGCGGGC	GTAGGTAAAA	400
	CCGTCAACAT	GATGGAGCTT	ATTGCTAACA	TTGCGGCTGA	GCACTCAGGT	450
35	TTCTCGGTAT	TTGCCGGTGT	GGGTGAGCGT	ACCCGTGAAG	GTAACGACTT	500
	CTACCACGAA	ATGACCGACT	CCAACGTTAT	CGACAAAGTT	TCGCTGGTCT	550
	ATGGTCAGAT	GAACGAGCCA	CCGGGTAACC	GTCTGCGCGT	TGCGCTGACC	600
	GGTCTGACCA	TGGCGGAGAA	GTTCCGTGAC	GAAGGTCGTG	ACGTACTGCT	650
	GTTTATCGAT	AACATCTATC	GTTACACCCT	GGCCGGTACT	GAAGTCTCCG	700
40	CTCTGCTGGG	TCGTATGCCT	TCTGCGGTAG	GTTACCAGCC	AACGCTGGCG	750
	GAAGAGATGG	GCGTTCTGCA	GGAACGTATC			780

45 2) INFORMATION FOR SEQ ID NO: 1653

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 545 bases
 (B) TYPE: Nucleic acid
 50 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Fonsecaea pedrosoi*

(B) STRAIN: ATCC 18831

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1653

TGTGTTTCATT CAGGAGCTGA TTGTGAGTAC CCCGGAGATT TTCCTGCGAT 50
 TGCGCATGAA GCAAGCGCTG ACGTCCATCT AGAACAACAT CGCCAAGGCT 100
 10 CACGGTGGTT ACTCCGTGTT CTGCGGTGTC GCGGAGCGTA CTCGTGAGGG 150
 TAACGATTTG TACCACGAAA TGCAGGAGAC CGGTGTCTATC AACCTCGAGG 200
 GCGAGTCCAA GGTGCGCCCTT GTCTTCGGTC AGATGAACGA GCGCCCGGGA 250
 GCGCGTGCCC GTGTCGCCCTT TACTGGTCTT ACCGTCGCTG AGTAAGTTTT 300
 GACAACCAGA AGCGAGTATT GCCACAATTA CTGACTAAAA ATCAAGATAT 350
 15 TTCCGTGACG AGGAGGGCCA GGATGTGCTT CTCTTCATTG ACAACATTTT 400
 CCGTTTCACC CAGGCCGGTT CTGAGGTGTC CGCTCTTCTC GGCCGTATTC 450
 CCTCTGCCGT CGGTTACCAG CCCACTCTCG CCGTCGACAT GGGTATGATG 500
 CAGGAGCGTA TCACCACCAC CCAGAAGGGT TCCATCACTT CCGTC 545

20

2) INFORMATION FOR SEQ ID NO: 1654

(i) SEQUENCE CHARACTERISTICS:

25

(A) LENGTH: 564 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

30

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Fusarium moniliforme*

(B) STRAIN: WSA-213

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1654

TGTGTTTATT CAGGAGCTCA TCAACAACAT CGCCAAGGCC CACGGTGGTT 50
 ACTCTGTCTT CACTGGTGTC GGTGAGCGAA CCCGTGAGGG TAACGATCTG 100
 40 TACCACGAAA TGCAGGAGAC TTCCGTTATT CAGCTTGATG GCGAGTCCAA 150
 GGTTGCCCTG GTTTTCGGTC AGATGAACGA GCGCCCTGGA GCTCGTGCCC 200
 GTGTCGCTCT TACCGGGTAA GTTGATAGAT AGTGCCTTCC CTTCTGTTT 250
 CAACACCTCA ACACCACCAC TCCCCAAGAC ATTGCTACTC ATACTGCACC 300
 ATGATATTAT ATTTACGCCT CTTGGACGCT AGCTAATGTT GTATCGACAG 350
 45 TTTGACTGTT GCTGAGTACT TCAGAGACGA GGAGGGTCAG GACGTGCTGC 400
 TTTTCATTGA CAACATTTTC CGATTCACTC AGGCCGGTTC CGAGGTGTCT 450
 GCCCTTCTCG GTCGTATCCC CTCTGCCGTC GGTACCAGC CCACTCTGGC 500
 CGTCGACATG GGTGGTATGC AGGAGCGTAT TACCACCACC ACCAAGGGT 550
 CCATTACCTC AGTC 564

50

2) INFORMATION FOR SEQ ID NO: 1655

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 776 bases
 (B) TYPE: Nucleic acid
 5 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

10 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Klebsiella oxytoca*
 (B) STRAIN: ATCC 13182

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1655

15 CGTACCGCGC GTGTACGAGG CTCTTGAGGT ACAAATGGT AGTGAGAATC 50
 TGGTGCTGGA AGTTCAGCAG CAGCTCGGCG GCGGTATTGT TCGTACCATC 100
 GCCATGGGTT CTTCCGACGG TCTGCGTCGC GGTCTGGAAG TCAAAGACCT 150
 CGAGCATCCG ATCGAAGTCC CGGTAGGTAA AGCAACGCTG GGTCGTATCA 200
 20 TGAACGTA CTGCTGGAAA CCGGCATCAA AGTTATCGAC CTGATGTGTC 250
 GAGCGTTGGG CGATTACCG CGCAGCGCCT TCCTACGAAG AGTTGTCAA 300
 CTCTCAGGAA CTGCTGGAAA CCGGCATCAA AGTTATCGAC CTGATGTGTC 350
 CGTTTGCGAA GGGCGGTAAA GTTGGTCTGT TCGGTGGTGC GGGTGTAGGT 400
 AAAACCGTAA ACATGATGGA GCTGATCCGT AACATCGCGA TCGAGCACTC 450
 25 CGTTTACTCC GTGTTTGCGG GCGTAGGTGA ACGTACTCGT GAGGGTAACG 500
 ACTTCTACCA CGAAATGACC GACTCCAACG TTATCGATAA AGTATCCCTG 550
 GTGTATGGCC AGATGAACGA GCCGCCGGA AACCGTCTGC GCGTTGCGCT 600
 GACCGGCCTG ACCATGGCTG AGAAGTCCG TGACGAAGGT CGTGACGTTT 650
 TGCTGTTCTG CGATAACATC TATCGTTACA CCCTGGCCGG TACTGAAGTA 700
 30 TCCGCACTGC TGGGTCGTAT GCCTTCAGCG GTAGGTTACC AGCCGACTCT 750
 GCGGAAGAG ATGGGCGTTC TGCAGG 776

35 2) INFORMATION FOR SEQ ID NO: 1656

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 572 bases
 (B) TYPE: Nucleic acid
 40 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

45 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Microsporium audouinii*
 (B) STRAIN: ATCC 11347

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1656

50 GTGTTTCATCC AGGAGTTGAT TGTAAGTGAT TATATTCCCC TAGAAAGAAA 50
 TGTTTTGAAC AAAAGTCTCG AATTAGAAAA TTCTTTTCAG ATACTAATTT 100
 ACTATAGAAC AACATTGCCA AGGCTCACGG TGTTTACTCC GTCTTCACCG 150

GTGTCGGAGA GCGAACCCGT GAAGGAAACG ATCTGTACCA TGAAATGCAG 200
 GAAACTCGTG TCATCCAAC T GATGGCGAG TCCAAGGTCG CCCTGGTCTT 250
 CGGTCAGATG AACGAGCCCC CAGGTGCCCG TGCCCGTGTT GCTCTTACTG 300
 GTTTGACCAT TGCTGAGTAC TTCCGTGATG AGGAAGGTCA AGACGGTATG 350
 5 TTCTTTAAAT TAGATATCTT CTGGAGAAAC AGCGTCTAAC AAATTCTTCC 400
 AGTGCTTCTC TTCATCGACA ACATCTTCCG TTTCACTCAG GCTGGTTCGG 450
 AAGTGTCTGC CCTGCTTGGT CGTATTCCAT CTGCCGTCGG TTACCAACCC 500
 ACTCTTGCCG TCGACATGGG TGGTATGCAG GAACGTATTA CCACCACCAA 550
 GAAGGGATCC ATTACCTCCG TC 572
 10

2) INFORMATION FOR SEQ ID NO: 1657

- 15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 790 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
 20
 (ii) MOLECULE TYPE: Genomic DNA
 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Obesumbacterium proteus*
 25 (B) STRAIN: ATCC 12841

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1657

GCCTAAAGTG TATAACGCAC TTGAGGTGAA AGGCGGTGCC ACTAAACTGG 50
 30 TACTGGAAGT TCAGCAGCAG CTAGGCGGCG GCGTTGTACG CTGTATCGCT 100
 ATGGGTACTT CTGACGGTCT GCGTCGCGGA CTGGACGTTG TTGACCTGGA 150
 GCACCCGATT GAAGTCCCAG TAGGTAAAGC GACCTTAGGC CGCATTATGA 200
 ACGTACTGGG TGAGCCAATT GATATGAAGG GTGATATCGG CGAAGAAGAT 250
 CGCTGGGCTA TTCACCGTGA AGCTCCAAGC TACGAAGAAC TGTCTAACTC 300
 35 GCAAGAACTG CTGGAAACCG GTATCAAGGT AATGGACTTG ATTTGTCCGT 350
 TCGCTAAGGG CGGTAAAGTC GGTCTGTTCTG GTGGTGCGGG TGTTGGTAAA 400
 ACAGTAAACA TGATGGAGCT GATCCGTAAC ATCGCGATCG AGCACTCAGG 450
 TTA CTCTGTA TTTGCCGGCG TGGGTGAACG TACTCGTGAG GGTAACGACT 500
 TCTACCACGA AATGACCGAC TCCAACGTAT TGGACAAAGT ATCACTGGTT 550
 40 TATGGCCAGA TGAACGAGCC ACCAGGAAAC CGTCTGCGCG TTGCGCTGAC 600
 CGGTCTGACT ATGGCTGAGA AGTTCCGTGA CGAAGGTCGT GACGTACTGC 650
 TGTTTCATCGA TAACATCTAC CGTTATACCT TGGCCGGTAC CGAAGTATCT 700
 GCACTGCTGG GTCGTATGCC TTCTGCGGTA GGTTATCAGC CAACGCTGGC 750
 GGAAGAGATG GGTGTTCTGC AAGAACGTAT CACCTCTACC 790
 45

2) INFORMATION FOR SEQ ID NO: 1658

- 50 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 622 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

5 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Paracoccidioides brasiliensis*

(B) STRAIN: ATCC 200443

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1658

10
 TGTCTTCATT CAGGAGCTTA TCAACAACAT CGCCAAGGCC CACGGTGGTT 50
 ACTCCGTCTT CACTGGTGTG GGAGAGCGCA CTCGTGAGGG AAACGACTTG 100
 TATCACGAGA TGCAAGAGAC TTCCGTTATC CAGCTCGAAG GCGAATCCAA 150
 GGTTGCCCTC GTCTTCGGTC AAATGAACGA GCCTCCGGGT GCTCGTGCTC 200
 15 GTGTTGCTCT CACCGGTCGT AAGTGCTCCT TCCCAGATTT CTCTTCCCCA 250
 GTTTCTGGAC CCACTTTTTC CTTCCACCAC CATTCTACTG GGTAGGACCA 300
 AGATAGCACT GCCTATTCTG GTGCCTTCCT ACCGCCTACT CTACTGCCTA 350
 TTCCACCACC TTTTCTACCG CCTCTTCTAC TTGCTATTGT ATACTAACTT 400
 ACTCAAACAG TTACTATTGC TGAGTACTTC CGTGACGCTG AGGGCCAGGA 450
 20 TGTGCTTCTC TTCATCGACA ACATTTTCCG TTTCACCCAG GCCGGTTCGG 500
 AGGTGTCCGC TCTTCTCGGT CGTATCCCCT CCGCCGTCGG TTACCAGCCC 550
 ACCCTTGCCG TCGACATGGG TGGTATGCAG GAGCGTATCA CCACCACCAA 600
 GAAGGGATCC ATTACCTCCG TC 622

25

2) INFORMATION FOR SEQ ID NO: 1659

(i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 794 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

35 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Plesiomonas shigelloides*

(B) STRAIN: ATCC 14029

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1659

GACGCTGTAC CTCAGGTGTA CGATGCACTG ACAGTTGAGG GTGCTGAGCT 50
 GGTACTGGAA GTGCAGCAGC AGCTGGGTGG TGGTGTGTGTT CGCTGTATCG 100
 45 CGATGGGTGC CTCTGATGGC CTCAAGCGCG GTCTGAAAGC GCACAATACT 150
 GGTGCTCCTA TCACTGTACC GGTGGGTGTG GAAACACTGG GCCGGATCAT 200
 GGATGTGTTG GGTAACCCGA TTGACCAGAA AGGTCCAATC GGTGAACAAG 250
 ATCGCTGGGT GATCCACCGT GAAGCACCAA GCTACGAAGA TCAGGCTAAC 300
 AGCACTGAAC TGCTGGAAAC CGGTATCAAG GTTATCGACC TGGTATGCCC 350
 50 GTTTGCGAAA GCGGGTAAAG TCGGTCTGTT CGGTGGTGCC GGTGTAGGTA 400
 AAACCGTAAA CATGATGGAG CTGATCCGTA ACATCGCGAT CGAGCACTCC 450
 GGTATTCCG TGTGTCGGG CGTGGGTGAG CGTACCCGTG AAGGTAACGA 500
 CTTCTACCAC GAAATGACAG ACTCCAACGT ACTGGACAAA GTATCCCTGG 550

	TGTACGGTCA	GATGAACGAG	CCGCCAGGTA	ACCGTCTGCG	CGTAGCACTG	600
	ACCGGCCTGA	CCATTGCGGA	GAAATTCCGT	GATGAAGGTC	GTGACGTACT	650
	GCTGTTTCATC	GATAACATCT	ACCGTTATAC	CCTGGCGGGG	ACCGAAGTAT	700
	CGGCACTGCT	GGGCCGTATG	CCTTCTGCGG	TAGGTTATCA	GCCAACGCTG	750
5	GCGGAAGAGA	TGGGTGTACT	GCAAGAGCGT	ATTACCTCTA	CCCG	794

2) INFORMATION FOR SEQ ID NO: 1660

10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 799 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

15

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

20

- (A) ORGANISM: *Shewanella putrefaciens*
- (B) STRAIN: ATCC 8071

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1660

25	AGGTATATGA	CGCTSTGAAG	ATCACAGGTG	AAGGCGCCTG	TAATGGTTTG	50
	GTGCTGGAAG	TTCAGCAACA	GCTAGGCGGT	GGTGTAGTTC	GTACTATCGC	100
	TATGGGTTCT	TCTGATGGTC	TGCGTCGTGG	TCTTGAGGTT	GTAACTCAG	150
	GTTCACCTAT	TTCTGTTCCCT	GTTGGTACCG	CCACGCTTGG	CCGTATCATG	200
	AACGTATTAG	GTGAGCCTAT	TGATGAAGCG	GGTCCAATCG	GTGAAGAAGA	250
30	GCGTTATGTT	ATTACCCGTG	CAGCACCTTC	ATATGAAGAT	CAATCGAACA	300
	CTACTGAACT	GTTAGAGACA	GGTATCAAGG	TTATTGACCT	TGTTTGTCCA	350
	TTCGCTAAGG	GTGGTAAAGT	AGGTCTGTTC	GGTGGTGCGG	GTGTTGGTAA	400
	AACAGTTAAC	ATGATGGAAC	TGATTAACAA	CATCGCTAAA	GCTCACTCGG	450
	GTCTTTCCGGT	GTTCCGCCGGT	GTGGGTGAAC	GTAATCGTGA	AGGTAACGAC	500
35	TTCTACTACG	AGATGAAAAG	TTCTGGCGTT	CTCGACAAAG	TGGCCATGGT	550
	TTATGGTCAG	ATGAACGAGC	CACCAGGAAA	CCGTTTACGC	GTAGCACTGT	600
	CAGGTCTGAC	AATGGCTGAG	AAGTTCCGTG	ACGAAGGTCG	TGACGTATTG	650
	TTGTTTCGTTG	ACAACATCTA	CCGTTATACC	TTAGCCGGTA	CTGAAGTATC	700
	TGCACTGTTA	GGCCGTATGC	CTTCTGCGGT	AGGTTATCAA	CCAACATTGG	750
40	CTGAAGAAAT	GGGCGTTCTG	CAAGAGCGTA	TTACTTCAAC	TAAGACGGG	799

2) INFORMATION FOR SEQ ID NO: 1661

45

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1661

TGGGAAGCGA AAATCCTG

18

5.

2) INFORMATION FOR SEQ ID NO: 1662

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 774-bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

15 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Campylobacter curvus*
 (B) STRAIN: ATCC 35224

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1662

CTATGCCTCA AACTAGAGAG CATATCTTGC TATCTCGCCA AGTAGGCGTT 50
 CCATATATCG TTGTATTTAT GAACAAAGCC GATATGGTCG ATGACGCTGA 100
 25 GCTTCTTGAG CTAGTCGAGA TGGAAATTCG CGAGCTTCTT AACGAGTACA 150
 ACTTCCCTGG CGATGATACT CCTATCATAT CAGGTTCTGC TCTTAAAGCC 200
 CTCGAAGAGG CTAAAGCAGG CGTTGATGGC GAGTGGTCAG CAAAAGTTCT 250
 TGAGCTTATG GATAAAGTCG ATGAGTATAT CCCAACTCCA GTTCGTGCTA 300
 CCGATAAAGA CTCCTGATG CCTATCGAAG ACGTTTTCTC TATCTCAGGT 350
 30 CGTGGAACGG TCGTTACTGG TAGGATCGAA AAAGGTGTCG TAAAAGTTGG 400
 CGATACTATC GAGATCGTTG GTATCAAACC TACTCAAAC TACGACAGTTA 450
 CTGGCGTTGA GATGTTTAGG AAAGAGATGG AACAAGGCGA GGCCGGTGAT 500
 AACGTAGGTG TTCTTTTAAG AGGTACTAAA AAAGAAGACG TCGAGCGCGG 550
 CATGGTTCTT TGTAAGCCAA AATCAATCAC TCCTCATACA AAATTTGAGG 600
 35 GTGAGGTTTA TATCCTAACA AAAGAGGAAG GCGGACGCCA CACTCCATTC 650
 TTTAACAAC TATAGACCACA ATTTTATGTA AGAACAACAG ACGTTACAGG 700
 TTCTATCACA CTTCCAGAAG GAACTGAGAT GGTATGCCT GGAGATAATG 750
 TCAGAATTTC CGTTGAACTC ATCG 774

10

2) INFORMATION FOR SEQ ID NO: 1663

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 791 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

50 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Campylobacter rectus*

(B) STRAIN: ATCC 33238

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1663

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5  TTCTGCGGCT GACGGCCCAA TGCCACAAAC TAGAGAGCAC ATCTTGCTAT      50
   CTCGCCAAGT AGGCGTTCCG TATATCGTTG TTTTATGAA CAAAGCCGAT      100
   ATGGTCGATG ATGCCGAGCT TCTTGAGCTG GTTGAGATGG AGATTCGCGA      150
   GCTTCTAAAC GAGTATGATT TCCCTGGTGA CGATACTCCA ATCGTAGCAG      200
   GCTCTGCTCT TCAAGCTCTT AATGAAGCCA AAGCCGGAAC AGAAGGCGAG      250
10- TGGTCTGCAA AAATTCTTGA GCTTATGGCT AAAGTTGACG AGTATATCCC      300
   GACTCCGGTT CGTGCAACGG ATAAAGACTT CTTGATGCCT ATTGAGGACG      350
   TTTTCTCTAT CTCCGGTCGC GGCACCGTCG TTACCGGCAG AATCGAAAAA      400
   GGTATCGTAA AAGTCGGTGA TACTATCGAG ATCGTAGGTA TCCGCGATAC      450
   TCAAACAACCT ACCGTTACCG GCGTTGAGAT GTTCAGAAAA GAGATGGATC      500
15  AAGGCGAAGC GGGCGATAAC GTAGGCGTTC TTCTAAGAGG CACTAAAAAA      550
   GAAGACGTTG AGCGCGGTAT GGTTCCTTTC AAACCTAAAT CAATCACTCC      600
   TCACACTAAA TTTGAGGGAG AGGTTTATAT CTTAACTAAA GAGGAAGGCG      650
   GACGCCATAC TCCATTCTTT AATAACTATA GACCGCAGTT TTATGTAAGA      700
   ACTACCGACG TTACCGGTTT TATCACTCTT CCGGAAGGAA CAGAGATGGT      750
20  TATGCCTGGC GATAACTTAA AGATAAGCGT TGAGCTTATC G              791

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2) INFORMATION FOR SEQ ID NO: 1664

25

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 810 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

30

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

35

(A) ORGANISM: *Fonsecaea pedrosoi*

(B) STRAIN: ATCC 18831

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1664

```

40  CGACGGACAG ATGCCCCAGA CCAGGGAGCA CTTGCTCCTC GCCCGCCAGG      50
   TCGGTGTCAA GCGCATTGTC GTCTTCGTCA ACAAGGTCGA TGCCATTGAG      100
   GACAAGGAGA TGTTGGAGCT CGTCGAGATG GAGATGCGTG AGCTTCTCTC      150
   CAGCTACGGC TTCGAGGGTG ACGACACTCC CATCGTCATG GGTTCGCCCC      200
   TTTGCGCCAT TGAGGGCCGC GAGCCCGACA TTGGTGTCGA GAAGATTGAC      250
45  GAGCTCCTCG AGCACGTCGA CACCTGGATC CCCACCCCG AGCGTGACAT      300
   CGCCAAGCCT TTCCTCATGT CCGTTGAGGA CGTCTTCTCC ATTCCCGGCC      350
   GTGGTACCGT CGCTTCTGGC CGTGTCGAGC GTGGTGTCCT GAAGAAGGAT      400
   TCCGAAGTCG AGCTTGTCGG CAAGAACAAG AACCCCATCA AGACCAAGGT      450
   TACCGACATC GAGACCTTCA AGAAGTCTTG CGACGAGTCC CGCGCTGGTG      500
50  ACAACTCCGG TCTCCTTCTC CGTGGTGTCA AGCGTGACGA TGTCTCCGT      550
   GGCATGGTCG TTGTCCAGCC CGGCACCACC AAGGCCACAA AGAAGTTCCT      600
   TGCCTCCATG TACGTCCTCA CCAAGGAGGA GGGTGGCCGC CACACTGGTT      650
   TCGCCAACAA CTACAAGCCC CAGATGTTCA TCCGTACCGC CGATGAGGCC      700

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GCCACTCTTA CCTGGCCCGA GGGTACCGAG GAGGACAAGA TGGTCATGCC 750
CGGTGACAAT GTCGAGATGA TCTGCGAGAT CCACAAGCCC ATTGCCGTCG 800
AGCAAGGCCA 810

5

2) INFORMATION FOR SEQ ID NO: 1665

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 19 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

15 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1665

CAGTACAGGT AGACTTCTG

19

20

2) INFORMATION FOR SEQ ID NO: 1666

25 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 888 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

30

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 35 (A) ORGANISM: *Microsporium audouinii*
(B) STRAIN: ATCC 11347

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1666

ATGATTGCGA AACCTACTTG CTGTGGAAGA ATTTGGATAT TCTAACATTT 50
40 CTCTAGGCCT CAAACCAGAG AGCATCTGCT CCTTGCCCGC CAGGTCGGTG 100
TTCAGAAGCT CGTCGTTTTC GTTAACAAGG TCGACGCTGT TGAGGACCCA 150
GAGATGTTGG AACTTGTCGA GCTAGAGATG CGTGAGCTGC TCAGCCACTA 200
TGGTTTCGAG GGTGAGGAGA CCCCATCAT TTTTGGCTCT GCTCTCTGCG 250
CCCTTGAATC TCGACGACCA GAATTGGGTG TTGAGAAGAT CGATGAGCTA 300
45 TTGAACGCTG TGGATACCTG GATTCCCACC CCAGAGCGTG CCACTGATAA 350
GCCTTTCCTT ATGTCCATTG AGGAAGTTT CTCCATCTCT GGTCGTGGTA 400
CCGTCGTTTC CGGTCGTGTC GAGCGTGGTA TCCTCAAGAA GGA CTCTGAT 450
GTCGAAATTG TGGGTGGATC TGATACACCC ATCAAGACGA AGGTCACCGA 500
CATTGAAACC TTCAAGAAGT CTTGTGACGA ATCCCGAGCT GGTGACAACT 550
50 CCGGTCTACT TCTCCGAGGT GTCAAGCGTG AGGACTTGAG ACGTGGAATG 600
GTTGTTGCTG CTCCCGGATC GACCAAGGCT CATAACCGACT TCATGGTCTC 650
CCTTTATGTT CTGACCGAGG CTGAGGGTGG CCGTTCCAAT GGATTCACCC 700
ACAAGTACCG CCCACAGATG TTCATCCGTA CTGCCGGTAT GTAAACCCTT 750

TTTCTACCAT	TCACTTTGTT	TCACCACTGA	CTTGTATACT	TTACCGCAGA	800
CGAAGCCGCA	TCTTTCAGCT	GGCCTGGAGA	GGATCAAGAC	AAGAAGGCCA	850
TGCCTGGTGA	CAATGTCGAG	ATGATTTGCA	AGACCCTC		888

5

2) INFORMATION FOR SEQ ID NO: 1667

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 793 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

15 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Piedraia hortai*
 (B) STRAIN: ATCC 24292

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1667

ATGCCGCAGA	CCCGCGAGCA	CTTGCTGCTC	GCCCCGTCAGG	TCGGTGTCCA	50
GAAGATCGTT	GTTTTTCGTCA	ACAAGGTTGA	TGCTATCGAC	GACCCGGAGA	100
25 TGCTGGAGCT	TGTCGAGATG	GAGATGCGTG	AACTTCTCAG	CACATACGGT	150
TTCGAGGGTG	ACGAGACCCC	TGTTATTATG	GGCTCCGCGC	TCATGGCTCT	200
CAACAACCAG	CGCCCCGAGA	TTGGTCAACA	GAAGATTGAT	GAAGTCATGG	250
CCGCTGTCTGA	CGAGTGGATC	CCTACTCCCC	AGCGTGACCT	CGACAAGCCT	300
TTCCTGATGT	CTGTTGAGGA	TGTCTTCTCC	ATTGCTGGCC	GTGGTACCGT	350
30 TGTGTCCGGC	CGTGTGGAGC	GCGGTACCCT	CAAGCGTGAT	GAGGAAGTCG	400
AGCTTGTCGG	CAAGGGTGTC	GACCCCATCA	AGACCAAGGT	CACCGATATC	450
GAGACTTTCA	AGAAGTCCTG	CGAGGAGGCT	CAGGCTGGTG	ACAACTCTGG	500
TCTTCTGATC	CGTGGTGTCC	GCCGCGAGGA	TGTTTCGTCG	GGTATGGTTG	550
TCTCCAAGCC	CGGCACCGTC	AAGTCTCACA	CTCAGTTCCT	GGCCTCGCTT	600
35 TACGTTCTCA	CCAAGGAGGA	GGGTGGTCGC	CACACTGGTT	TCGGCGAGCA	650
CTACCGTCCC	CAGCTCTACC	TCCGTACCTC	AGACGAGTCT	GTCGATCTGA	700
CCTTCCCCGA	GGGAAGTGAG	GATCACCCT	CCAAGATCGT	CATGCCTGGT	750
GACAACATCG	AGATGGTCGT	CACGATGACT	CACGCCAACG	CTA	793

40

2) INFORMATION FOR SEQ ID NO: 1668

(i) SEQUENCE CHARACTERISTICS:

- 45 (A) LENGTH: 891 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

50 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Escherichia coli*

(B) STRAIN: K-12 KL1699

(C) ACCESSION NUMBER: J01717

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1668

5
AACATGATCA CCGGTGCTGC GCAGATGGAC GGCGCGATCC TGGTAGTTGC 50
TGCGACTGAC GGCCCGATGC CGCAGACTCG TGAGCACATC CTGCTGGGTC 100
GTCAGGTAGG CGTTCCGTAC ATCATCGTGT TCCTGAACAA ATGCGACATG 150
GTTGATGACG AAGAGCTGCT GGAAGTGGTT GAAATGGAAG TTCGTGAACT 200
10 TCTGTCTCAG TACGACTTCC CGGGCGACGA CACTCCGATC GTTCGTGGTT 250
CTGCTCTGAA AGCGCTGGAA GGCGACGCAG AGTGGGAAGC GAAAATCCTG 300
GAACTGGCTG GCTTCCTGGA TTCTTACATT CCGGAACCAG AGCGTGCGAT 350
TGACAAGCCG TTCCTGCTGC CGATCGAAGA CGTATTCTCC ATCTCCGGTC 400
GTGGTACCGT TGTTACCGGT CGTGTAGAAC GCGGTATCAT CAAAGTTGGT 450
15 GAAGAAGTTG AAATCGTTGG TATCAAAGAG ACTCAGAAGT CTACCTGTAC 500
TGGCGTTGAA ATGTTCCGCA AACTGCTGGA CGAAGGCCGT GCTGGTGAGA 550
ACGTAGGTGT TCTGCTGCGT GGTATCAAAC GTGAAGAAAT CGAACGTGGT 600
CAGGTACTGG CTAAGCCGGG CACCATCAAG CCGCACACCA AGTTCGAATC 650
TGAAGTGTAC ATTCTGTCCA AAGATGAAGG CGGCCGTCAT ACTCCGTTCT 700
20 TCAAAGGCTA CCGTCCGCAG TTCTACTTCC GTACTACTGA CGTGACTGGT 750
ACCATCGAAC TGCCGGAAGG CGTAGAGATG GTAATGCCGG GCGACAACAT 800
CAAAATGGTT GTTACCCTGA TCCACCCGAT CGCGATGGAC GACGGTCTGC 850
GTTTCGCAAT CCGTGAAGGC GGCCGTACCG TTGGCGCGGG C 891

25

2) INFORMATION FOR SEQ ID NO: 1669

(i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 805 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

35 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Saksenaea vasiformis*
(B) STRAIN: ATCC 60625

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1669

TCCTCGTGGT CGCCGCCACC GACGGCCCGA TGCCGCAGAC CAAGGAGCAC 50
GTGCTCCTGG CCCGCCAGGT CGGCGTTCCG TACATCGTCG TCGCCCTCAA 100
45 CAAGGCCGAC ATGGTGGACG ACGAGGAGAT CCTGGAGCTC GTCGAGCTCG 150
AGGTCCGTGA GCTCCTCTCC GAGTACGAGT TCCC GGCGCA CGACGTTCCC 200
GTCGTCAAGG TCTCCGCTCT GAAGGCCCTC GAGGGCGACA AGGAGTGGGG 250
CAACTCGGTT CTCGAGCTCA TGAACGCCGT CGACACGGCG ATCCCCGAGC 300
CCGAGCGTGA CGTCGACAAG CCGTTCCCTCA TGCCGATCGA GGACGTCTTC 350
50 ACGATCACCG GTCGCGGTAC GGTGCTCACC GGCCGTATCG AGCGTGGTGT 400
CCTGAAGGTC AACGAGACCG TCGACATCAT CGGCATCAAG ACCGAGAAGA 450
CCACCACCAC GGTCAACGGC ATCGAGATGT TCCGGAAGCT CCTCGACGAG 500
GGCCAGGCCG GTGAGAACGT CGGTCTGCTC CTCCGTGGCA TCAAGCGCGA 550

	GGACGTCGAG	CGCGGCCAGG	TCATCATCAA	GCCGGGCTCG	GTCACGCCGC	600
	ACACGGAGTT	CGAGGCGCAG	GCCTACATCC	TGTCCAAGGA	CGAGGGTGGC	650
	CGCCACACGC	CGTTCCTTCAA	CAACTACCGC	CCGCAGTTCT	ACTTCCGTAC	700
	GACGGACGTG	ACCGGCGTGG	TGACCCTCCC	CGAGGGCACC	GAGATGGTCA	750
5	TGCCGGGTGA	CAACACCGAG	ATGAAGGTGG	AGCTCATCCA	GCCCCGTCGCC	800
	ATGGA					805

10 2) INFORMATION FOR SEQ ID NO: 1670

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 935 bases
 (B) TYPE: Nucleic acid
 15 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

20 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Trichophyton tonsurans*
 (B) STRAIN: ATCC 56185

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1670

25	GCTTCTGACG	GTCAAATGTA	ATTGAATGCC	CGCCCAGACA	GATGAAAGGA	50
	TTTGACGTTT	CTAACATCAG	TCTAGGCCCTC	AGACCAGAGA	ACATTTGCTC	100
	CTTGCCCGCC	AGGTCGGTGT	CCAGAAGCTG	GTCGTTTTTCG	TTAACAAGGT	150
	CGATGCCGTT	GAGGACCCAG	AGATGTTGGA	GCTTGTCGAA	CTTGAAATGC	200
30	GTGAACCTCT	CAGCCACTAC	GGTTTCGAGG	GTGAGGAGAC	CCCCATCATT	250
	TTTGGCTCTG	CTCTCTGTGC	CCTCGAGTCC	CGTCGACCTG	AGCTTGGTGT	300
	CGAGAAGATT	GACGAGCTAT	TGAACGCCGT	CGACACCTGG	ATCCCCACCC	350
	CAGAGCGCGC	CACTGATAAG	CCTTTCCTCA	TGTCCATTGA	GGAAGTGTTT	400
	TCTATCTCTG	GTCGTGGTAC	CGTCGTCTCC	GGTCGTGTTG	AGCGTGGTAT	450
35	CCTCAAGAAG	GATTCGGACG	TCGAAATTGT	TGGTGGCTCT	ACCACCCCTA	500
	TCAAGACCAA	GGTCACCGAT	ATCGAAACCT	TCAAGAAGTC	CTGCGATGAA	550
	TCTCGAGCTG	GTGACAACTC	TGGTCTCCTT	CTCCGAGGTA	TCAAGCGTGA	600
	GGAATTGAAG	CGTGGAATGG	TTGTTGCTGC	CCCCGGATCC	ACCAAGGCTC	650
	ACACCGACTT	CATGGTCTCC	CTCTACGTCC	TGACTGAGGC	TGAGGGTGGT	700
40	CGTTCCAACG	GCTTCACCCA	CAAGTACCGC	CCCCAAATGT	TCATCCGTAC	750
	TGCTGGTATG	TAACCCAAAGT	TTCCGCTATT	TACTAAGTAG	ATCATTGCTA	800
	ACTTGTATTT	CCTTCCGTAG	ACGAAGCCGC	ATCTTTCAGC	TGGCCTGGAG	850
	AAGACCAAGA	CAAGAAGGCT	ATGCCTGGTG	ACAACGTCGA	GATGATTTGC	900
45	AAGACCCTCC	ACCCCATTCG	TGCCGAGGCT	GGCCA		935

2) INFORMATION FOR SEQ ID NO: 1671

50 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 772 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

5 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Enterobacter aerogenes*

(B) STRAIN: ATCC 13048

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1671

10
 ACGATGCCCT TGAGGTACAG AATGGTAATG AGAGCCTGGT GCTGGAAGTT 50
 CAGCAGCAGC TCGGCGGTGG CGTAGTCCGT GCTATCGCCA TGGGTCTTC 100
 CGACGGTCTG CGTCGTGGTC TGGAAGTTAA AGACCTGAG CACCCGATCG 150
 AAGTCCCGGT AGGTAAAGCG ACTCTGGGCC GTATCATGAA CGTCCTGGGT 200
 15 CAGCCGATCG ACATGAAAGG CGACATCGGC GAAGAAGAAC GTTGGGCTAT 250
 CCACCGCGCG GCGCCTTCCT ATGAAGAGCT GTCCAGCTCT CAGGAACTGC 300
 TGGAAACCGG CATCAAAGTT ATCGACTTGA TGTGTCCGTT CGCTAAGGGC 350
 GGTAAAGTTG GTCTGTTCGG TGGTGCGGGT GTAGGTAAAA CCGTAAACAT 400
 GATGGAGCTG ATCCGTAACA TCGCGATCGA GCACTCCGGT TACTCCGTGT 450
 20 TTGCGGGCGT TGGTGAGCGT ACTCGTGAGG GTAACGACTT CTATCACGAA 500
 ATGACCGACT CCAACGTTCT GGATAAAGTA TCCCTGGTTT ACGGCCAGAT 550
 GAACGAGCCG CCGGGAAACC GTCTGCGCGT TGCCTGACC GGCCTGACCA 600
 TGGCTGAGAA ATTCCGTGAC GAAGGTCGTG ACGTTCTGCT GTTCGTCGAT 650
 AACATCTATC GTTACACCCT GGCCGGTACT GAAGTATCTG CACTGCTGGG 700
 25 CCGTATGCCT TCAGCGGTAG GTTATCAGCC GACTCTGGCG GAAGAGATGG 750
 GCGTTCTGCA GGAACGTATC AC 772

30 2) INFORMATION FOR SEQ ID NO: 1672

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1401 bases

(B) TYPE: Nucleic acid

35 (C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

40 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Bordetella pertussis*

(B) STRAIN: Tohama 1

(C) ACCESSION NUMBER: Genome project

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1672

ATGAGCAACG GAACCATCGT TCAGTGCATC GGCGCCGTGG TGGATATTCA 50
 GTTCCCCCGC GATAACATGC CCAAGATCTA CGAAGCGCTC ACCCTGGTCG 100
 ACGAGGGTTC CTCGTTCGCC GAGAAGGGCT TGACGCTGGA AGTGCAACAA 150
 50 CAGCTGGGCG ACGGCGTGGT GCGTACCATC GCGCTGGGTT CCAGCGACGG 200
 GCTGCGCCGC GGCATGCAAG TGGCCGGCAC CGGCGCACCG ATCTCGGTGC 250
 CCGTGGGCCA CGGCACCTG GGCCGCATCA TGGACGTGCT GGGCCGTCCC 300
 ATCGACGAAG CCGGTCCCAT CGCCTCCGAC GAGAAGCGCG CCATCCACCA 350

	GCCCCGCGCC	CGTTTCGACG	AGCTGTCGCC	GTCGGTCGAG	CTGCTGGAAA	400
	CCGGCATCAA	GGTTATCGAC	CTGGTGTGCC	CGTTCGCCAA	GGGCGGCAAG	450
	GTCGGCCTGT	TCGGCGGCGC	CGGCGTGGGC	AAGACCGTCA	ACATGATGGA	500
	ACTGATCAAC	AACATCGCCA	AGCAGCACAG	CGGCTTGTCG	GTGTTGCGCC	550
5	GCGTGGGCGA	GCGTACCCGC	GAAGGCAACG	ACTTCTACCA	CGAAATGGAA	600
	GAGTCGAACG	TTCTGGACAA	GGTGGCCATG	GTGTTCGGCC	AGATGAACGA	650
	GCCCCCGGGC	AACCGCCTGC	GCGTGGCGCT	GACCGGCCTG	ACCATGGCCG	700
	AGAAGTTCCG	CGACGAAGGC	CGTGACATCC	TGTTCTTCGT	CGACAACATC	750
	TACCGCTACA	CCCTGGCCCG	TACCGAAGTG	TCGGCGCTGC	TGGGCCGTAT	800
10	GCCGTCGGCG	GTGGGCTACC	AGCCTACGCT	GGCCGAGGAA	ATGGGCGTGC	850
	TGCAAGAGCG	CATCACCTCG	ACCAAGACCG	GTTTCGATCAC	CTCGATCCAG	900
	GCCGTGTACG	TGCCTGCCGA	CGACTTGACC	GACCCGTCGC	CCGCCACGAC	950
	CTTCCAGCAC	TTGGAATCGA	CCGTCTGTCT	GTCGCGTGAC	ATCGCTGCGC	1000
	TGGGCATCTA	TCCCGCCGTG	GACCCGCTGG	ATTCTCTCCAG	CCGCCAGCTC	1050
15	GACCCGCAAG	TCGTGGGCGA	AGAGCACTAC	CAGGTGGCCC	GTGGCGTGCA	1100
	GCAGACGCTG	CAGCGCTACA	AGGAAGTGGC	CGACATCATC	GCGATTCTGG	1150
	GCATGGACGA	ACTGTCGCCG	GAAGACAAGC	AGGCCGTGGC	CCGCGCGCGC	1200
	AAGATCCAGC	GCTTCTGTG	GCAGCCCTTC	TACGTGGCCG	AAGTGTTTAC	1250
	CGGCTCGCCG	GGCAAGTACG	TGTCGCTGGC	CGAAACGATC	CGTGGCTTCA	1300
20	AGATGATCGT	CGACGGCGAG	TGCGACGCGC	TGCCCAGGCA	GGCGTTCTAC	1350
	ATGGTTCGGC	CGATCGACGA	GGCCTTCGAG	AAGGCCAAGA	AACTCCAATA	1400
	A					1401

25

2) INFORMATION FOR SEQ ID NO: 1673

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 797 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Arcanobacterium haemolyticum*
 (B) STRAIN: ATCC 9345

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1673

	CAGCTACCGA	CGGTCCAATG	GCTCAGACCC	GCGAGCACGT	TCTTCTTGCT	50
	CGCCAGGTTG	GCGTTCCACA	GATCATCGTT	GCTCTCAACA	AGGCTGACAT	100
	GGTTGACGAC	GAGGAAATCC	TCGAACTCGT	CGAAATGGAA	GTTCGTGAGC	150
45	TTCTCTCTTC	CCAGGAGTAC	CCAGGTGACG	ACCTCCAGT	CGTCAAGATC	200
	TCGGCACTCA	AGGCTCTCGA	AGGCGATGCC	GAATGGAGCA	AGGCAATCGA	250
	AGATCTCATG	GAAGCTGTCT	ATACCTACTT	CGACGATCCA	GTGCGTGACC	300
	TCGATAAGCC	ATTCCTCATG	CCAATCGAAG	ACGTCTTCAC	CATCACCAGT	350
	CGTGGCACC	TTGTTACCGG	CCGTGCAGAG	CGCGGTATGC	TCAACTTGAA	400
50	CGAAGAAGTT	GAAATCCTCG	GTATCCGTGC	ACCACAGAAG	ACAACCGTTA	450
	CCGGTATCGA	AATGTTCCAC	AAGTCGATGG	ATCACGCAGA	TGCAGGCGAA	500
	AACTGTGGTC	TTCTCCTCCG	TGGCACCAAG	CGCGAAGATG	TTGAACGTGG	550
	TCAGGTTGTT	GCCAAGCCAG	GCACCATCAC	CCCACACACC	AACTTCGAAG	600

CTCAGGTCTA	CGTGCTCGGT	AAGGAAGAAG	GTGGCCGTCA	CAACCCATTC	650
TTCTCCAAC	ACCGTCCACA	GTTCTACTTC	CGTACCACGG	ATGTTACCGG	700
CGTGATCACC	CTTCCAGAGG	GCACCGAAAT	GGTTATGCCA	GGCGACAACA	750
CCGACATGAC	AGTTGAGCTC	ATCCAGCCAA	TCGCTATGGA	AGAGGGC	797

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2) INFORMATION FOR SEQ ID NO: 1674

10 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 785 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

15

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Butyrivibrio fibrisolvens*
- (B) STRAIN: ATCC 19171

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1674

CTGATGGTCC	TATGCCACAG	ACCCGTGAGC	ACATCCTATT	AGCACGTCAG	50
GTAGGCGTAC	CATACATCAT	CGTATTCCTA	AACAAGTGCG	ATATGGTTGA	100
CGACGAGGAA	TTATTAGAGT	TAGTTGAGAT	GGACGTACGT	GATCTATTAA	150
ATCAGTACCA	GTTCCCAGGC	GACGACACTC	CAATCATCCG	TGGTTCAGCA	200
CTAGGTGCAT	TAAACGGCGA	AGAGAAGTGG	AAAGAGGCAA	TCTATCAGTT	250
AGCAGACACT	CTAGATTCAT	ACATTCCAGA	GCCAAAGCGT	GATATCGATG	300
ATCCATTCTT	ATTACCAATC	GAAGATATCT	TCTCAATCTC	AGGTCGTGGT	350
ACTGTAGTAA	CCGGCCGTGT	AGAGCGTGGT	ATTGTACACG	TAGGTGACGA	400
AGTTGAAATC	GTTGGTATTC	GTCCAACCAC	CAAGACCACT	GTAAGTGGCG	450
TTGAAATGTT	CCGTAAGTTA	CTAGACGAAG	GTCGTGCAGG	TGATAACGTT	500
GGTGTCTTAC	TACGTGGTAC	CAAGCGTGAT	GAGGTTGAGC	GTGGTCAGGT	550
TCTAGCTGCT	CCAGGCACAA	TCACTCCACA	CACCAAGTTC	ACTGGTCAGG	600
TTTACGTACT	AAGCAAGGAT	GAAGGTGGTC	GTCACACTCC	ATTCTTCAAG	650
GGCTACCGTC	CACAGTTCTT	CTTCCGTACA	ACCGATATTA	CCGGTTCTAT	700
CGATCTGAAA	GAGGGCGTAG	AGATGGTAAT	GCCAGGTGAT	AACACCGACA	750
TGACCGTAAC	CCTAATCCAC	CCAGTAGCTA	TGGCT		785

40

2) INFORMATION FOR SEQ ID NO: 1675

45 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 835 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Campylobacter jejuni* subsp. *doylei*

(B) STRAIN: ATCC 49349

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1675

5
 TGGGGCGATC TTGGTTGTTT CTGCTGCAGA TGGTCCTATG CCACAAACTA 50
 GAGAGCACAT TCTTCTTTCT CGTCAAGTAG GCGTTCCATA TATTGTTGTT 100
 TTTATGAATA AAGCAGATAT GGTTGATGAT GCTGAGCTTT TAGAGTTAGT 150
 TGAAATGGAA ATTAGAGAAT TATTAAGCTC TTATGATTTT CCAGGCGATG 200
 10 ATACACCTAT TATTTCTGGT TCTGCTTTAA AAGCTCTTGA AGAAGCTAAA 250
 GCTGGACAAG ATGGTGAATG GTCAGCAAAA ATTATGGATC TTATGGCTGC 300
 AGTTGATAGT TATATTCCAA CTCCAACCTCG TGATACTGAA AAAGACTTCT 350
 TGATGCCAAT TGAAGACGTT TTCTCAATTT CAGGTCGTGG TACTGTTGTT 400
 ACAGGTAGAA TTGAAAAAGG TGTTGTAAAA GTAGGTGATA CTATCGAAAT 450
 15 CGTTGGTATT AAAGACACTC AAACAACAAC TGTAACAGGT GTTGAAATGT 500
 TCAGAAAAGA AATGGATCAA GGCGAGGCAG GAGATAACGT AGGTGTTCTT 550
 CTTCTGGTGA CTA AAAAAGA AGAAGTTATT CGCGGTATGG TTCTTGCTAA 600
 ACCAAAATCA ATTACTCCAC AACTGACTT CGAAGCTGAA GTTTATATCT 650
 TAAATAAAGA TGAAGGTGGT AGACATACTC CATTCTTTAA CAACTATAGA 700
 20 CCACAGTTTT ATGTAAGAAC AACTGATGTT ACAGGTTCTGA TTAAATTAGC 750
 TGATGGTGTG GAAATGGTTA TGCCAGGTGA AAATGTGAGA ATTACTGTAA 800
 GCTTGATCGC TCCAGTAGCA CTTGAAGAAG GAACT 835

25

2) INFORMATION FOR SEQ ID NO: 1676

(i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 812 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

35

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Campylobacter lari*

(B) STRAIN: ATCC 43675

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1676

TTCTGCAGCA GACGGCCCTA TGCCACAAAC TAGAGAGCAT ATCTTACTTT 50
 CTCGTCAAGT AGGTGTACCA TATATTGTTG TTTTCATGAA CAAAGCTGAT 100
 ATGGTTGATG ATGCAGAATT ATTAGAATTA GTTGAAATGG AAATTAGAGA 150
 45 ATTACTAAGC TCTTATGATT TCCCAGGAGA TGATACTCCA ATTATTTTCAG 200
 GTTCAGCATT ACAAGCTCTT GAAGAAGCAA AAGCTGGTCA AGATGGTGAA 250
 TGGTCTAAAA AAATCTTAGA TCTTATGGCT GCAGTTGATG ATTATATTCC 300
 AACTCCGGCT CGTGATACAG ATAAAGATTT CTTGATGCCA ATCGAAGATG 350
 TTTTCTCAAT CTCAGGTCGT GGAAGTGTG TTACCGGTAG AATTGAAAAA 400
 50 GGTGTTGTAA AAGTTGGTGA TACTATAGAA ATCGTTGGTA TTAGAGACAC 450
 TCAAACAACC ACAGTTACTG GTGTTGAAAT GTTTAGAAAA GAAATGGATC 500
 AAGGTGAAGC TGGTGATAAT GTTGGTGTAT TACTTCGTGG AACTAAAAAA 550
 GAAGATGTTG AACGTGGTAT GGTTCTTGCT AAACCAAAAT CAATCACTCC 600

	ACATACTGAT	TTTGAAGCAG	AAGTTTATAT	CTTAAATAAA	GATGAAGGTG	650
	GTCGTCATAC	TCCATTCTTT	AATAATTATA	GACCGCAATT	TTATGTAAGA	700
	ACAACTGATG	TTACAGGTGC	TATTAACTT	GCAGAAGGCG	TTGAGATGGT	750
	TATGCCAGGC	GATAATGATA	GAATTACTGT	AAGTCTTATT	GCTCCAGTTG	800
5	CACTTGAGGA	AG				812

2) INFORMATION FOR SEQ ID NO: 1677

10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 828 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- 15 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 20 (A) ORGANISM: *Campylobacter sputorum* subsp. *sputorum*
- (B) STRAIN: ATCC 35980

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1677

25	GCTATTCTTG	TATGTTGAGC	TGCAGATGGT	CCAATGCCAC	AGACTAGAGA	50
	GCATATTCTA	CTATCAAGAC	AAGTTGGTGT	TCCATACATA	GTTGTTTTCT	100
	TAAATAAAGA	AGATATGGTT	GATGATGCTG	AGCTTATAGA	GTTGGTTGAA	150
	GTTGAGGTTA	GAGATTTATT	AAATGAATAT	GATTTCCCTG	GAGATGATAC	200
	TCCAATCGTA	ATAGGTTCTG	CTCTTAAAGC	TTTAGAAGAA	GCAAAAGCTG	250
30	GAACAGAGGG	TGAATGGTCT	GCTAAAATTA	TGAAACTTAT	GGATGCTGTT	300
	GATAGCTATA	TCCCAACTCC	AACAAGAGAT	ACAGATAAAG	ATTCCTTAT	350
	GCCAATCGAA	GATATCTTCT	CAATTTCTGG	TCGTGGTACA	GTTGTAACAG	400
	GTAGAATTGA	AAAAGGTGTA	GTAAAAGTTG	GCGAGACTAT	TGAGATAGTT	450
	GGTATTAGAC	CTACTCAAAC	AACAACAGTT	ACTGGTGTG	AAATGTTTAA	500
35	AAAAGAGCTA	GATCAAGGTG	AAGCTGGAGA	TAATGTTGGT	ATCTTGTTAA	550
	GAGGTACAAA	AAAAGAAGAT	GTTGAAAGAG	GTATGGTTTT	ATGTAAACCA	600
	AAATCAATCA	CTCCTCACAA	GAAATTTGAA	GGCGAAGTTT	ATATTCTTAC	650
	AAAAGATGAA	GGTGGTAGAC	ATACTCCTTT	CTTTAGTAAC	TATAGACCAC	700
	AATTTTATGT	TAGAACAACA	GATGTAACAG	GTTCTATATC	TCTTCCTGAG	750
40	GGAACAGAGA	TGGATATGCC	TGGTGATAAT	GTAAAACCTTA	CAGTTGAACT	800
	TATAAACCCA	ATTGCTCTTG	AGCAAGGA			828

45 2) INFORMATION FOR SEQ ID NO: 1678

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 820 bases
- (B) TYPE: Nucleic acid
- 50 (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Campylobacter upsaliensis*
 (B) STRAIN: ATCC 49815

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1678

CGATTTTGGT TGTTCCTGCT GCTGATGGTC CTATGCCACA AACTAGAGAG 50
 CACATTTTGC TTTCTCGTCA AGTGGGTGTT CCTTATATCG TAGTTTTTAT 100
 10 GAATAAGGCT GATATGGTTG ATGATGCAGA GCTTTTAGAA TTGGTTGAAA 150
 TGGAAATTAG AGAACTTTTA AGCTCTTATG ATTTCCCGGG CGATGACACT 200
 CCTATCATTT CAGGCTCTGC TCTTCAAGCC TTAGAAGAGG CTAAGGCGGG 250
 ACAAGATGGC GAGTGGTCAG CTAAGATTTT AGAGCTTATG AAGGCAGTTG 300
 ATGAGTATAT CCCAACTCCT GTTCGCGATA CTGAAAAAGA TTTCTTGATG 350
 15 CCTATTGAAG ATGTTTTTTC AATTTCTGGT CGTGGAAGT TGTAAACAGG 400
 TAGAATTGAA AAAGGTGTGG TTAAAGTCGG CGATACTATT GAGATAGTAG 450
 GTATCAAAGA TACTCAAAC ACAACAGTTA CAGGCGTTGA GATGTTTAGA 500
 AAAGAAATGG ATCAAGGTGA GGCTGGCGAT AATGTCGGTG TGCTTTTAAG 550
 AGGAACAAAA AAAGAAGATG TTCTTCGTGG TATGGTTCTT GCAAAGCCTA 600
 20 AATCTATCAC TCCTCATACT GATTTTGAAG CAGAAGTTTA TATTCTAAAT 650
 AAAGATGAGG GCGGTCGCCA TACTCCTTTC TTAAACAATT ATCGTCCGCA 700
 GTTTTATGTA AGAACGACTG ATGTAAGTGG TTCTATTAAA TTAGCTGATG 750
 GTGTTGAGAT GGTTATGCCG GGTGAAAATG TAAGAATTAC AGTTAGCCTT 800
 ATCGCTCCAG TTGCACTTGA 820

25

2) INFORMATION FOR SEQ ID NO: 1679

30 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 783 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Globicatella sanguis*
 40 (B) STRAIN: ATCC 51173

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1679

CTGCAGCTGA TGGTCCAATG CCTCAAACAC GTGAACATAT CTTATTATCA 50
 45 CGTCAAGTAG GTGTTCTTA CATGGTTGTC TTCTTAAACA AAGTTGACAT 100
 GGTGACGAT GAAGAATTAT TAGAATTAGT TGAAATGGAA GTTCGTGATT 150
 TATTATCTGA ATACGAATTC CCTGGAGACG ACGTTCCAGT AATCGCTGGT 200
 TCAGCTTTAA AAGCTTTAGA AGGCGAAGAA CAATATGAAG CAAAAGTATT 250
 AGAATTAATG GAAGCTGTAG ATACATACAT TCCAGAACCA GTTCGTGATA 300
 50 CTGAAAAACC ATTCATGATG CCAGTTGAAG ATGTGTTCTC AATCACAGGT 350
 CGTGGTACAG TTGCTACTGG ACGTGTGAA CGTGACAAG TTAAAGTTGG 400
 TGACGAAGTT GAAATCGTTG GTATTGCTGA AGAAATTAGC AAAACAACCTG 450
 TAACTGGTGT TGAAATGTTC CGTAAATTAT TAGATTACGC TGAAGCTGGA 500

	GATAACATTG	GTGCGTTATT	ACGTGGTGT	ACACGTGAAC	AAATCCAACG	550
	TGGTCAAGTA	TTAGCAAAAC	CAGGAACAAT	TACACCTCAT	ACTAAATTCTG	600
	AGGCGGAAGT	TTACGTATTA	TCAAAAAGAAG	AAGGTGGACG	TCATACTCCA	650
	TTCTTCGCTA	ACTACCGTCC	TCAATTCTAC	TTCCGTACAA	CTGACGTTAC	700
5	AGGTGTTGTA	GAATTACCAG	AAGGTACAGA	AATGGTAATG	CCTGGAGATA	750
	ACGTATCAAT	GACAGTTGAA	TTAATTCACC	CAA		783

10 2) INFORMATION FOR SEQ ID NO: 1680

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 823 bases
 (B) TYPE: Nucleic acid
 15 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

20 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Lactobacillus acidophilus*
 (B) STRAIN: ATCC 4356

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1680

25	GCTATCTTAG	TTGTTGCTGC	AACTGATGGT	CCTATGCCAC	AAACTCGTGA	50
	ACACATTTTG	CTTGCTCGTC	AAGTTGGTGT	TAACATACATC	GATGATTCT	100
	TGAACAAGTG	CGATTTAGTT	GACGACCCAG	AATTGATCGA	CTTGGTTGAA	150
	ATGGAAGTTC	GTGACTTGTT	GACTGAATAC	GATTACCCTG	GTGATGATAT	200
30	TCCAGTTGTT	CGTGGTTCAG	CATTAAAGGC	TTTACAAGGT	GACAAGGAAG	250
	CTCAAGACCA	AATCATGAAG	TTGATGGACA	TTGTTGATGA	ATACATCCCA	300
	ACTCCAGAAC	GTCAAACCTGA	CAAGCCATTC	TTGATGCCAG	TTGAAGACGT	350
	ATTCATATC	ACTGGTCGTG	GACTGTGTC	TTCAGGTCGT	ATCGACCGTG	400
	GACTGTAA	GGTCGGTGAC	GAAGTTGAA	TCGTTGGTTT	GGTAGATAAA	450
35	GTTCTTAAGT	CAGTTGTAC	TGGTTTGAA	ATGTTCCACA	AGACTTTGGA	500
	CTTAGGTGAA	GCCGGCGATA	ACGTTGGTGT	ATTGCTTCGT	GGTGTTGACC	550
	GTGATCAAGT	TGTTCTGGT	CAAGTATTGG	CTGCACCCGG	CTCAATCCAA	600
	ACTCATAAGA	AGTTTAAGGC	ACAAGTTTAT	GTTTGAAGA	AGGACGAAGG	650
	TGGTCGTCAC	ACTCCATTCT	TCTCAGACTA	CCGTCCACAA	TTCTACTTCC	700
40	ACACCACTGA	TATTACTGGT	GAAATTGAAT	TGCCAGAAGG	TACTGAAATG	750
	GTTATGCCTG	GTGATAACAC	TGAATTCAC	GTTACTTTGA	TCAAGCCAGC	800
	TGCCATCGAA	AAGGGTACTA	AGT			823

45

2) INFORMATION FOR SEQ ID NO: 1681

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 793 bases
 50 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 5 (A) ORGANISM: *Leuconostoc mesenteroides* subsp.
dextranicum
(B) STRAIN: ATCC 19255

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1681

```
10 GCTGCAACTG ATGGTCCTAT GCCACAAACA CGTGAAGACA TCTTGTTGGC 50
   ACGTCAAGTT GGTGTTGACT ACTTGTTGT CTTCTTGAAC AAGACTGATT 100
   TGGTTGATGA TGAAGAATTA GTTGAATTGG TTGAAATGGA AGTTCGTGAA 150
   TTGTTGTCAG AATATGACTT CCCAGGTGAC GATATTCCTG TACTTAAGGG 200
   TTCAGCTTTG AAGGCTTTGG AAGGTGATCC TGAACAAGTT AAGGTTATCG 250
15 AAGAATTGAT GGATACTGTT GATTCATACA TTCCAGAACC AGCACGTGAA 300
   ACAGACAAGC CATTCTTGAT GCCTGTCGAA GACGTCTTCA CAATCACTGG 350
   TCGTGGTACA GTTGCTTCTG GTCGTGTTGA CCGTGGTGTA TTGACTACAG 400
   GAACTGAAAT TGAAATCGTT GGTTTGAAGG ACGAAGTTCA AAAGACTACT 450
   GTTACAGGTA TCGAAATGTT CCGTAAGACT TTGGAAGAAG CTCAAGCGGG 500
20 TGATAACATT GGTGCATTGT TGC GTGTTGT TGATCGTAGC AACATTGAAC 550
   GTGGTCAAGT TTTGGCAAAG CCAGGTTCAA TTAAGACACA CAAGAAGTTC 600
   AAGGCTGAAG TTTATGTCTT GACAAAGGAA GAAGGTGGTC GTCATACACC 650
   ATTCTTCACT AACTACCGTC CACAATTCTA CTTCCACACA ACTGATGTTA 700
   CAGGTGTTGT TGAATTGCCA GCCGGTGTG AAATGGTTAT GCCTGGTGAC 750
25 CAAGTGACAT TCGAAATCGA ATTGATCTCA CCAGTTGCCA TCG 793
```

2) INFORMATION FOR SEQ ID NO: 1682

30

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 796 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
35 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 40 (A) ORGANISM: *Prevotella buccalis*
(B) STRAIN: ATCC 35310

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1682

```
45 TATCCTTGTA GTTGCTGCTA CTGATGGTCC TATGCCACAG ACACGTGAGC 50
   ACGTGCTTTT GGCTCGTCAG GTAAACGTTT CTCGTTTGGT TGTGTTTCATG 100
   AACAAAGTGT ACTTGGTAGA AGACGAAGAG ATGCTTGAAC TCGTTGAAAT 150
   GGAGTTGCGC GAACTTCTTG AGCAATACGA ATTCGAAGAG GATACTCCAA 200
   TCGTTTCGTG TTCTGCACTG GGTGCATTGA ATGGTGTTGA CAAGTGGGTT 250
50 GACAGCGTGA TGACGTTGAT GGACACTGTT GACGAGTGGA TTCAAGAGCC 300
   AGAGCGTGAC CTTGACAAAC CTTTCTTGAT GCCAGTAGAG GACGTGTTCT 350
   CTATCACAGG TCGTGGTACC GTTGTAACAG GACGTATTGA GACTGGTAAG 400
   GTAAAGGTTG GCGACGAGAT TCAGTTGCTC GGTCTTGGTG AGGACAAGAA 450
```

	GTCTGTTGTA	ACAGGCGTTG	AAATGTTCCG	TAAGATTCTT	TCTGAAGGTG	500
	AAGCAGGTGA	TAACGTAGGA	CTTTTGCTCC	GCGGTATCGA	TAAGGATGAA	550
	GTAAAGCGTG	GTATGGTTGT	TGTACACCCA	GGTGCCATCA	CTCCTCACGA	600
	TCAC TTCAAG	GCTTCCATCT	ATGTATTGAA	GAAGGAAGAG	GGTGGACGTC	650
5	ATACTCCATT	CGGAAACAAG	TATCGTCCTC	AGTTCTATCT	CCGTACAATG	700
	GACTGTACAG	GTGAGATCAC	TTTGCCAGAA	GCGGTAGAGA	TGGTGATGCC	750
	TGGTGACAAC	G TAGAGATTG	AGGTTACCTT	GATTTACAAG	GTTGCC	796

10

2) INFORMATION FOR SEQ ID NO: 1683

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 800 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

20

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Ruminococcus bromii*
 (B) STRAIN: ATCC 27255

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1683

	GGTTGCTGCT	ACTGACGGCC	CGATGCCTCA	GA CTCTGAG	CACGTTCTGC	50
	TCGCTCGTCA	GGTGGGTGTG	CCCGCCATCG	TCGTCGCCCT	CAACAAGTGC	100
	GACATGGTTG	ACGATGAGGA	GCTCATTGAG	CTTGTCGAGA	TGGAGGTCCG	150
30	CGAGCTGCTG	ACCTCGCAGG	AGTTCGACGG	CGACAACTGC	CCTGTCGTTT	200
	GCATCTCCGC	CTTCCAGGCC	CTCCAGGGTG	ACGAGAAGTG	GACCCAGTCG	250
	ATCCTCGACC	TCATGGACGC	CGTGGACGAG	TACATCCCGC	AGCCTGAGCG	300
	CGATCTCGAC	AAGCCCTTCC	TTATGCCGAT	CGAGGACGTC	TTCACCATCA	350
	CCGGCCGTGG	CACCGTTGTC	ACCGGTCGTG	TCGAGCGTGG	TGTCGTCAAG	400
35	ACTGGCGAAG	AGGTCGAGAT	CGTCGGTATC	CACGAGAAGA	CCCAGAAGAC	450
	CACCGTTACC	GGTGTGAGAA	TGTTCCGTAA	GATCCTCGAC	GAGGGCCGCG	500
	CTGGTGAGAA	CGTCCGCGTT	CTGCTCCGTG	GCACCAAGAA	GGAGGACGTC	550
	GTTCCGCGCA	TGGTCTCTCT	CAAGCCTGGT	TCCACCACCC	CCCACACCGA	600
	CTTCGAGGGC	CAGGTCTACG	TCCTCAAGAA	GGATGAGGGT	GGCCGCCACA	650
40	AGCCGTTCTT	CTCCCATTAC	AGCCCCCAGT	TCTACTTCCG	TACCACGGAC	700
	GTGACTGGCA	CTGTTGAGCT	CCCCGAGGGC	ACCGAGATGG	TCATGCCTGG	750
	CGACAACACC	GACATGACTG	TGCACCTGAT	TCACCCGGTT	GCCATGGAGG	800

45

2) INFORMATION FOR SEQ ID NO: 1684

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 545 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Paracoccidioides brasiliensis*

5 (B) STRAIN: ATCC 32075

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1684

10 TGTCTTTATT CAGGAAGTGA TTGTATGTTT CTTCTCGTTT ATATATAACA 50
 TACCTTCTAT ATTTTCATGTG TTTCTAACGA ACTCATAGAA CAACATTGCC 100
 AAGGCTCACG GTGGTTACTC CGTGTTTACC GGTGTCGGTG AGCGTACCCG 150
 TGAAGGAAAC GATCTGTACC ACGAAATGCA GGAAACCCGC GTCATCCAGC 200
 TGGACGGCGA GTCCAAAGTC GCCCTCGTCT TCGGCCAGAT GAACGAGCCC 250
 CCCGGAGCCC GTGCCCCTGT TGCCCTGACC GGTCTGACCA TCGCTGAATA 300
 15 CTTCCGTGAC GAAGAAGGCC AAGATGGTAC GTTCCCCCAT TCCATATATG 350
 TTTCTTGTGC GCTTTGCCAA CTAAACACCA CCTAGTGCTC CTCTTCATCG 400
 ACAATATCTT CCGCTTCACC CAAGCCGGTT CCGAAGTGTC CGCCCTGCTA 450
 GGCCGCATCC CCTCCGCCGT CGGCTATCAA CCCACCCTCG CCGTCGACAT 500
 GGGTGGTATG CAGGAGCGCA TCACAACCTAC AACAAAAGGC TCCAT 545
 20

2) INFORMATION FOR SEQ ID NO: 1685

25 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1020 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

30

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Candida norvegica*

35 (B) STRAIN: ATCC 36586

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1685

40 GATATCGCTT TATGGAAATT CGAAACTCCA AAATTCCACG TTACYGTTAT 50
 CGATGCTCCA GGTCACAGAG ATTTTCATCAA GAATATGATT ACYGGTACCT 100
 CCCAAGCTGA TTGTGCTATT TTAATCATTG CTGGTGGTGT TGGTGAATTC 150
 GAAGCTGGTA TCTCCAAAGA TGGTCAAACC AGAGAACACG CTTTGTTAGC 200
 TTTCACCTTA GGTGTYYAAC AATTGATTGT TGCCGTTAAC AAAATGGACT 250
 CTGTCAAATG GGATCAATCC CGTTTCGAAG AAATCGTCAA GGAAGCTTCC 300
 45 GGTTCATCA AGAAAGTTGG TTACAACCCA AAGACTGTTC CATTCGTTCC 350
 AATCTCTGGT TGGAAATGGT ACAACATGAT TGAAGTYTCW GCTAACGCYC 400
 CATGGTACAA AGGTTGGGAA AAGGAAACCA AAGCYGGTGT CGTTAAAGGT 450
 AAAACTTTAT TAGAAGCCAT TGATGCTATT GAACCACCTT CAAGACCAAC 500
 TGAAAACCA TTGAGATTGC CATTGCAAGA TGTCTACAAG ATTGGTGGTA 550
 50 TCGGAACCGT ACCAGTCGGT ARAGTTGAAA CCGGTGTCAT TAAACCAGGT 600
 ATGATTGTTA CTTTCGCCCC AGCCGGTGTT ACTACTGAAG TCAAATCTGT 650
 TGAAATGCAT CACGAACAAT TAGAAGCTGG TTACCCAGGT GACAATGTTG 700
 GTTTCACCGT CAAGAATGTT TCAGTTAAAG AAATCAGAAG AGGTAAGHTT 750

	GCTGGTGA	CT	CAACGC	800
	TCAAGTTATT	GTCTTGAACC	ATCCAGGTCA	850
	CAGTTTTGGA	TTGTCACACT	GCCCACATTG	900
	TTGGAAGAA	TTGACAGAAG	ATCCGGTAAG	950
5	ATTCATCAA	TCTGGTGACG	CTGCTAWTGT	1000
	CATTRTGTGT	TGAAGCTTTC		1020

10 2) INFORMATION FOR SEQ ID NO: 1686

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 929 bases
 (B) TYPE: Nucleic acid
 15 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

20 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Aspergillus nidulans*
 (B) STRAIN: WSA-176

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1686

25	TGCTGCTTCC	GATGGTCAAA	TGTACGATTG	ATATTCCTTC	CAGCCAGTCA	50
	GGATAACAGC	TGATACCACT	TGCAATAGG	CCCCAGACTC	GTGAGCACTT	100
	GTTGCTTGCC	CGTCAGGTTG	GTGTCCAGAA	GATCGTTGTC	TTCGTCAACA	150
	AGGTTGACGC	TGTCGATGAC	CCTGAGATGT	TGGAGCTTGT	TGAGCTCGAG	200
30	ATGCGTGAGC	TCCTCAACAC	TTACGGTTTC	GAGGGAGAGG	AGACCCCTAT	250
	CATCTTCGGT	TCCGCCCTGT	GCGCTCTCGA	AGGCCGCCGC	GAGGACATTG	300
	GTA	CTCAGCG	TATTGACTCC	CTCCTCGAGG	CCGTTGACAC	350
	ACCCCCAGC	GTGACTTGGA	CAAGCCCTTC	CTGATGTCCA	TTGAGGAAGT	400
	TTTCTCCATT	GGTGGTCGTG	GTACCGTCGC	CTCTGGTCGT	GTCGAGCGTG	450
35	GTCTCCTCAA	GAAGGATACC	GAAGTTGAAA	TTCACGGTGC	TGATGGTATT	500
	CTGAAGACCA	AGGTCACCGA	CATTGAGACC	TTCAAGAAGA	GCTGCGATGA	550
	GTCTCGTGCT	GGTGACAAC	CCGGTCTTCT	CCTCCGTGGT	ATCCGTCGTG	600
	AGGATGTTTC	TCGTGGTATG	GTCATCGCTG	CCCCTGGCTC	CATCAAGGCC	650
	TCCAAGAAGT	TCATGGTCTC	CATGTACGTC	TTGACTGAGG	CTGAAGGTGG	700
40	CCGCAAGAAC	GGCTTCGGTG	CCA	ACTACCG	CCCCCAGGCT	750
	CTGCTGGTAA	GTTTCGAACT	ATTTGATTCA	TTGATCACGT	CCCTAACTGT	800
	TACTTTAGAC	GAGGCTTGCG	ACCTTCATTT	CCCTGATGAG	GCCGACAAGG	850
	ACCGCCACGT	CATGCCCGGT	GACAACGTCG	AAATGGTCCT	CAACCTCAAC	900
	AACCCCGTTG	CTGCTGAGGC	TGGACAGCG			929

45

2) INFORMATION FOR SEQ ID NO: 1687

50 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 951 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

5 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Aspergillus terreus*

(B) STRAIN: WSA-174

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1687

```

10 TGCCGCTTCC GATGGTCAGA TGTACGCTCA AGCCCCAGTT TCCATATAAA      50
   CATAAACGAT CTATCATCAG CACAACGCTG ACTTCTTCGC TTCCAGGCCCC      100
   CAGACCCGTG AGCACTTGCT GTTGGCCCGT CAGGTCGGTG TCCAGAAGAT      150
   CGTGGTCTTC GTCAACAAGG TCGATGCCGT TGATGACCCG GAGATGTTGG      200
15 AGCTCGTTGA GCTGGAAATG CGCGAGCTCC TGACCAGCTA CGGATTTCGAG      250
   GGTGAAGAGA CCCCCATCAT CTTCGGTTCT GCTCTCTGCG CTCTTGAGGG      300
   CCGCCGTCCT GAGATTGGTA CTGAGAAGAT TGACGAGCTG ATGCACGCCG      350
   TCGACACCTG GATCCCCACC CCCCAGCGTG ACCTCGACAA GCCCTTCCTG      400
   ATGTCCGTCG AGGAAGTCTT CTCCATTGCT GGTCGTGGTA CCGTCGCTTC      450
20 CGGCCGTGTC GAGCGTGGTA TTCTGAAGAA GGATAGCGAA GTCGAGATCA      500
   TCGGTGGTGC TTTCGACGCC ACGAAGACCA AGGTCACTGA CATCGAGACC      550
   TTCAAGAAGT CTTGCGACGA GTCTCGCGCT GGTGACAACT CTGGTCTCCT      600
   CCTCCGTGGT ATCCGTCGTG AGGATGTTCT GCGTGGTATG GTCATTGCTG      650
   CTCCTGGCAG CACCAAGGCC CACGACAAGT TCCTTGTCTC TATGTACGTC      700
25 CTCACTGAGG CTGAGGGTGG CCGTCGTACC GGATTCGGTA CCAACTACCG      750
   CCCCCAGGTC TTCATCCGTA CTGCCGGTAA GTGTTCTTGG AAGAGGCTTT      800
   GAGCCTATAT AGGATCTCGG ATAATTTACT AATCCACCAT ATAGATGAGG      850
   CCGCTGACCT CAGCTTCCCC GACAACGATG ACTCCCGCCG TGTCATGCCC      900
   GGTGACAACG TTGAGATGGT CCTGAAGACC CACCGCCCCG TGGCTGCTGA      950
30 G                                                                951

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2) INFORMATION FOR SEQ ID NO: 1688

35

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 823 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

40

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

45

(A) ORGANISM: *Candida norvegica*

(B) STRAIN: ATCC 36586

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1688

```

50 CGTTGCCGCT ACCGATGGTC AAATGCCTCA AACTAGAGAA CATTGCTAT      50
   TGGCTAGACA GGTGGTGTG CAACACATTG TCGTGTTTGT TAACAAGGTT      100
   GACACTATTG ATGATCCAGA AATGTTGGAA TTGGTTGAAA TGGAATGAG      150
   AGAGTTGATT GCCACTTATG GTTTCGATGG TGATAACACC CCAGTTATCA      200

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	TGGGTTCTGC	TCTATGTGCT	TTGGAAGGTC	GTGAACCTGA	AATCGGTGCT	250
	CAATCAATCG	ACAGATTGTT	GGAAGCCGTT	GATGAATACA	TTCCAACCTCC	300
	AACTAGAGAT	TTGGAAAAAC	CATTCTTGAT	GGGTGTTGAA	GATGTCTTCT	350
	CCATTTCTGG	TAGAGGTACC	GTCTGTACCG	GTCGTGTTGA	AAGAGGTAAC	400
5	TTGAAGAAAG	GTGATGAAAT	CGAAATTGTC	GGCTACAACA	AGACTCCAAT	450
	CAAAACCAAC	GTCACCGGTA	TTGAGATGTT	CAAAAAGGAA	TTAGACCAAG	500
	CTATGGCTGG	TGATAACTGT	GGTATCTTAT	TACGTGGTGT	TAAGAGAGAT	550
	GATATCAAGA	GAGGTATGGT	TATCTCTAAA	GTCAACACCG	TTTCCGCACA	600
	CACCAAATTC	TTGGCCTCTT	TATACGTCTT	GACTAAAGAA	GAAGGTGGTC	650
10	GTCATTGAGG	TTTTGCTGAA	AACTACAGAC	CTCAATTGTT	CATCAGAACC	700
	GGTGATGTCA	CTGTTACTTT	AACCTTCCCA	GAAGATGCTG	ATCACTCTCA	750
	GCAAGTCTTA	CCAGGTGACA	ACGTTGAAAT	GGAATGTACC	TTGGTTCATC	800
	CAACTGCTCT	TGAAACCGGT	CAA			823

15

2) INFORMATION FOR SEQ ID NO: 1689

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 803 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

25 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Candida parapsilosis*

(B) STRAIN: ATCC 201076

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1689

	GCTGCTACTG	ACGGTCAAAT	GCCTCAAAC	AGGGAACATA	TGTTGTTGGC	50
	GAGACAAGTT	GGTATCCAAA	ACTTGGTTGT	TTTTGTTAAC	AAAGTTGATA	100
35	CCATTGATGA	CCCAGAAATG	TTGGAATTGG	TTGAAATGGA	AATGAGGGAA	150
	TTATTGAGCT	CTTATGGGTT	TGATGGTGAA	AACACTCCAG	TTATCATGGG	200
	ATCAGCCTTG	TGTGCTTTAG	AAGGTAAACA	ACCAGAAATC	GGTGTTCAAG	250
	CCATTCAAAA	ATTATTGGAT	GCTGTTGATG	AATATATTCC	AACTCCAGAA	300
	AGAGATGCTG	ACCAACCATT	TTTGATGCCA	GTGGAAGATG	TGTTTTCTAT	350
40	TTCAGGTAGA	GGAACCGTTG	TCACCGGAAG	AGTTGAAAGA	GGTATGTTGA	400
	AGAAAGGTGA	AGAAGTAKAA	GTCATTGGTG	AAAACCTCATT	TAAGGCTACT	450
	TCCACGGGTA	TTGAGATGTT	CAAAAAGGAA	TTGGATGCCG	CTATGGCCGG	500
	TGACAACTGT	GGTATTTTGT	TGAGAGGTGT	CAAGAGAGAC	GAAGTCAAGA	550
	GGGGTATGGT	TTTGCCCAAA	CCAGGTACCA	CCACCCACAC	CCAAAAGTTT	600
45	TTGGCTTCCA	TTTATATCTT	GACTGCTGAA	GAAGGTGGAC	GTAGTACCCC	650
	TTTCAGTGAA	GGATACAAAC	CACAATGTTT	CTTTAGAACT	AGTGATGTTA	700
	CCACGACATT	TACTTTCCCA	GAAGGTGAAG	GTGTTGACCA	CTCACAAATG	750
	GTTATGCCAG	GAGRCAATGT	TGAAATGGTG	GGAACCTTAA	TCAAGAAAGC	800
	TCC					803

50

2) INFORMATION FOR SEQ ID NO: 1690

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 bases
(B) TYPE: Nucleic acid
5 (C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1690

CAGGTCCTGT TGCGACTGAA GAA

23

15

2) INFORMATION FOR SEQ ID NO: 1691

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 bases
20 (B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1691

CACAGATAAA CCTGAGTGTG CTTTC

25

30

2) INFORMATION FOR SEQ ID NO: 1692

- (i) SEQUENCE CHARACTERISTICS:
35 (A) LENGTH: 24 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

40 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1692

GGTGAGAACT GTGGTATCTT ACTT

24

45

2) INFORMATION FOR SEQ ID NO: 1693

- 50 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1693

CATTCAACG CCTTCTTTCA ACTG

24

10

2) INFORMATION FOR SEQ ID NO: 1694

(i) SEQUENCE CHARACTERISTICS:

15

(A) LENGTH: 20 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1694

AAGGCAAGGA TGACAACGGC

20

25

2) INFORMATION FOR SEQ ID NO: 1695

(i) SEQUENCE CHARACTERISTICS:

30

(A) LENGTH: 21 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

35 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1695

ACGATTTCCTTCTTCCTG G

21

40

2) INFORMATION FOR SEQ ID NO: 1696

45 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1696

ATGTTCTGT AGTTGCTGGA

20

5

2) INFORMATION FOR SEQ ID NO: 1697

- (i) SEQUENCE CHARACTERISTICS:
- 10 (A) LENGTH: 22 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

- 15 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1697

20 TTTCTTCAGC AATACCAACA AC

22

2) INFORMATION FOR SEQ ID NO: 1698

- 25 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 23 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - 30 (D) TOPOLOGY: Linear

- (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1698

35 GGAATCAACA GATGGTTTAC AAA

23

2) INFORMATION FOR SEQ ID NO: 1699

- 40 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 20 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - 45 (D) TOPOLOGY: Linear

- (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1699

50 GCATCTTCTG GGAAAGGTGT

20

2) INFORMATION FOR SEQ ID NO: 1700

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: DNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1700

AAGATGCGGA AAGAAGCGAA

20

2) INFORMATION FOR SEQ ID NO: 1701

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 23 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: DNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1701

ATTATGGATC AGTTCTTGGA TCA

23

2) INFORMATION FOR SEQ ID NO: 1702

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 213 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus gordonii*
 (B) STRAIN: Challis V288
 (C) ACCESSION NUMBER: L20574
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1702

TTCATAGACG	CTGAGCACGC	TTTGGATCCA	TCTTACGCGG	CTGCTCTAGG	50
TGTAAATATT	GATGAGCTGT	TGCTATCTCA	ACCAGATTCT	GGTGAGCAAG	100
GTTTAGAAAT	TGCAGGAAAA	TTGATTGACT	CTGGGGCAGT	TGATTTAGTT	150

GTCATCGACT	CTGTTGCAGC	TCTTGTACCA	CGTGCGGAAA	TCGATGGAGA	200
TATCGGTGAT	AGC				213

5

2) INFORMATION FOR SEQ ID NO: 1703

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 692 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

15

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus mutans*
 (B) STRAIN: strain GS-5
 (C) ACCESSION NUMBER: M61897

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1703

GGGCCGGAAT	CTTCTGGTAA	GACAACTGTC	GCTCTTCATG	CTGCTGCTCA	50
GGCGCAAAAA	GATGGCGGTA	TTGCCGCTTT	CATTGATGCA	GAACATGCCC	100
TTGATCCAGC	CTATGCTGCT	GCTCTTGCGC	TTAATATTGA	TGAGCTTTTG	150
CTTTCACAAC	CAGATTCAGG	AGAACAGGGT	CTTGAAATTG	CAGGGAAATT	200
GATTGATTCT	GGCGCTGTTG	ATTTAGTTGT	TGTTGACTCA	GTGGCAGCTT	250
TAGTACCACG	TGCGGAGATT	GACGGAGATA	TTGGTAATAG	TCATGTTGGC	300
TTACAAGCAC	GCATGATGAG	TCAAGCGATG	CGTAAATTAT	CAGCTTCAAT	350
CAATAAAACA	AAAACCATTG	CTATTTTAT	TAATCAATTG	CGGGAAAAAG	400
TTGGTATTAT	GTTTGGTAAT	CCAGAAACAA	CCCCTGGCGG	GCGTGCCTTG	450
AAGTTTTATT	CTTCTGTGCG	TCTTGATGTC	CGCGGCAATA	CTCAAATTAA	500
AGGAACCGGG	GAACAAAAG	ACAGCAATAT	TGGTAAAGAG	ACCAAAATTA	550
AAGTTGTAA	AAATAAAGTT	GCTCCACCAT	TTAAGGAAGC	TTTTGTAGAA	600
ATTATATATG	GTGAAGGCAT	TTCTCGTACA	GGTGAATTAG	TTAAGATTGC	650
CAGTGATTTC	GGAATTATCC	AAAAAGCTGG	AGCTTGGTAC	TC	692

40 2) INFORMATION FOR SEQ ID NO: 1704

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1204 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

50

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
 (C) ACCESSION NUMBER: Z17307

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1704

	ATGGCGAAAA	AACCAAAAAA	ATTAGAAGAA	ATTTCAAAAA	AATTTGGGGC	50
	AGAACGTGAA	AAGGCCTTGA	ATGACGCTCT	TAAATTGATT	GAGAAAGACT	100
5	TTGGTAAAGG	ATCAATCATG	CGTTTGGGTG	AACGTGCGGA	GCAAAAAGGTG	150
	CAAGTGATGA	GCTCAGGTTC	TTTAGCTCTT	GACATTGCCC	TTGGCTCAGG	200
	TGGTTATCCT	AAGGGACGTA	TCATCGAAAT	CTATGGCCCA	GAGTCATCTG	250
	GTAAGACAAC	GGTTGCCCTT	CATGCAGTTG	CACAAGCGCA	AAAAGAAGGT	300
	GGGATTGCTG	CCTTTATCGA	TGCGGAACAT	GCCCTTGATC	CAGCTTATGC	350
10	TGCGGCCCTT	GGTGTCAATA	TTGACGAATT	GCTCTTGTCT	CAACCAGACT	400
	CAGGAGAGCA	AGGTCTTGAG	ATTGCGGGAA	AATTGATTGA	CTCAGGTGCA	450
	GTTGATCTTG	TCGTAGTCGA	CTCAGTTGCT	GCCCTTGTTT	CTCGTGCGGA	500
	AATTGATGGA	GATATCGGAG	ATAGCCATGT	TGGTTTGCAG	GCTCGTATGA	550
	TGAGCCAGGC	CATGCGTAAA	CTTGGCGCCT	CTATCAATAA	AACCAAAACA	600
15	ATTGCCATTT	TTATCAACCA	ATTGCGTGAA	AAAGTTGGAG	TGATGTTTGG	650
	AAATCCAGAA	ACAACACCGG	GCGGACGTGC	TTTGAAATTC	TATGCTTCAG	700
	TCCGCTTGGA	TGTTCTGTGGT	AATACACAAA	TTAAGGGAAC	TGGTGATCAA	750
	AAAGAAACCA	ATGTCGGTAA	AGAACTAAG	ATTAAGGTTG	TAAAAAATAA	800
	GGTAGCTCCA	CCGTTTAAGG	AAGCCGTAGT	TGAAATTATG	TACGGAGAAG	850
20	GAATTTCTAA	GACTGGTGAG	CTTTTGAAGA	TTGCAAGCGA	TTTGATATT	900
	ATCAAAAAG	CAGGGGCTTG	GTATTCTTAC	AAAGATGAAA	AAATTGGGCA	950
	AGGTTCTGAG	AATGCTAAGA	AATACTTGGC	AGAGCACCCA	GAAATCTTTG	1000
	ATGAAATTGA	TAAGCAAGTC	CGTTCTAAAT	TTGGCTTGAT	TGATGGAGAA	1050
	GAAGTTTCAG	AACAAGATAC	TGAAAACAAA	AAAGATGAGC	CAAAGAAAGA	1100
25	AGAAGCAGTG	AATGAAGAAG	TTCCGCTTGA	CTTAGGCGAT	GAACCTGAAA	1150
	TCGAAATTGA	AGAATAAGCT	GTAAAGCAG	TGGAGAAATC	CGCTACTTTT	1200
	TCGA					1204

30.

2) INFORMATION FOR SEQ ID NO: 1705

(i) SEQUENCE CHARACTERISTICS:

35

- (A) LENGTH: 981 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

40

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

45

- (A) ORGANISM: *Streptococcus pyogenes*
- (B) STRAIN: NZ131
- (C) ACCESSION NUMBER: U21934

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1705

	ATGCGTTCAG	GAAGTCTAGC	TCTTGATATT	GCTTGGATAG	CTGGTGGTTA	50
	TCCTAAAGGA	CGTATCATCG	AAATCTATGG	TCCAGAGTCT	TCCGGTAAAA	100
50	CGACTGTGGC	TTTACATGCT	GTAGCACAAG	CTCAAAAAGA	AGGTGGAATC	150
	GCAGCCTTTA	TCGATGCCGA	GCATGCGCTT	GATCCAGCTT	ATGCTGCTGC	200
	GCTTGGGGTT	AATATTGATG	AACCTCTCTT	GTCTCAACCA	GATTCTGGAG	250
	AACAAGGACT	TGAAATTGCA	GGTAAATTGA	TTGATTCTGG	TGCGGTGAC	300

	CTGGTTGTTG	TCGATTCAGT	AGCAGCTTTA	GTGCCACGTG	CTGAAATTGA	350
	TGGTGATATT	GGCGATAGCC	ATGTCCGATT	GCAAGCACGT	ATGATGAGTC	400
	AGGCCATGCG	TAAATTATCA	GCTTCTATTA	ATAAAACAAA	AACTATCGCA	450
	ATCTTTATCA	ACCAATTGCG	TGAAAAAGTT	GGTGTGATGT	TTGGAAATCC	500
5	TGAAACAACA	CCAGGTGGTC	GAGCTTTGAA	ATTCTATGCT	TCTGTTCGGC	550
	TGGATGTGCG	TGGAAACAAC	CAAATTAAAG	GAAGTGGTGA	CCAAAAGATA	600
	GCCAGCATTG	GTAAGGAGAC	CAAATCAAG	GTTGTTAAAA	ACAAGGTCGC	650
	TCCGCCATTT	AAGGTAGCAG	AAGTTGAAAT	CATGTATGGG	GAAGGTATTT	700
	CTCGTACAGG	GGAGCTTGTC	AAAATTGCTT	CTGATTGGA	CATTATCCAA	750
10	AAAGCAGGTG	CTTGTTCTC	TTATAATGGT	GAGAAGATTG	GCCAAGGTTC	800
	TGAAATGCT	AAGCGTTATT	TGGCCGATCA	TCCACAATTG	TTTGATGAAA	850
	TCGACCGTAA	AGTACGTGTT	AAATTTGGTT	TGCTTGAAGA	AAGCGAAGAA	900
	GAATCTGCTA	TGGCAGTAGC	ATCAGAAGAA	ACCGATGATC	TTGCTTTAGA	950
	TTTAGATAAT	GGTATTGAAA	TTGAAGATTA	A		981
15						

2) INFORMATION FOR SEQ ID NO: 1706

20 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 312 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

25

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus salivarius* subsp. *thermophilus*
- (C) ACCESSION NUMBER: M94062

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1706

35	GCGTATGCAC	GAGCTCTAGG	TGTTAATATC	GATGAGCTTC	TTTTGTGCGCA	50
	GCCTGATTCT	GGTGAGCAAG	GTCTCGAAAT	TGCAGGTAAG	CTGATTGACT	100
	CTGGTGCAGT	GGATTTAGTT	GTTGTTGACT	CAGTTGCGGC	CTTCGTACCA	150
	CGTGACAGAA	TTGATGGAGA	TAGTGGTGAC	AGTCATGTAG	GACTTCAAGC	200
	GCGTATGATG	AGTCAAGCCA	TGCGTAAACT	TTCTGCATCT	ATTAATAAAA	250
40	CAAAAACGAT	TGCTATCTTT	ATTAACCACT	TGCGTGAAAA	AGTTGGTATC	300
	ATGTTTGGTA	AC				312

45 2) INFORMATION FOR SEQ ID NO: 1707

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 831 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Escherichia coli*

(C) ACCESSION NUMBER: J02967

5.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1707

	ATGAAAAACA	CAATACATAT	CAACTTCGCT	ATTTTTTTTAA	TAATTGCAAA	50
	TATTATCTAC	AGCAGCGCCA	GTGCATCAAC	AGATATCTCT	ACTGTTGCAT	100
10	CTCCATTATT	TGAAGGAACT	GAAGGTTGTT	TTTTACTTTA	CGATGCATCC	150
	ACAAACGCTG	AAATTGCTCA	ATTCAATAAA	GCAAAGTGTG	CAACGCAAAT	200
	GGCACCAGAT	TCAACTTTCA	AGATCGCATT	ATCACTTATG	GCATTTGATG	250
	CGGAAATAAT	AGATCAGAAA	ACCATATTCA	AATGGGATAA	AACCCCCAAA	300
	GGAATGGAGA	TCTGGAACAG	CAATCATACA	CCAAAGACGT	GGATGCAATT	350
15	TTCTGTTGTT	TGGGTTTCGC	AAGAAATAAC	CCAAAAAATT	AGATTAAATA	400
	AAATCAAGAA	TTATCTCAAA	GATTTTGATT	ATGGAAATCA	AGACTTCTCT	450
	GGAGATAAAG	AAAGAAACAA	CGGATTAACA	GAAGCATGGC	TCGAAAGTAG	500
	CTTAAAAATT	TCACCAGAAG	AACAAATTCA	ATTCCTGCGT	AAAATTATTA	550
	ATCACAATCT	CCCAGTTAAA	AACTCAGCCA	TAGAAAACAC	CATAGAGAAC	600
20	ATGTATCTAC	AAGATCTGGA	TAATAGTACA	AACTGTATG	GGAAAAGTGG	650
	TGCAGGATTC	ACAGCAAATA	GAACCTTACA	AAACGGATGG	TTTGAAGGGT	700
	TTATTATAAG	CAAATCAGGA	CATAAATATG	TTTTTGTGTC	CGCACTTACA	750
	GGAAACTTGG	GGTCGAATTT	AACATCAAGC	ATAAAAGCCA	AGAAAAATGC	800
25	GATCACCATT	CTAAACACAC	TAAATTTATA	A		831

2) INFORMATION FOR SEQ ID NO: 1708

30 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 846 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Enterococcus faecalis*

40 (B) STRAIN: HH22

(C) ACCESSION NUMBER: M60253

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1708

45	TTGAAAAAGT	TAATATTTTT	AATTGTAATT	GCTTTAGTTT	TAAGTGCATG	50
	TAATTCAAAC	AGTTCACATG	CCAAAGAGTT	AAATGATTTA	GAAAAAAAAT	100
	ATAATGCTCA	TATTGGTGTT	TATGCTTTAG	ATACTAAAAG	TGGTAAGGAA	150
	GTAATTTTAA	ATTCAGATAA	GAGATTTGCC	TATGCTTCAA	CTTCAAAAGC	200
	GATAAATAGT	GCTATTTTGT	TAGAACAAGT	ACCTTATAAT	AAGTTAAATA	250
50	AAAAAGTACA	TATTAACAAA	GATGATATAG	TTGCTTATTC	TCCTATTTTA	300
	GAAAAATATG	TAGGAAAAGA	TATCACTTTA	AAAGCACTTA	TTGAGGCTTC	350
	AATGACATAT	AGTGATAATA	CAGCAAACAA	TAAAATTATA	AAAGAAATCG	400
	GTGGAATCAA	AAAAGTTAAA	CAACGTCTAA	AAGAAGTAGG	AGATAAAGTA	450

	ACAAATCCAG	TTAGATATGA	GATAGAATTA	AATTACTATT	CACCAAAGAG	500
	CAAAAAAGAT	ACTTCAACAC	CTGCTGCTTT	CGGTAAGACT	TTAAATAAAC	550
	TTATCGCAA	TGGAAAATTA	AGCAAAGAAA	ACAAAAAATT	CTTACTTGAT	600
	TTAATGTAA	ATAATAAAAG	CGGAGATACT	TTAATTAAAG	ACGGTGTTCC	650
5	AAAAGACTAT	AAGGTTGCTG	ATAAAAGTGG	TCAAGCAATA	ACATATGCTT	700
	CTAGAAATGA	TGTTGCTTTT	GTTTATCCTA	AGGGCCAATC	TGAACCTATT	750
	GTTTTAGTCA	TTTTTACGAA	TAAAGACAAT	AAAAGTGATA	AGCCAAATGA	800
	TAAGTTGATA	AGTGAAACCG	CCAAGAGTGT	AATGAAGGAA	TTTTAA	846

10

2) INFORMATION FOR SEQ ID NO: 1709

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 555 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

20 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Pseudomonas aeruginosa*
 (C) ACCESSION NUMBER: M29695

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1709

	ATGTCCGCGA	GCACCCCCC	CATAACTCTT	CGCCTCATGA	CCGAGCGCGA	50
	CCTGCCGATG	CTCCATGACT	GGCTCAACCG	GCCGCACATC	GTTGAGTGGT	100
30	GGGGTGGCGA	CGAAGAGCGA	CCGACTCTTG	ATGAAGTGCT	GGAACACTAC	150
	CTGCCCAGAG	CGATGGCGGA	AGAGTCCGTA	ACACCGTACA	TCGCAATGCT	200
	GGGCGAGGAA	CCGATCGGCT	ATGCTCAGTC	GTACGTCGCG	CTCGGAAGCG	250
	GTGATGGCTG	GTGGGAAGAT	GAAACTGATC	CAGGAGTGCG	AGGAATAGAC	300
	CAGTCTCTGG	CTGACCCGAC	ACAGTTGAAC	AAAGGCCTAG	GAACAAGGCT	350
35	TGTCCGCGCT	CTCGTTGAAC	TACTGTTCTC	GGACCCCACC	GTGACGAAGA	400
	TTCAGACCGA	CCCGACTCCG	AACAACCATC	GAGCCATACG	CTGCTATGAG	450
	AAGGCAGGAT	TCGTGCGGGA	GAAGATCATC	ACCACGCCTG	ACGGGCCGGC	500
	GTTTTACATG	GTTCAAACAC	GACAAGCCTT	CGAGAGAAAG	CGCGGTGTTG	550
	CCTAA					555

40

2) INFORMATION FOR SEQ ID NO: 1710

45 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 732 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Staphylococcus aureus*

(C) ACCESSION NUMBER: K02987

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1710

5
 ATGAACCAGA AAAACCCTAA AGACACGCAA AATTTTATTA CTTCTAAAAA 50
 GCATGTAAAA GAAATATTGA ATCACACGAA TATCAGTAAA CAAGACAACG 100
 TAATAGAAAT CGGATCAGGA AAAGGACATT TTACCAAAGA GCTAGTCAAA 150
 ATGAGTCGAT CAGTTACTGC TATAGAAATT GATGGAGGCT TATGTCAAGT 200
 10 GACTAAAGAA GCGGTAAACC CCTCTGAGAA TATAAAAGTG ATTCAAACGG 250
 ATATTCTAAA ATTTTCCTTC CCAAAACATA TAAACTATAA GATATATGGT 300
 AATATTCCTT ATAACATCAG TACGGATATT GTCAAAAGAA TTACCTTTGA 350
 AAGTCAGGCT AAATATAGCT ATCTTATCGT TGAGAAGGGA TTTGCGAAAA 400
 GATTGCAAAA TCTGCAACGA GCTTTGGGTT TACTATTAAT GGTGGAGATG 450
 15 GATATAAAAA TGCTCAAAAA AGTACCACCA CTATATTTTC ATCCTAAGCC 500
 AAGTGTAGAC TCTGTATTGA TTGTTCTTGA ACGACATCAA CCATTGATTT 550
 CAAAGAAGGA CTACAAAAAG TATCGATCTT TTGTTTATAA GTGGGTAAAC 600
 CGTGAATATC GTGTTCTTTT CACTAAAAAC CAATTCCGAC AGGCTTTGAA 650
 GCATGCAAAAT GTCACTAATA TTAATAAACT ATCGAAGGAA CAATTTCTTT 700
 20 CTATTTTCAA TAGTTACAAA TTGTTTCACT AA 732

2) INFORMATION FOR SEQ ID NO: 1711

25
 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 738 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

30 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

35 (A) ORGANISM: *Escherichia coli*

(B) STRAIN: BM2570

(C) ACCESSION NUMBER: M19270

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1711

40
 ATGAACAAAA ATATAAAATA TTCTCAAAAC TTTTAAACGA GTGAAAAAGT 50
 ACTCAACCAA ATAATAAAAC AATTGAATTT AAAAGAAACC GATACCGTTT 100
 ACGAAATTGG AACAGGTAAA GGGCATTTAA CGACGAAACT GGCTAAAATA 150
 AGTAAACAGG TAACGTCTAT TGAATTAGAC AGTCATCTAT TCAACTTATC 200
 45 GTCAGAAAAA TTAATAATCGA ATACTCGTGT CACTTTAATT CACCAAGATA 250
 TTCTACAGTT TCAATTCCCT AACAAACAGA GGTATAAAAT TGTTGGGAAT 300
 ATTCCTTACC ATTTAAGCAC ACAAATTATT AAAAAAGTGG TTTTGTAAAG 350
 CCATGCGTCT GACATCTATC TGATTGTTGA AGAAGGATTC TACAAGCGTA 400
 CCTTGGATAT TCACCGAACA CTAGGGTTGC TCTTGCACAC TCAAGTCTCG 450
 50 ATTCAGCAAT TGCTTAAGCT GCCAGCGGAA TGCTTTCATC CTAAACCAAG 500
 AGTAAACAGT GTCTTAATAA AACTTACCGG CCATACCACA GATGTTCCAG 550
 ATAAATATTG GAAGCTATAT ACGTACTTTG TTTCAAAATG GGTCAATCGA 600
 GAATATCGTC AACTGTTTAC TAAAAATCAG TTTTCATCAAG CAATGAAACA 650

CGCCAAAGTA	AACAATTTAA	GTACCGTTAC	TTATGAGCAA	GTATTGTCTA	700
TTTTTAATAG	TTATCTATTA	TTTAACGGGA	GGAAATAA		738

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2) INFORMATION FOR SEQ ID NO: 1712

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 735 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear.

(ii) MOLECULE TYPE: Genomic DNA

15

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus aureus*
(B) STRAIN: RN451
(C) ACCESSION NUMBER: M17990

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1712

ATGAACGAGA	AAAATATAAA	ACACAGTCAA	AACTTTATTA	CTTCAAAACA	50
TAATATAGAT	AAAATAATGA	CAAATATAAG	ATTAAATGAA	CATGATAATA	100
25 TCTTTGAAAT	CGGCTCAGGA	AAAGGGCATT	TTACCCTTGA	ATTAGTACAG	150
AGGTGTAATT	TCGTAAGTGC	CATTGAAATA	GACCATAAAT	TATGCAAAAC	200
TACAGAAAAT	AACTTGTTG	ATCACGATAA	TTTCCAAGTT	TTAAACAAGG	250
ATATATTGCA	GTTTAAATTT	CCTAAAAACC	AATCCTATAA	AATATTTGGT	300
AATATACCTT	ATAACATAAG	TACGGATATA	ATACGCAAAA	TTGTTTTTGA	350
30 TAGTATAGCT	GATGAGATTT	ATTTAATCGT	GGAATACGGG	TTTGCTAAAA	400
GATTATTAAA	TACAAAACGC	TCATTGGCAT	TATTTTAAAT	GGCAGAAGTT	450
GATATTTCTA	TATTAAGTAT	GGTTCCAAGA	GAATATTTTC	ATCCTAAACC	500
TAGAGTGAAT	AGCTCACTTA	TCAGATTAAA	TAGAAAAAAA	TCAAGAATAT	550
CACACAAAGA	TAAACAGAAG	TATAATTATT	TCGTTATGAA	ATGGGTTAAC	600
35 AAAGAATACA	AGAAAATATT	TACAAAAAAT	CAATTTAACA	ATTCCTTAAA	650
ACATGCAGGA	ATTGACGATT	TAAACAATAT	TAGCTTTGAA	CAATTCTTAT	700
CTCTTTTCAA	TAGCTATAAA	TTATTTAATA	AGTAA		735

40

2) INFORMATION FOR SEQ ID NO: 1713

(i) SEQUENCE CHARACTERISTICS:

- 45 (A) LENGTH: 1029 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

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(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus faecalis*
(B) STRAIN: V583

(C) ACCESSION NUMBER: U00456

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1713

5	ATGAATAAAA	TAAAAGTCGC	AATTATCTTC	GGCGGTTGCT	CGGAGGAACA	50
	TGATGTGTCG	GTAAAATCCG	CAATAGAAAT	TGCTGCGAAC	ATTAATACTG	100
	AAAAATTCTGA	TCCGCACTAC	ATCGGAATTA	CAAAAAACGG	CGTATGGAAG	150
	CTATGCAAGA	AGCCATGTAC	GGAATGGGAA	GCCGATAGTC	TCCCCGCCAT	200
	ATTCTCCCCG	GATAGGAAAA	CGCATGGTCT	GCTTGTCATG	AAAGAAAGAG	250
10	AATACGAAAC	TCGGCGTATT	GACGTGGCTT	TCCCGGTTTT	GCATGGCAAA	300
	TGCGGGGAGG	ATGGTGCGAT	ACAGGGTCTG	TTTGAATTGT	CTGGTATCCC	350
	CTATGTAGGC	TGCGATATTC	AAAGCTCCGC	AGCTTGCAATG	GACAAATCAC	400
	TGGCCTACAT	TCTTACAAAA	AATGCGGGCA	TCGCCGTCCC	CGAATTTCAA	450
	ATGATTGAAA	AAGGTGACAA	ACCGGAGGCG	AGGACGCTTA	CCTACCCTGT	500
15	CTTTGTGAAG	CCGGCACGGT	CAGGTTGCTC	CTTTGGCGTA	ACCAAAGTAA	550
	ACAGTACGGA	AGAACTAAAC	GCTGCGATAG	AAGCAGCAGG	ACAATATGAT	600
	GGAAAAATCT	TAATTGAGCA	AGCGATTTTCG	GGCTGTGAGG	TCGGCTGCGC	650
	GTCATGGGA	AACGAGGATG	ATTTGATTGT	CGGCGAAGTG	GATCAAATCC	700
	GGTTGAGCCA	CGGTATCTTC	CGCATCCATC	AGGAAAACGA	GCCGGAAAAA	750
20	GGCTCAGAGA	ATGCCGATGAT	TATCGTTCCA	GCAGACATTC	CGGTCGAGGA	800
	ACGAAATCGG	GTGCAAGAAA	CGGCAAAGAA	AGTATATCGG	GTGCTTGGAT	850
	GCAGAGGGCT	TGCTCGTGTT	GATCTTTTTT	TGCAGGAGGA	TGGCGGCATC	900
	GTTCTAAACG	AGGTCAATAC	CCTGCCCCGGT	TTTACATCGT	ACAGCCGCTA	950
	TCCACGCATG	GCGGCTGCCG	CAGGAATCAC	GCTTCCCGCA	CTAATTGACA	1000
25	GCCTGATTAC	ATTGGCGATA	GAGAGGTGA			1029

2) INFORMATION FOR SEQ ID NO: 1714

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 818 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

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(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

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- (A) ORGANISM: *Campylobacter jejuni* subsp. *jejuni*
- (B) STRAIN: ATCC 33292

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1714

45	GCACAGGTTT	AGTTGGGCTT	GATCTTGCTT	TAGGTATAGG	CGGTGTTCCA	50
	AAAGGAAGAA	TTATAGAAAT	TTATGGRCTT	GAAAGTTCAG	GTAAAACCAC	100
	TCTAACTCTA	CACATTATCG	CAGAATGCCA	AAAAGCAGGT	GGRGTTTGTG	150
	CTTTTATCGA	TGCAGAACAT	GCRCTTGATG	TRAAATATGC	TAAAAATTTG	200
	GGTGTAATA	CAGATGATTT	GTATGTTTCT	CAGCCTGATT	TTGGAGARCA	250
50	AGCCTTAGAA	ATTGTAGAAA	CTATAGCAAG	AAGTGGCGCA	GTAGATCTTA	300
	TCGTAGTAGA	TAGCGTTGCA	GCGCTTACCC	CAAAGCAGA	AATTGAAGGC	350
	GATATGGGTG	ATCAACATGT	AGGACTTCAA	GCAAGACTTA	TGTCTCAAGC	400
	TCTAAGAAAA	CTTACAGGTA	TAGTTCATAA	AATGAATACC	ACAGTAATTT	450

	TYATCAACCA	AATTCGTATG	AAAATCGGTG	CTATGGGTTA	TGGTACTCCT	500
	GAAACCACAA	CAGGTGGAAA	TGCATTAAAA	TTTTATGCTT	CTGTGCGTTT	550
	AGATGTTAGA	AAAGTAGCAA	CCTTAAAACA	AAACGAAGAA	CCTATAGGAA	600
	ACCGCGTTAA	AGTAAAAGTA	GTTAAAAATA	AAGTTGCTCC	TCCATTGAGA	650
5	CAAGCTGAAT	TTGATGTGAT	GTTTGGAGAG	GGTTTAAGCC	GTGAAGGTGA	700
	ATTGATCGAT	TATGGTGTAA	AACTTGATAT	CGTAGATAAA	AGTGGTGCCT	750
	GGTTTTCTTA	TAAAGATAAA	AAACTTGGAC	AAGGTAGAGA	AAATTCAAAA	800
	GCTTTCTTAA	AAGAAAAC				818

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2) INFORMATION FOR SEQ ID NO: 1715

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 809 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

20 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Abiotrophia adiacens*
 (B) STRAIN: ATCC 49175
 25 (C) ACCESSION NUMBER: AF124224

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1715

	TGGTGCTATC	TTAGTAGTAT	CTGCAGCTGA	TGGTCCAATG	CCTCAAACAC	50
30	GTGAACACAT	CTTATTATCA	CGTCAAGTAG	GTGTTCTTA	CATCGTTGTA	100
	TTCTTAAACA	AAGTTGACAT	GGTTGACGAT	GAAGAATTAT	TAGAATTAGT	150
	AGAAATGGAA	GTTCTGACT	TATTATCAGA	ATACGATTTT	CCAGGCGATG	200
	ACACTCCAGT	TGTTGCAGGT	TCTGCTTTAC	GCGCTTTAGA	AGGCGACGCT	250
	TCATACRAAG	AAAAAATCTT	AGAATTAATG	GCTGCTGTTG	ACGAATACAT	300
35	TCCAACCTCA	GAACGYGACG	TTGACAAACC	ATTCATGATG	CCAGTTGAAG	350
	ACGTGTTCTC	AATCACAGGT	CGTGGTACTG	TTGCTACAGG	TCGTGTTGAA	400
	CGTGGAACAAG	TTCGTGTTGG	TGACGAAGTT	GAAATCGTTG	GTATTTTACA	450
	AGAAACTTCA	AAAACAACCTG	TAAGTGGTGT	TGAAATGTTT	CGTAAATTGT	500
	TAGACTACGC	TGAAGCAGGG	GATAACATTG	GTACATTATT	ACGTGGTGTT	550
40	ACACGTGACA	ACATCGAACG	TGGACAAGTT	CTTGCTAAAC	CAGGAACAAT	600
	CACTCCACAT	ACTAAATTCA	AAGCTGAAGT	TTACGTATTA	ACTAAAGAAG	650
	AAGGTGGACG	TCATACTCCA	TTCTTCTCTA	ACTACCGTCC	TCAATTCTAC	700
	TTCCGTACAA	CAGACATCAC	TGGTGTTTGT	GTGTTACCAG	AAGGCGTTGA	750
	AATGGTAATG	CCTGGTGATA	ACGTAACTAT	GGAAGTTGAA	TTAATTCACC	800
45	CAGTAGCGA					809

2) INFORMATION FOR SEQ ID NO: 1716

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 817 bases
 (B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

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(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Abiotrophia defectiva*

(B) STRAIN: ATCC 49176

(C) ACCESSION NUMBER: AF124225

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1716

	CGGCGCGATC	CTCGTTGTAT	CTGCTGCTGA	CGGCCCAATG	CCACAAACTC	50
	GTGAACACAT	CCTCTTGTCT	CGTCAAGTTG	GTGTTCCCTTA	CATCGTAGTA	100
15	TTCTTGAACA	AAGTTGACAT	GGTTGACGAC	GAAGAATTGC	TCGAATTAGT	150
	TGAAATGGAA	GTTCGTGACC	TCTTGTCTGA	ATACGACTTC	CCAGGCGACG	200
	ACACTCCAGT	TATCGCTGGT	TCAGCTTTGA	AAGCTTTAGA	AGGCGACGCT	250
	AACTACGAAG	CTAAAGTTTT	AGAATTGATG	GAACAAGTTG	ATGCTTACAT	300
	TCCAGAACCA	GAACGTGACA	CTGACAAGCC	ATTCATGATG	CCAGTCGAAG	350
20	ACGTATTCTC	TATCACTGGT	CGTGGTACTG	TTGCAACTGG	TCGTGTTGAA	400
	CGTGGTCAAG	TTCGCGTTGG	TGACGAAGTT	GAAATCGTTG	GTATCGAAGA	450
	AGAAACTTCT	AAGACTACCG	TTACCGGTGT	TGAAATGTTC	CGTAAGTTAT	500
	TGGATTACGC	TGAAGCTGGG	GACAACGTTG	GTACCTTGTT	ACGTGGTGTA	550
	ACTCGTGACC	AAATCCAACG	TGGTCAAGTA	TTATCTAAAC	CAGGTTCAAT	600
25	CACTCCGYAC	ACTAAGTTCG	AAGCTGAAGT	GTACGTATTG	TCTAAAGAAG	650
	AAGGTGGTCG	TCACACTCCA	TTCTTCTCTA	ACTACCGTCC	ACAATTCTAC	700
	TTCCGTACAA	CTGACGTAAAC	TGGTGTGTTT	ACTTTACCAG	AAGGTACTGA	750
	AATGGTTATG	CCAGGCGACA	ACGTACAAAT	GGTTGTTGAA	TTGATCCACC	800
30	CAATCGCGAT	CGAAGAA				817

2) INFORMATION FOR SEQ ID NO: 1717

35 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 814 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

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(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Corynebacterium accolens*

45 (B) STRAIN: ATCC 49725

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1717

	CGGCGCTATC	CTGGTTGTTG	CTGCAACCGA	TGGCCCGATG	CCGCAGACCC	50
50	GCGAGCACGT	TCTGCTTGCT	CGCCAGGTTG	GCGTTCCTTA	CATCCTCGTT	100
	GCACTGAACA	AGTGCGACAT	GGTTGATGAT	GAGGAAATCA	TCGAGCTCGT	150
	GGAGATGGAG	ATCTCCGAGC	TGCTCGCAGA	GCAGGACTAC	GATGAGGAAG	200
	CTCCTATCGT	TCACATCTCC	GCTCTGAAGG	CACTCGAGGG	TGACGAGAAG	250

	TGGGTACAGT	CCATCGTTGA	CCTGATGGAT	GCCTGCGACA	ACTCCATCCC	300
	TGATCCGGAG	CGCGCTACCG	ATCAGCCGTT	CTTGATGCCT	ATCGAGGACA	350
	TCTTCACCAT	TACCGGCCCG	GGTACCGTTG	TTACCGGCCG	TGTTGAGCGT	400
	GGTCGTCTGA	ACGTCAACGA	GGACGTTGAG	ATCATCGGTA	TCCAGGAGAA	450
5	GTCCCAAGAAC	ACCACCGTTA	CCGGTATCGA	GATGTTCCGC	AAGATGATGG	500
	ACTACACCGA	GGCTGGCGAC	AACTGTGGTC	TGCTTCTGCG	TGGTACCAAG	550
	CGTGAGGACG	TTGAGCGTGG	CCAGGTTGTT	ATCAAGCCGG	GCGCTTACAC	600
	CCCTCACACC	AAGTTCGAGG	GTTCCGTCTA	CGTCCTGAAG	AAGGAAGAGG	650
	GCGGCCGCCA	CACCCCGYTC	ATGAACAAC	ACCGTCCTCA	GTTCTACTTC	700
10	CGCACCACCG	ACGTTACCGG	TGTTGTGAAC	CTGCCCTGAGG	GCACCGAGAT	750
	GGTTATGCCT	GGCGACAACG	TTGAGATGTC	TGTTGAGCTC	ATCCAGCCTG	800
	TTGCTATGGA	CGAG				814

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2) INFORMATION FOR SEQ ID NO: 1718

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 814 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

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(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Corynebacterium genitalium*
 (B) STRAIN: ATCC 33031

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1718

	CGGCGCCATC	CTGGTTGTTG	CTGCAACCGA	TGGCCCGATG	CCGCAGACCC	50
	GTGAGCACGT	TCTGCTGGCT	CGCCAGGTTG	GCGTTCGGTA	CATCCTAGTT	100
	GCACTGAACA	AGTGCGACAT	GGTTGATGAT	GAGGAGCTGC	TGGAGCTCGT	150
35	CGAGATGGAG	GTCCGCGAGC	TGCTGGCTGA	GCAGGACTTC	GACGAGGAAG	200
	CACCTGTTGT	TCACATCTCC	GCACTGAAGG	CCCTGGAGGG	CGACGAGAAG	250
	TGGGCTAAGC	AGATCCTGGA	GCTCATGGAG	GCTTGCGACA	ACTCCATCCC	300
	GGATCCGGAG	CGCGAGACCG	ACAAGCCGTT	CCTGATGCCG	GTTGRGGACA	350
	TCTTCACCAT	TACCGGCCCG	GGTACCGTTG	TTACCGGCCG	TGTTGAGCGT	400
40	GGCGTCCTGA	ACCTGAACGA	CGAGGTCGAG	ATCCTGGGCA	TCCGCGAGAA	450
	GTCCACCAAG	ACCACCGTTA	CCTCCATCGA	GATGTTCAAC	AAGCTGCTGG	500
	ACACCGCAGA	GGCTGGCGAC	AACGCCGCAC	TGCTGCTGCG	TGGCCTGAAG	550
	CGCGAAGATG	TTGAGCGTGG	TCAGATCGTT	GCTAAGCCGG	GCGAGTACAC	600
	CCCGCACACC	GAGTTCGAGG	GCTCCGTCTA	CGTTCTGTCC	AAGGACGAGG	650
45	GTGGCCGCCA	CACCCCGTTC	TTCGACAAC	ACCGTCCGCA	GTTCTATTTC	700
	CGCACCACCG	ACGTTACCGG	TGTTGTGAAG	CTGCCGGAGG	GCACCGAGAT	750
	GGTTATGCCG	GGCGACAACG	TTGACATGTC	CGTCACCCTG	ATCCAGCCCG	800
	TTGCTATGGA	CGAG				814

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2) INFORMATION FOR SEQ ID NO: 1719

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 814 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 5 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 10 (A) ORGANISM: *Corynebacterium jeikeium*
 (B) STRAIN: ATCC 43216

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1719

15	CGGCGCCATC	CTGGTTGTTG	CCGCAACCGA	TGGCCCGATG	CCGCAGACCC	50
	GCGAGCACGT	TCTGCTGGCY	CGCCAGGTTG	GCGTTCCGTA	CATCCTGGTT	100
	GCACTGAACA	AGTGTGACAT	GGTTGACGAT	GAGGAGCTGC	TGGAGCTCGT	150
	CGAGATGGAG	GTCCGCGAGC	TGCTGGCTGA	GCAGGACTTC	GACGAGGAAG	200
	CTCCGGTTGT	TCACATCTCC	GCACTGAAGG	CCCTGGAGGG	CGACGAGAAG	250
20	TGGGCTAACC	AGATTCTCGA	GCTGATGCAG	GCTTGCGACG	AGTCTATCCC	300
	GGATCCGGAG	CGCGAGACCG	ACAAGCCGTT	CCTGATGCCG	GTTGWGGACA	350
	TCTTCACCAT	TACCGGTCGC	GGTACCGTTG	TTACCGGCCG	TGTTGAGCGT	400
	GGCATCCTGA	ACCTGAACGA	CGAGGTTGAG	ATCCTGGGTA	TCCGCGAGAA	450
	GTCCCAGAAG	ACCACCGTTA	CCTCCATCGA	GATGTTCAAC	AAGCTGCTGG	500
25	ACACCGCAGA	GGCTGGCRAC	AACGCTGCAC	TGCTGCTGCG	TGGTCTGAAG	550
	CGCGAGGACG	TTGAGCGTGG	CCAGATCATC	GCTAAGCCGG	GCGAGTACAC	600
	CCCGCACACC	GAGTTCGAGG	GCTCCGTCTA	CGTTCTGTCC	AAGGACGAGG	650
	GCGGCCGCCA	CACCCCGTTC	TTCGACAAC	ACCGTCCGCA	GTTCTACTTC	700
	CGCACCACCG	ACGTTACCGG	TGTTGTGAAG	CTGCCTGAGG	GCACCGAGAT	750
30	GGTTATGCCG	GGCGACAACG	TYGACATGTC	CGTCACCCTG	ATCCAGCCCG	800
	TTGCTATGGA	CGAG				814

35 2) INFORMATION FOR SEQ ID NO: 1720

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 748 bases
 (B) TYPE: Nucleic acid
 40 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 45 (A) ORGANISM: *Corynebacterium pseudodiphtheriticum*
 (B) STRAIN: ATCC 10700

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1720

50	CGGCGCTATC	TTGGTTGTTG	CAGCTACCGA	CGGCCCAATG	CCACAGACTC	50
	GCGAGCACGT	TCTGCTGGCT	CGCCAGGTTG	GCGTTCCTTA	CATCCTGGTT	100
	GCACTAAACA	AGTGCGACAT	GGTTGACGAC	GAGGAAATCC	TCGAGCTCGT	150

	CGAGATGGAG	ATCCGCGAAT	TGCTGGCTGA	CCAGGAATTC	GACGAAGAAG	200
	CTCCAATCGT	TCACATCTCC	GCAGTCGGCG	CCTTGAAGG	CGAAGAGAGG	250
	TGGGTAAACG	CCATCGTTGA	ACTGATGGAT	GCTTGTGACG	AGTCGATCCC	300
	TGATCCAGAC	CGTGCTACCG	ACAAGCCATT	CCTGATGCCT	ATCGAGGACA	350
5	TCTTCACCAT	TACCGGTCGT	GGCACCGTTG	TTACGGGTCG	TGTTGAGCGT	400
	GGTTCCTGA	AGGTCAACGA	AGAAGTCGAG	ATCATCGGCA	TCAAGGAAAA	450
	GTCCCAGAAG	ACCACCATCA	CCGGTATCGA	AATGTTCCGC	AAGATGCTGG	500
	ACTACACCGA	GGCCGGCGAC	AACGCTGGTC	TGCTGCTTCG	CGGTACCAAG	550
	CGTGAAGACG	TTGAGCGTGG	ACAGGTTATC	GTTGCTCCAG	GTGCTTACAG	600
10	CACCCACAAG	AAGTTCGAAG	GTTCCGTCTA	CGTTCTTTCC	AAGGACGAGG	650
	GCGGCCGCCA	CACCCCGTTC	TTCGACAAC	ACCGTCCTCA	GTTCTACTTC	700
	CGCACCACCG	ACGTTACCGG	TGTTGTTACC	CTGCCTGAGG	GCACCGAG	748

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2) INFORMATION FOR SEQ ID NO: 1721

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 813 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

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(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Corynebacterium striatum*
 (B) STRAIN: ATCC 6940

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1721

	GGCGCTATCT	TGGTTGTTGC	TGCAACCGAT	GGCCCGRTGC	CGCAGACCCG	50
	CGAGCACGTT	CTTCTGGCTC	GCCAGGTTGG	CGTTCCTTAC	ATCCTCGTTG	100
	CACTGAACAA	GTGCGACATG	GTTGACGACG	AGGAAATTAT	CGAGCTCGTC	150
35	GAGATGGAGA	TCCGCGAACT	GCTCGCAGAG	CAGGACTACG	ATGAGGAAGC	200
	TCCGATCGTT	CACATCTCTG	CTCTGAAGGC	TCTTGAGGGC	GRCGAGAAGT	250
	GGGTACAGGC	TATCGTTGAC	CTGATGCAGG	CTTGCGATGA	CTCCATCCCG	300
	GATCCGGAGC	GCGAGCTGGA	CAAGCCGTTT	CTGATGCCAA	TCGAGGACAT	350
	CTTCACCATC	ACCGGCCGCG	GTACCGTTGT	TACTGGCCGT	GTTGAGCGTG	400
40	GCTCCCTGAA	CGTCAACGAG	GACGTTGAGA	TCATCGGTAT	CCAGGACARG	450
	TCCATCTCCA	CCACCGTTAC	CGGTATCGAG	ATGYTCCGCA	AGATGATGGA	500
	CTACACCGAG	GCTGGCGACA	ACTGTGGTCT	GCTTCTGCGT	GGTACCAAGC	550
	GTGAAGAGGT	TGAGCGCGGC	CAGGTTGTTA	TTAAGCCGGG	CGCTTACACC	600
	CCTCACACCC	AGTTCGAGGG	TTCCGTCTAC	GTCCTGAAGA	AGGAAGAGGG	650
45	CGGCCGCCAC	ACCCCGTTCA	TGGACAAC	CCGTCCGCAG	TTCTACTTCC	700
	GCACCACCGA	CGTTACCGGC	GTCATCAAGC	TGCCTGAGGG	CACCGAGATG	750
	GTTATGCCTG	GCGACAACGT	CGAGATGTCY	GTCGAGCTGA	TCCAGCCGGT	800
	CGCTATGGAC	GAG				813

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2) INFORMATION FOR SEQ ID NO: 1722

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 817 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 10 (A) ORGANISM: *Enterococcus avium*
(B) STRAIN: ATCC 14025
(C) ACCESSION NUMBER: AF124220

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1722

15 CGGAGCTATC TTAGTAGTAT CTGCTGCTGA TGGCCCTATG CCTCAAACCTC 50
GTGAACACAT CTTGTTATCT CGTAACGTTG GTGTTCCCTA CATCGTTGTA 100
TTCTTAAACA AAATGGATAT GGTGACGAT GAAGAATTAC TTGAATTAGT 150
TGAAATGGAA GTTCGTGACT TATTAAGTGA ATACGACTTC CCAGGCGACG 200
20 ACACTCCAGT TATCGCAGGT TCAGCGTTGA AAGCTTTAGA AGGCGACGCT 250
TCATACGAAG AAAAAATCTT AGAATTAATG GCTGCTGTTG ACGAATATAT 300
CCCAACACCA GTTCGTGATA CTGACAAACC ATTCATGATG CCAGTCGAAG 350
ACGTATTCTC AATCACTGGT CGTGGTACTG TTGCAACTGG TCGTGTGAA 400
CGTGGACAAG TTCGCGTTGG TGACGAAGTT GAAATCGTAG GTATCGCTGA 450
25 CGAAACTGCT AAAACAACCTG TTACAGGTGT TGAAATGTTT CGTAAATTGT 500
TAGACTACGC TGAAGCAGGT GACAACATCG GTGCTTTGTT ACGTGGTGTT 550
GCACGTGAAG ATATCCAACG TGGACAAGTA TTGGCTAAAC CAGCTTCAAT 600
CACTCCACAT ACAAATTCT CTGCAGAACT TTATGTTCTA ACTAAAGAAG 650
AAGGTGGACG TCATACTCCA TTCTTCACTA ACTACCGTCC TCAGTTCTAC 700
30 TTCCGTACAA CTGACGTAAC TGGTGTAGTT GATCTACCAG AAGGTACTGA 750
AATGGTWTAT CCTGGGGATA ACGTAACTAT GGAAGTTGAA TTGATYCACC 800
CAATYGCGGT AGAAGAC 817

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2) INFORMATION FOR SEQ ID NO: 1723

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 823 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

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(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Gardnerella vaginalis*
(B) STRAIN: ATCC 14018

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1723

TGGCGCAATC CTCGTGGTTG CTGCTACCGA CGGTCCAATG GCTCAGACCC 50
GTGAACACGT CTTGCTTGCT AAGCAGGTCG GCGTTCCAAA AATTCTTGTT 100

	GCTTTGAACA	AGTGCGATAT	GGTTGACGAC	GAAGAGCTTA	TCGATCTCGT	150
	TGAAGAAGAG	GTCCGTGACC	TCCTCGAAGA	AAACGGCTTC	GATCGCGATT	200
	GCCCAGTCYT	CCGTACTTCC	GCTTACGGCG	CTTTGCATGA	TGACGCTCCA	250
	GACCACGACA	AGTGGGTAGA	GACCGTCAAG	GAATCATGA	AGGCTGTTGA	300
5	CGAGTACATC	CCAACCCCAA	CTCACGATCT	TGACAAGCCA	TTCTTGATGC	350
	CAATCGAAGA	TGTGTTCAAC	ATCTCCGGTC	GTGGTYCCGT	TGTCACCGGT	400
	CGTGTTGAGC	GTGGTAAGCT	CCCAATCAAC	ACCCAGTTG	AGATCGTTGG	450
	TTTGCGCGAT	ACCCAGACCA	CCACCGTCAC	CTCTATCGAG	ACCTTCCACA	500
	AGCAGATGGA	TGAGGCAGAG	GCTGGCGATA	ACACTGGTCT	TCTTCTCCGC	550
10	GGTATCAACC	GTACCGACGT	TGAGCGTGGT	CAGGTTGTGG	CTGCTCCAGG	600
	TTCTGTGACT	CCACACACCA	AGTTCGAAGG	CGAAGTTTAC	GTCTTGACCA	650
	AGGACGAAGG	TGGCCGTCAC	TCGCCATTCT	TCTCCAATA	CCGTCCACAG	700
	TTCTACTTCC	GTACCACCGA	TGTTACTGGC	GTTATCACCT	TGCCAGACGG	750
	CATCGAAATG	GTTAGCCAG	GCGATCACGC	AACCTTCACT	GTTGAGTTGA	800
15	TCCAGGCTAT	CGCAATGGAA	GAG			823

2) INFORMATION FOR SEQ ID NO: 1724

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 817 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

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(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

30

- (A) ORGANISM: *Listeria innocua*
- (B) STRAIN: ATCC 33090

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1724

35	CGGAGCTATC	TTAGTAGTAT	CTGCTGCTGA	TGGCCCAATG	CCACAAACTC	50
	GTGAACATAT	CTTACTTTCA	CGTCAAGTTG	GTGTTCCATA	CATCGTTGTA	100
	TTCATGAACA	AATGTGACAT	GGTTGACGAT	GAAGAATTAC	TAGAATTAGT	150
	TGAAATGGAA	ATTCGTGATC	TATTAAGTGA	ATATGAATTC	CCTGGCGATG	200
	ACATTCCCTGT	AATCAAAGGT	TCAGCTCTTA	AAGCACTTCA	AGGTGAAGCT	250
40	GACTGGGAAG	CTAAAATTGA	CGAGTTAATG	GAAGCTGTAG	ATTCTTACAT	300
	TCCAACCTCA	GAACGTGATA	CTGACAAACC	ATTCATGATG	CCAGTTGAGG	350
	ATGTATTCTC	AATCACTGGT	CGTGGAACAG	TTGCAACTGG	ACGTGTTGAA	400
	CGTGGACAAG	TTAAAGTTGG	TGACGAAGTA	GAAGTTATCG	GTATTGAAGA	450
	AGAAAGCAAA	AAAGTAGTAG	TAAGTGGAGT	AGAAATGTTC	CGTAAATTAC	500
45	TAGACTACGC	TGAAGCTGGC	GACAACATTG	GCGCACTTCT	ACGTGGTGTT	550
	GCTCGTGAAG	ATATCCAACG	TGGTCAAGTA	TTAGCTAAAC	CAGGTTTCAT	600
	TACTCCACAC	ACTAACTTCA	AAGCTGAAAC	TTATGTTTTA	ACTAAAGAAG	650
	AAGGTGGACG	TCACACTCCA	TTCTTCAACA	ACTACCGCCC	ACAATTCTAT	700
	TTCCGTACTA	CTGACGTAAC	TGGTATTGTT	ACACTTCCAG	AAGGTACTGA	750
50	AATGGTAATG	CCTGGTGATA	ACATTGAGCT	TGCAGTTGAA	CTAATTGCAC	800
	CAATCGCTAT	CGAAGAC				817

2) INFORMATION FOR SEQ ID NO: 1725

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 818 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

10

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Listeria ivanovii*
 (B) STRAIN: ATCC 19119

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1725

	CGGAGCTATC	TTAGTAGTAT	CTGCTGCTGA	TGGTCCAATG	CCACAAACTC	50
	GTGAACATAT	TCTTACTTTC	ACGTCAAGTT	GGTGTTCAT	ACATCGTTGT	100
	ATTCATGAAC	AAATGTGACA	TGGTTGACGA	TGAAGAATTA	CTTGAATTAG	150
20	TTGAAATGGA	AATTCGTGAT	CTATTAAC TG	AATATGAATT	CCCTGGCGAC	200
	GACATTCC TG	TAATCAAAGG	TTCAGCTCTT	AAAGCACTTC	AAGGTGAAGC	250
	TGATTGGGAA	GCTAAAATTG	ACGAGTTAAT	GGAAGCTGTA	GATTCTTACA	300
	TTCCA ACTCC	AGAACGTGAT	ACTGACAAAC	CATTCATGAT	GCCAGTTGAG	350
	GATGTATTCT	CAATCACTGG	TCGTGGAACA	GTTGCAACTG	GACGTGTTGA	400
25	ACGTGGACAA	GTTAAAGTTG	GTGACGAAGT	AGAAGTTATC	GGTATTGAAG	450
	AAGAAAGCAA	AAAAGTAGTA	GTA ACTGGAG	TAGAAATGTT	CCGTAAATTA	500
	CTAGACTACG	CTGAAGCTGG	CGACAACATT	GGCGCACTTC	TACGTGGTGT	550
	TGCTCGTGAA	GATATCCAAC	GTGGTCAAGT	ATTAGCTAAA	CCAGGTT CGA	600
	TTACTCCACA	TACTAACTTC	AAAGCTGAAA	CTTATGTTTT	AACTAAAGAA	650
30	GAAGGTGGAC	GTCATACTCC	ATTCTTCAAC	AACTACCGCC	CACAATTCTA	700
	TTTCCGTA CT	ACTGACGTAA	CTGGTATTGT	TACACTTCCA	GAAGGTACTG	750
	AAATGGTAAT	GCCTGGTGAT	AACATTGAGC	TTGCAGTTGA	ACTAATTGCA	800
	CCAATCGCTA	TCGAAGAC				818

35

2) INFORMATION FOR SEQ ID NO: 1726

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 817 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

45 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Listeria monocytogenes*
 (B) STRAIN: LSPQ 5093202

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1726

CGGAGCTATC	TTAGTAGTAT	CTGCTGCTGA	TGGCCCAATG	CCACAAACTC	50
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	GTGAACATAT	CTTACTTTCA	CGTCAAGTTG	GTGTTCCATA	CATCGTTGTA	100
	TTCATGAACA	AATGTGACAT	GGTTGACGAT	GAAGAATTAC	TAGAATTAGT	150
	TGAAATGGAA	ATTCGTGATC	TATTAAGTGA	ATATGAATTC	CCTGGCGATG	200
	ACATTCCTGT	AATCAAAGGT	TCAGCTCTTA	AAGCACTTCA	AGGTGAAGCT	250
5	GACTGGGAAG	CTAAAATTGA	CGAGTTAATG	GAAGCTGTAG	ATTCTTACAT	300
	TCCAACCTCCW	GAACGTGATA	CTGACAAACC	ATTCATGATG	CCAGTTGAGG	350
	ATGTATTCTC	AATCACTGGT	CGTGGAACAG	TTGCAACTGG	ACGTGTTGAA	400
	CGTGGAACAAG	TTAAAGTTGG	TGACGAAGTA	GAAGTTATCG	GTATCGAAGA	450
	AGAAAGCAAA	AAAGTAGTAG	TAAGTGGAGT	AGAAATGTTC	CGTAAATTAC	500
10	TAGACTACGC	TGAAGCTGGC	GACAACATTG	GCGCACTTCT	ACGTGGTGTG	550
	GCTCGTGAAG	ATATCCAACR	TGGTCAAGTA	TTAGCTAAAC	CAGGTTTCGAT	600
	TACTCCACAC	ACTAACTTCA	AAGCTGAAAC	TTATGTTTTA	ACTAAAGAAG	650
	AAGGTGGACG	TCACACTCCA	TTCTTCAACA	ACTACCGCCC	ACAATTCTAT	700
	TTCCGTACTA	CTGACGTAAC	TGGTATTGTT	ACACTTCCAG	AAGGTACTGA	750
15	AATGGTAAYG	CCTGGTGATA	ACATTGAGCT	TGCAGTTGAA	CTAATTGCAC	800
	CAATCGCTAT	CGAAGAC				817

20 2) INFORMATION FOR SEQ ID NO: 1727

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 817 bases
 (B) TYPE: Nucleic acid
 25 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

30 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Listeria seeligeri*
 (B) STRAIN: ATCC 35967

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1727

35	CGGAGCTATC	TTAGTAGTAT	CTGCTGCTGA	TGGCCCAATG	CCACAAACTC	50
	GTGAACATAT	CTTACTTTCA	CGTCAAGTTG	GTGTTCCATA	CATCGTTGTA	100
	TTCATGAACA	AATGTGACAT	GGTTGACGAT	GAAGAATTAC	TTGAATTAGT	150
	TGAAATGGAA	ATTCGTGATC	TATTAAGTGA	ATATGAATTC	CCTGGTGATG	200
40	ACATTCCTGT	AATCAAAGGT	TCAGCTCTTA	AAGCACTTCA	AGGTGAAGCT	250
	GACTGGGAAG	CTAAAATTGA	CGAGTTAATG	GAAGCTGTAG	ATTCTTACAT	300
	TCCAACCTCCA	GAACGTGATA	CTGACAAACC	ATTCATGATG	CCAGTTGAGG	350
	ATGTATTCTC	AATCACTGGT	CGTGGAACAG	TTGCAACTGG	ACGTGTTGAA	400
	CGTGGAACAAG	TTAAAGTTGG	TGACGAAGTA	GAAGTTATCG	GTATTGAAGA	450
45	AGAAAGCAAA	AAAGTAATAG	TAAGTGGAGT	AGAAATGTTC	CGTAAATTAC	500
	TAGACTACGC	TGAAGCTGGC	GACAACATTG	GCGCACTTCT	ACGTGGTGTG	550
	GCTCGTGAAG	ATATCCAACG	TGGTCAAGTA	TTAGCTAAAC	CAGGTTTCGAT	600
	TACTCCACAT	ACTAACTTCA	AAGCTGAAAC	TTATGTTTTA	ACTAAAGAAG	650
	AAGGTGGACG	TCACACTCCA	TTCTTCAACA	ACTACCGCCC	ACAATTCTAT	700
50	TTCCGTACTA	CTGACGTAAC	TGGTATTGTT	ACACTTCCAG	AAGGTACTGA	750
	AATGGTAATG	CCTGGTGATA	ACATTGAGCT	TGCAGTTGAA	CTAATTGCAC	800
	CAATCGCTAT	CGAAGAC				817

2) INFORMATION FOR SEQ ID NO: 1728

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 814 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

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(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus aureus*
(B) STRAIN: ATCC 25923

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1728

	CGGTGGTATC	TTAGTAGTAT	CTGCTGCTGA	CGGTCCAATG	CCACAAACTC	50
	GTGAACACAT	TCTTTTATCA	CGTAACGTTG	GTGTACCAGC	ATTAGTAGTA	100
	TTCTTAAACA	AAGTTGACAT	GGTTGACGAT	GAAGAATTAT	TAGAATTAGT	150
20	AGAAATGGAA	GTTTCGTGACT	TATTAAGCGA	ATATGACTTC	CCAGGTGACG	200
	ATGTACCTGT	AATCGCTGGT	TCAGCATTAR	AAGCTTTAGA	AGGCGATGCT	250
	CAATACGAAG	AAAAAATCTT	AGAATTARTG	GAAGCTGTAG	ATACTTACAT	300
	TCCAACGCCA	GAACGTGATT	CTGACAAACC	ATTCATGATG	CCAGTTGAGG	350
	ACGTATTCTC	AATCACTGGT	CGTGGTACTG	TTGCTACAGG	CCGTGTTGAA	400
25	CGTGGTCAAA	TCAAAGTTGG	TGAAGAAGTT	GAAATCATCG	GTTTACATGA	450
	CACATCTAAA	ACAACGTGTA	CAGGTGTTGA	AATGTTCCGT	AAATTATTAG	500
	ACTACGCTGA	AGCTGGTGAC	AACATTGGTG	CATTATTACG	TGGTGTGCT	550
	CGTGAAGACG	TACAACGTGG	TCAAGTATTA	GCTGCTCCTG	GTTCAATTAC	600
	ACCACATACT	GAATTCAAAG	CAGAAGTATA	CGTATTATCA	AAAGACGAAG	650
30	GTGGACGTCA	CACTCCATTC	TTCTCAAAC	ATCGTCCACA	ATTCTATTTT	700
	CGTACTACTG	ACGTAACTGG	TGTTGTTTAC	TTACCAGAAG	GTAAGTAAAT	750
	GGTAATGCCT	GGTGATAACG	TTGAAATGAC	AGTAGAATTA	ATCGCTCCAA	800
	TCGCGATTGA	AGAC				814

35

2) INFORMATION FOR SEQ ID NO: 1729

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 817 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

45

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus saprophyticus*
(B) STRAIN: ATCC 15305

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1729

CGGAGCTATC	TTAGTAGTAT	CTGCTGCTGA	TGGCCCAATG	CCACAAACTC	50
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	GTGAACACAT	TCTTTTATCA	CGTRACGTTG	GTGYTCCAGC	ATTAGTTGTA	100
	TTCTTAAACA	AAGTTGACAT	GGTTGACGAY	GAAGAATTAT	TAGAATTRGT	150
	AGAAATGGAA	GTTTCGTGRCT	TATTAAGCGA	ATATGACTTC	CCAGGTGACG	200
	ATGTACCTGT	AATCTCTGGT	TCTGCATTAA	AAGCTTTAGA	AGGCGACGCT	250
5	GACTATGAGC	AAAAAATCTT	AGACTTAATG	CAAGCTGTTG	ATGACTYCAT	300
	TCCAACACCA	GAACGTGATT	CTGACAAACC	ATTCATGATG	CCAGTTGAGG	350
	ACGTATTCTC	AATCACTGGT	CGTGGTACTG	TTGCTACAGG	CCGTGTTGAA	400
	CGTGGTCAAA	TCAAAGTCGG	TGAAGAAATC	GARATCATCG	GTATGCAAGA	450
	AGAATCAAGC	AAAACAACCTG	TTACTGGTGT	AGAAATGTTC	CGTAAATTAT	500
10	TAGACTACGC	TGAAGCTGGT	GACAACATTG	GTGCATTATT	ACGTGGTGTG	550
	TCACGTGATG	ATGTACAACG	TGGTCAAGTT	TTAGCTGCTC	CTGGTACTAT	600
	CACACCACAT	ACAAAATTCA	AAGCGGATGT	TTACGTTTTA	TCTAAAGATG	650
	AAGGTGGTCG	TCATACGCCA	TTCTTCACTA	ACTACCGCCC	ACAATTCTAT	700
	TTCCGTACTA	CTGACGTAAC	TGGTGTGTTT	AACTTACCAG	AAGGTACTGA	750
15	AATGGTTATG	CCTGGCGATA	ACGTTGAAAT	GGATGTTGAA	TTAATTTCTC	800
	CAATCGCTAT	TGAAGAC				817

20 2) INFORMATION FOR SEQ ID NO: 1730

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 817 bases
 (B) TYPE: Nucleic acid
 25 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

30 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus simulans*
 (B) STRAIN: ATCC 27848

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1730

35	CGGCGGTATC	TTAGTAGTAT	CTGCTGCAGA	TGGTCCAATG	CCACAAACTC	50
	GTGAACACAT	CTTATTATCA	CGTAACGTTG	GTGTACCAGC	TTTAGTTGTA	100
	TTCTTAAACA	AAGCTGACAT	GGTTGACGAC	GAAGAATTAT	TAGAATTAGT	150
	TGAAATGGAA	GTTTCGTGACT	TATTATCTGA	ATACGACTTC	CCTGGTGACG	200
40	ATGTACCAGT	TATCGTTGGT	TCTGCATTAA	AAGCTTTAGA	AGGCGACCCA	250
	GAATACGAAC	AAAAAATCTT	AGACTTAATG	CAAGCTGTAG	ATGACTACAT	300
	CCCAACTCCA	GAACGTGACT	CTGATAAACC	ATTCATGATG	CCAGTTGAGG	350
	ACGTATTCTC	AATCACTGGT	CGTGGTACTG	TAGCAACAGG	CCGTGTTGAA	400
	CGTGGTCAAA	TCAAAGTCGG	TGAAGAAGTT	GAAATCATCG	GTATCACTGA	450
45	AGAAAGCAAG	AAAACAACAG	TTACAGGTGT	AGAAATGTTC	CGTAAATTAT	500
	TAGACTACGC	TGAAGCTGGT	GACAACATCG	GTGCTTTATT	ACGTGGTGTG	550
	GCACGTGAAG	ACGTACAACG	TGGACAAGTA	TTAGCAGCTC	CTGGCTCTAT	600
	TACTCCACAC	ACAAAATTCA	AAGCTGATGT	TTACGTTTTA	TCTAAAGAAG	650
	AAGGTGGACG	TCATACTCCA	TTCTTCACTA	ACTACCGCCC	ACAATTCTAC	700
50	TTCCGTACTA	CTGACGTAAC	TGGCGTTGTT	CACTTACCAG	AAGGTACTGA	750
	AATGGTTATG	CCTGGCGATA	ACGTAGAAAT	GACTGTTGAA	TTGATCGCTC	800
	CAATCGCGAT	TGAAGAC				817

2) INFORMATION FOR SEQ ID NO: 1731

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 817 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 10 (A) ORGANISM: *Streptococcus agalactiae*
(B) STRAIN: ATCC 27591
(C) ACCESSION NUMBER:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1731

CGGAGCTATC CTTGTAGTTG CTTCAACTGA TGGACCAATG CCACAAACTC 50
GTGAGCACAT CCTTCTTTCA CGTCAAGTTG GTGTTAAACA CCTTATCGTA 100
20 TTCATGAACA AAGTTGACCT TGTTGATGAT GAAGAATTGC TTGAATTGGT 150
TGAAATGGAA ATTCGTGACC TTCTTTCAGA ATACGACTTC CCAGGTGATG 200
ACCTTCCAGT TATCCAAGGT TCAGCTCTTA AAGCACTTGA AGGCGACGAA 250
AAATACGAAG ACATCATCAT GGAATTGATG AGCACTGTTG ATGAGTACAT 300
TCCAGAACCA GAACGTGATA CTGACAAACC TTTACTTCTT CCAGTTGAAG 350
25 ATGTATTCTC AATCACTGGA CGTGGTACAG TTGCTTCAGG ACGTATCGAC 400
CGTGGTACTG TTCGTGTCAA CGACGAAGTT GAAATCGTTG GTATTAAAGA 450
AGATATCCAA AAAGCAGTTG TTAGTGGTGT TGAAATGTTT CGTAAACAAC 500
TTGACGAAGG TCTTGCAGGG GACAACGTTG GTGTTCTTCT TCGTGGTGT 550
CAACGTGATG AAATCGAACG TGGTCAAGTT CTTGCTAAAC CAGGTTCAAT 600
30 CAACCCACAC ACTAAATTTA AAGGTGAAGT TTACATCCTT TCTAAAGAAG 650
AAGGTGGACG TCATACTCCA TTCTTCAACA ACTACCGTCC ACAATTCTAC 700
TTCCGTACAA CTGACGTAAC AGGTTCAATC GAACTTCCAG CAGGAACAGA 750
AATGGTTATG CCTGGTGATA ACGTTACTAT CGAAGTTGAA TTGATTCACC 800
CAATCGCCGT AGAACAA 817

2) INFORMATION FOR SEQ ID NO: 1732

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 817 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 45 (A) ORGANISM: *Streptococcus pneumoniae*
50 (B) STRAIN: ATCC 27336

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1732

	CGGAGCTATC	CTTG TAGTAG	CTTCAACTGA	CGGACCAATG	CCACAAACTC	50
	GTGAGCACAT	CCTTCTTTCA	CGTCAGGTTG	GTGTTAAACA	CCTTATCGTC	100
	TTCATGAACA	AAGTTGACTT	GGTTGACGAC	GAAGAATTGC	TTGAATTGGT	150
	TGAAATGGAA	ATCCGTGACC	TATTGTCAGA	ATACGACTTC	CCAGGTGACG	200
5	ATCTTCCAGT	TATCCAAGGT	TCAGCACTTA	AAGCTCTTGA	AGGTGACTCT	250
	AAATACGAAG	ACATCGTTAT	GGAATTGATG	AACACAGTTG	ATGAGTATAT	300
	CCCAGAACCA	GAACGTGACA	CTGACAAACC	ATTGCTTCTT	CCAGTCGAGG	350
	ACGTATTCTC	AATCACTGGA	CGTGGTACAG	TTGCTTCAGG	ACGTATCGAC	400
	CGTGGTATCG	TTAAAGTCAA	CGACGAAATC	GAAATCGTTG	GTATCAAAGA	450
10	AGAAACTCRA	AAAGCAGTTG	TTACTGGTGT	TGAAATGTTC	CGTAAACAAC	500
	TTGACGAAGG	TCTTGCTGGA	GATAACGTAG	GTGTCCTTCT	TCGTGGTGTG	550
	CAACGTGATG	AAATCGAACG	TGGACAAGTT	ATCGCTAAAC	CAGGTTCAAT	600
	CAACCCACAC	ACTAAATTCA	AAGGTGAAGT	CTACATCCTT	ACTAAAGAAG	650
	AAGGTGGACG	TCACACTCCA	TTCTTCAACA	ACTACCGTCC	ACAATTCTAC	700
15	TTCCGTAATA	CTGACGTTAC	AGGTTCAATC	GAACCTCCAG	CAGGTACTGA	750
	AATGGTAATG	CCTGGTGATA	ACGTGACAAT	CGACGTTGAG	TTGATTCACC	800
	CAATCGCCGT	AGAACAA				817

20

2) INFORMATION FOR SEQ ID NO: 1733

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 817 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

30

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus salivarius*
 (B) STRAIN: ATCC 7073

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1733

	CGGTGCGATC	CTTG TAGTAG	CATCTACTGA	CGGACCAATG	CCACAAACTC	50
	GTGAGCACAT	CCTTCTTTCA	CGTCAGGTTG	GTGTTAAACA	CCTTATCGTC	100
	TTCATGAACA	AAGTTGACTT	GGTTGACGAT	GAAGAATTGC	TTGAATTGGT	150
40	TGAAATGGAA	ATCCGTGACC	TTCTTTCAGA	ATACGATTTT	CCAGGTGATG	200
	ACATTCCAGT	TATCCAAGGT	TCAGCTCTTA	AAGCTCTTGA	AGGTGATTCT	250
	AAATACGAAG	ACATCATCAT	GGACTTGATG	AACACTGTTG	ACGAATACAT	300
	CCCAGAACCA	GAACGTGACA	CTGACAAACC	ATTGTTGCTT	CCAGTCGAAG	350
	ACGTATTCTC	AATCACTGGT	CGTGGTACTG	TTGCTTCAGG	ACGTATCGAC	400
45	CGTGGTGTG	TTCGTGTCAA	TGACGAAGTT	GAAATCGTTG	GTCTTAAAGA	450
	AGACATCCAA	AAAGCAGTTG	TTACTGGTGT	TGAAATGTTC	CGTAAACAAC	500
	TTGACGRAGG	TATTGCCGGA	GATAACGTCG	GTGTTCTTCT	TCGTGGTATC	550
	CAACGTGATG	AAATCGAACG	TGGTCAAGTA	TTGGCTGCAC	CTGGTTCAAT	600
	CAACCCACAC	ACTAAATTCA	AAGGTGAAGT	TTACATCCTT	TCTAAAGAAG	650
50	AAGGTGGACG	TCACACTCCA	TTCTTCAACA	ACTACCGTCC	ACAGTTCTAC	700
	TTCCGTACAA	CTGACGTAAC	AGGTTCAATC	GAACCTCCTG	CAGGTACTGA	750
	AATGGTTATG	CCTGGTGATA	ACGTGACTAT	CGACGTTGAG	TTGATCCACC	800
	CAATCGCCGT	TGAACAA				817

2) INFORMATION FOR SEQ ID NO: 1734

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 897 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

10

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Agrobacterium tumefaciens*
 (C) ACCESSION NUMBER: x99673

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1734

	AACATGATCA	CCGGTGCTGC	CGAGATGGAC	GGCGCGATCC	TGGTTTGCTC	50
	GGCTGCCGAC	GGCCCGATGC	CACAGACCCG	CGAGCACATC	CTGCTTGCCC	100
	GTCAGGTGGG	CGTTCCGGCC	ATCGTCGTGT	TCCTCAACAA	GGTCGACCAG	150
20	GTTGACGACG	CCGAGCTTCT	CGAGCTCGTC	GAGCTTGAAG	TTCGCGAACT	200
	TCTGTCTGTC	TACGACTTCC	CGGGCGACGA	TATCCCGATC	ATCAAGGGTT	250
	CGGCACTTGC	TGCTCTTGAA	GATTCTGACA	AGAAGATCGG	TGAAGACGCG	300
	ATCCGCGAGC	TGATGGCTGC	TGTCGACGCC	TACATCCCGA	CGCCTGAGCG	350
	TCCGATCGAC	CAGCCGTTCC	TGATGCCGAT	CGAAGACGTG	TTCTCGATCT	400
25	CGGGTCGTGG	TACGGTTGTG	ACGGGTCGCG	TTGAGCGCGG	TATCGTCAAG	450
	GTTGGTGAA	AAGTCGAAAT	CGTCGGCATC	CGTCCGACCT	CGAAGACGAC	500
	TGTTACCGGC	GTTGAAATGT	TCCGCAAGCT	GCTCGACCAG	GGCCAGGCCG	550
	GCGACAACAT	CGGTGCACTC	GTTGCGGGCG	TTACCCGTGA	CGGCGTCGAG	600
	CGTGGTGAGA	TCCTGTGCAA	GCCGGGTTTCG	GTCAAGCCGC	ACAAGAAGTT	650
30	CATGGCAGAA	GCCTACATCC	TGACGAAGGA	AGAAGGCGGC	CGTCATACGC	700
	CGTTCTTCAC	GAACCTACCGT	CCGCAGTTCT	ACTTCCGTAC	GACTGACGTT	750
	ACCGGTATCG	TTTCGCTTCC	TGAAGGCACG	GAAATGGTTA	TGCCTGGCGA	800
	CAACGTCACT	GTTGAAGTCG	AGCTGATCGT	TCCGATCGCG	ATGGAAGAAA	850
35	AGCTGCGCTT	CGCTATCCGC	GAAGGCGGCC	GTACCGTCGG	CGCCGGC	897

2) INFORMATION FOR SEQ ID NO: 1735

40 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 885 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 45 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacillus subtilis*
 50 (B) STRAIN: 168
 (C) ACCESSION NUMBER: Z99104

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1735

	ATGATCACTG	GTGCTGCGCA	AATGGACGGA	GCTATCCTTG	TAGTATCTGC	50
	TGCTGATGGC	CCAATGCCAC	AAACTCGTGA	GCACATCCTT	CTTTCTAAAA	100
	ACGTTGGTGT	ACCATACATC	GTTGTATTCT	TAAACAAATG	CGACATGGTA	150
5	GACGACGAAG	AGCTTCTTGA	ACTAGTTGAA	ATGGAAGTTC	GCGATCTTCT	200
	TAGCGAATAC	GACTTCCCTG	GTGATGATGT	ACCAGTTGTT	AAAGGTCTG	250
	CTCTTAAAGC	TCTTGAAGGA	GACGCTGAGT	GGAAGCTAA	AATCTTCGAA	300
	CTTATGGATG	CGGTTGATGA	GTACATCCCA	ACTCCAGAAC	GCGACACTGA	350
	AAAACCATTC	ATGATGCCAG	TTGAGGACGT	ATTCTCAATC	ACTGGTCGTG	400
10	GTACAGTTGC	TACTGGCCGT	GTAGAACGCG	GACAAGTTAA	AGTCGGTGAC	450
	GAAGTTGAAA	TCATCGGTCT	TCAAGAAGAG	AACAAGAAAA	CAACTGTTAC	500
	AGGTGTTGAA	ATGTTCCGTA	AGCTTCTTGA	TTACGCTGAA	GCTGGTGACA	550
	ACATTGGTGC	CCTTCTTCGC	GGTGTATCTC	GTGAAGAAAT	CCAACGTGGT	600
	CAAGTACTTG	CTAAACCAGG	TACAATCACT	CCACACAGCA	AATTCAAAGC	650
15	TGAAGTTTAC	GTTCTTTCTA	AAGAAGAGGG	TGGACGTCAT	ACTCCATTCT	700
	TCTCTAACTA	CCGTCCTCAG	TTCTACTTCC	GTACAACTGA	CGTAACTGGT	750
	ATCATCCATC	TTCCAGAAGG	CGTAGAAATG	GTTATGCCTG	GAGATAACAC	800
	TGAAATGAAC	GTTGAACCTA	TTTCTACAAT	CGCTATCGAA	GAAGGAAGTC	850
	GTTTCTCTAT	TCGTGAAGGC	GGACGTACTG	TTGGT		885
20						

2) INFORMATION FOR SEQ ID NO: 1736

- 25 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 882 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Double
 - (D) TOPOLOGY: Linear
- 30 (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Bacteroides fragilis*
 - 35 (B) STRAIN: DSM 2151
 - (C) ACCESSION NUMBER: P33165
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1736

40	ATGGTTACTG	GTGCTGCTCA	GATGGACGGT	GCTATCATTG	TAGTTGCTGC	50
	TACTGATGGT	CCGATGCCTC	AGACTCGTGA	GCACATCCTT	TTGGCTCGTC	100
	AGGTAAACGT	TCCGAAGCTG	GTTGTATTCA	TGAACAAGTG	CGATATGGTT	150
	GAAGATGCTG	AGATGTTGGA	ACTTGTTGAA	ATGGAATGA	GAGAATTGCT	200
	TTCATTCTAT	GATTTGACG	GTGACAATAC	TCCGATCATT	CAGGGTTCTG	250
45	CTCTTGGTGC	ATTGAACGGC	GTAGAAAAAT	GGGAAGACAA	AGTAATGGAA	300
	CTGATGGAAG	CTGTTGATAC	TTGGATTCCA	CTGCCTCCGC	GCGATGTTGA	350
	TAAACCTTTC	TTGATGCCGG	TAGAAGACGT	GTTCTCTATC	ACAGGTCGTG	400
	GTAAGTAGC	TACAGGTCGT	ATCGAAACTG	GTGTTATCCA	TGTAGGTGAT	450
	GAAATCGAAA	TCCTCGGTTT	GGGTGAAGAT	AAGAAATCAG	TTGTAACAGG	500
50	TGTTGAAATG	TTCCGCAAAC	TTCTGGATCA	GGGTGAAGCT	GGTGACAACG	550
	TAGGTCTGTT	GCTTCGTGGT	GTTGACAAGA	ACGAAATCAA	ACGTGGTATG	600
	GTTCTTTGTA	AACCGGTCA	GATTAAACCT	CACTCTAAAT	TCAAAGCAGA	650
	GGTTTATATC	CTGAAGAAAG	AAGAAGGTGG	TCGTCACACT	CCATTCCATA	700

ACAAATATCG	TCCTCAGTTC	TACCTGCGTA	CTATGGACTG	TACAGGTGAA	750
ATCACTCTTC	CGGAAGGAAC	TGAAATGGTA	ATGCCGGGTG	ATAACGTAAC	800
TATCACTGTA	GAGTTGATCT	ATCCGGTTGC	ACTGAACATC	GGTCTTCGTT	850
TCGCTATCCG	CGAAGGTGGA	CGTACAGTAG	GT		882

5

2) INFORMATION FOR SEQ ID NO: 1737

10 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 888 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

15

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Borrelia burgdorferi*
- (B) STRAIN: U78183
- (C) ACCESSION NUMBER: U78183

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1737

25	AATATGATTA	CAGGAGCAGC	TCAAATGGAT	GCAGCGATAC	TTTtagTTGC	50
	TGCTGATAGT	GGTGCTGAGC	CTCAAACAAA	AGAGCATTTG	CTTCTTGCTC	100
	AAAGAATGGG	AATAAAGAAA	ATAATAGTTT	TTTTAAATAA	ATTGGACTTA	150
	GCAGATCCTG	AACTTGTTGA	GCTTGTTGAA	GTTGAAGTTT	TAGAACTTGT	200
	TGAAAAATAT	GGCTTTTCAG	CTGATACTCC	AATAATCAAA	GGTTCAGCTT	250
30	TTGGGGCTAT	GTCAAATCCA	GAAGATCCTG	AATCTACAAA	ATGCGTTAAA	300
	GAAGTTCTTG	AATCTATGGA	TAATTATTTT	GATCTTCCAG	AAAGAGATAT	350
	TGACAAGCCA	TTTTTGCTTG	CTGTTGAAGA	TGTATTTTCT	ATTTcAGGAA	400
	GAGGCACTGT	TGCTACTGGG	CGTATTGAAA	GAGGTATTAT	TAAAGTTGGT	450
	CAAGAAGTTG	AAATAGTTGG	AATTAAAGAA	ACCAGAAAAA	CTACTGTTAC	500
35	TGGTGTTGAA	ATGTTCCAGA	AAATTCTTGA	GCAAGGTCAA	GCAGGGGATA	550
	ATGTTGGTCT	TCTTTTGAGA	GGCGTTGATA	AAAAAGACAT	TGAGAGGGGG	600
	CAAGTTTGT	CAGCTCCAGG	TACAATTACT	CCACACAAGA	AATTTAAAGC	650
	TTCAATTTAT	TGTTTGACTA	AAGAAGAAGG	CGGTAGGCAC	AAGCCATTTT	700
	TCCCAGGGTA	TAGACCACAG	TTCTTTTTTA	GAACAACCGA	TGTTACTGGA	750
40	GTTGTTGCTT	TAGAGGGCAA	AGAAATGGTT	ATGCCTGGTG	ATAATGTTGA	800
	TATTATTGTT	GAGCTGATCT	CTTCAATAGC	TATGGATAAG	AATGTAGAAT	850
	TTGCTGTTCG	AGAAGGTGGA	AGAACCGTTG	CTTCAGGA		888

45

2) INFORMATION FOR SEQ ID NO: 1738

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 894 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Brevibacterium linens*
 (B) STRAIN: DSM 20425
 (C) ACCESSION NUMBER: X76863

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1738

10	AACATGATCA	CCGGTGCCGC	TCAGATGGAC	GGTGCGATCC	TCGTCGTCGC	50
	CGCTACCGAC	GGACCGATGC	CCCAGACCCG	TGAGCACGTG	CTGCTCGCGC	100
	GTCAGGTCGG	CGTTCCCTAC	ATCGTCGTGG	CTCTGAACAA	GTCCGACATG	150
	GTCGATGACG	AGGAGCTCCT	CGAGCTCGTC	GAATTCGAGG	TCCGCGACCT	200
	GCTCTCGAGC	CAGGACTTCG	ACGGAGACAA	CGCTCCGGTC	ATTCCGGTGT	250
15	CCGCTCTCAA	GGCGCTGGAA	GGCGACGAGA	AGTGGGTCAA	GAGCGTTCAG	300
	GATCTCATGG	CTGCCGTCGA	TGACAACGTT	CCGGAGCCGG	AGCGCGATGT	350
	CGACAAGCCG	TTCCTCATGC	CCGTCGAGGA	CGTCTTCACG	ATCACC GGTC	400
	GTGGAACCGT	CGTCACCGGT	CGTGTCGAGC	GCGGCGTGCT	CCTGCCTAAC	450
	GACGAAATCG	AAATCGTCGG	CATCAAGGAG	AAGTCGTCCA	AGACGACTGT	500
20	CACCGCTATC	GAGATGTTCC	GCAAGACCCCT	GCCGGATGCC	CGTGCAGGTG	550
	AGAACGTCGG	TCTGCTCCTC	CGCGGCACCA	AGCGCGAGGA	TGTTGAGCGC	600
	GGTCAGGTCA	TCGTGAAGCC	GGGTTCGATC	ACCCCGCACA	CCAAGTTCGA	650
	GGCTCAGGTC	TACATCCTGA	GCAAGGACGA	GGGCGGACGT	CACAACCCGT	700
	TCTACTCGAA	CTACCGTCCG	CAGTTCTACT	TCCGGACCAC	GGACGTCACC	750
25	GGTGTCATCA	CGCTGCCCCG	GGGCACCGAG	ATGGTCATGC	CCGGCGACAA	800
	CACCGATATG	TCGGTCGAGC	TCATCCAGCC	GATCGCTATG	GAGGACCGCC	850
	TCCGCTTCGC	AATCCGCGAA	GGTGCCGCA	CCGTCGGCGC	CGGT	894

30

2) INFORMATION FOR SEQ ID NO: 1739

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 888 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

40

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Chlamydia trachomatis*
 (B) STRAIN: F/IC-Cal-13
 (C) ACCESSION NUMBER: L22216

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1739

	ATGATCACGG	GCGCAGCGCA	GATGGACGGC	GCGATCCTGG	TTTGCTCGGC	50
	AGCAGACGGC	CCGATGCCGC	AAACGCGTGA	GCACATCCTG	CTGGCGCGTC	100
50	AGGTTGGTGT	TCCGTACATC	ATCGTGTTC	TGAACAAGTG	CGACAGTGTG	150
	GACGACGCTG	AACTGCTCGA	GCTGGTCGAG	ATGGAAGTTC	GCGAACTCCT	200
	GTCGAAGTAC	GACTTCCCGG	GCGACGACAC	GCCGATCGTG	AAGGGTTCGG	250
	CCAAGCTGGC	GCTGGAAGGC	GACACGGGCG	AGCTGGGCGA	AGTGGCGATC	300

	ATGAGCCTGG	CAGACGCGCT	GGACACGTAC	ATCCCGACGC	CGGAGCGTGC	350
	AGTTGACGGC	GCGTTCCTGA	TGCCGGTGGA	AGACGTGTTC	TCGATCTCGG	400
	GCCGTGGTAC	GGTGGTGACG	GGTCGTGTCTG	AGCGCGGCAT	CGTGAAGGTC	450
	GGCGAAGAAA	TCGAAATCGT	CGGTATCAAG	CCGACGGTGA	AGACGACCTG	500
5	CACGGGCGTT	GAAATGTTCC	GCAAGCTGCT	GGACCAAGGT	CAGGCAGGCG	550
	ACAACGTCGG	TATCCTGCTG	CGCGGCACGA	AGCGTGAAGA	CGTGGAGCGT	600
	GGCCAGGTTC	TGGCGAAGCC	GGGTTCGATC	ACGCCGCACA	CGCACTTCAC	650
	GGCTGAAGTG	TACGTGCTGA	GCAAGGACGA	AGGCGGCCGT	CACACGCCGT	700
	TCTTCAACAA	CTACCGTCCG	CAGTTCTACT	TCCGTACGAC	GGACGTGACG	750
10	GGCTCGATCG	AGCTGCCGAA	GGACAAGGAA	ATGGTGATGC	CGGGCGACAA	800
	CGTGTCGATC	ACGGTGAAGC	TGATTGCTCC	GATCGCGATG	GAAGAAGGTC	850
	TGCGCTTCGC	AATCCGTGAA	GGCGGCCGTA	CGGTCCGC		888

15

2) INFORMATION FOR SEQ ID NO: 1740.

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 891 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

25

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Fibrobacter succinogenes*
 (B) STRAIN: S85
 (C) ACCESSION NUMBER: X76866

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1740

	AACATGGTGA	CTGGTGCTGC	TCAGATGGAC	GGCGCTATCC	TCGTTGTTGC	50
	CGCTACTGAC	GGTCCGATGC	CGCAGACTCG	CGAACACATC	CTTCTCGCTC	100
35	ACCAGGTTGG	CGTGCCGAAG	ATCGTCGTGT	TCATGAACAA	GTGCGACATG	150
	GTTGACGATG	CTGAAATTCT	CGACCTCGTC	GAAATGGAAG	TTCGCGAACT	200
	CCTCTCCAAG	TATGACTTCG	ACGGTGACAA	CACCCCGATC	ATCCGTGGTT	250
	CCGCTCTCAA	GGCCCTCGAA	GGCGATCCGG	AATACCAGGA	CAAGGTCATG	300
	GAAGTCATGA	ACGCTTGCGA	CGAATACATC	CCGCTCCCGC	AGCGCGATAC	350
40	CGACAAGCCG	TTCCTCATGC	CGATCGAAGA	CGTGTTACG	ATTACTGGCC	400
	GCGGCACTGT	CGCTACTGGC	CGTATCGAAC	GCGGTGTCGT	TCGCTTGAAC	450
	GACAAGGTTG	AACGTATCGG	TCTCGGTGAA	ACCACCGAAT	ACGTCATCAC	500
	CGGTGTTGAA	ATGTTCCGTA	AGCTCCTCGA	CGACGCTCAG	GCAGGTGACA	550
	ACGTTGGTCT	CCTCCTCCGT	GGTGCTGAAA	AGAAGGACAT	CGTCCGTGGC	600
45	ATGGTTCTCG	CAGCTCCGAA	GTCTGTCACT	CCGCACACCG	AATTTAAGGC	650
	TGAAATCTAC	GTTCTCACGA	AGGACGAAGG	TGGCCGTCAC	ACGCCGTTCA	700
	TGAATGGCTA	CCGTCCGCAG	TTCTACTTCC	GCACCACCGA	CGTTACTGGT	750
	ACGATCCAGC	TCCCGGAAGG	TGTCGAAATG	GTTACTCCGG	GTGACACGGT	800
	CACGATCCAC	GTGAACCTCA	TCGCTCCGAT	CGCTATGGAA	AAGCAGCTCC	850
50	GCTTCGCTAT	CCGTGAAGGT	GGACGTACTG	TTGGTGCTGG	C	891

2) INFORMATION FOR SEQ ID NO: 1741

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 894 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

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(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Flavobacterium ferrugineum*
 (B) STRAIN: DSM 13524
 (C) ACCESSION NUMBER: X76867

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1741

	AACATGATCA	CCGGTGCTGC	CCAGATGGAC	GGTGCTATCT	TAGTTGTGGC	50
	TGCATCAGAC	GGTCCTATGC	CTCAAACAAA	AGAACACATC	CTGCTTGCTG	100
20	CCCAGGTAGG	TGTACCTAAA	ATGGTTGTGT	TTCTGAATAA	AGTTGACCTC	150
	GTTGACGACG	AAGAGCTCCT	GGAGCTGGTT	GAGATCGAGG	TTCGCGAAGA	200
	ACTGACTAAA	CGCGGTTTCG	ACGGCGACAA	CACTCCAATC	ATCAAAGGTT	250
	CCGCTACAGG	CGCCCTCGCT	GGTGAAGAAA	AGTGGGTAA	AGAAATTGAA	300
	AACCTGATGG	ACGCTGTTGA	CAGCTACATC	CCACTGCCTC	CTCGTCCGGT	350
25	TGATCTGCCG	TTCCTGATGA	GCGTAGAGGA	CGTATTCTCT	ATCACTGGTC	400
	GTGGTACTGT	TGCTACCGGT	CGTATCGAGC	GTGGCCGTAT	CAAAGTTGGT	450
	GAGCCTGTTG	AGATCGTAGG	TCTGCAGGAG	TCTCCCCTGA	ACTCTACCGT	500
	TACAGGTGTT	GAGATGTTCC	GCAAACCTCT	CGACGAAGGT	GAAGCTGGTG	550
	ATAACGCCGG	TCTCCTCCTC	CGTGGTGTG	AAAAAACACA	GATCCGTCGC	600
30	GGTATGGTAA	TCGTTAAACC	CGGTTCCATC	ACTCCGCACA	CGGACTTCAA	650
	AGGCGAAGTT	TACGTACTGA	GCAAAGACGA	AGGTGGCCGT	CACACTCCAT	700
	TCTTCAACAA	ATACCGTCCT	CAATTCTACT	TCCGTACAAC	TGACGTTACA	750
	GGTGAAGTAG	AACTGAACGC	AGGAACAGAA	ATGGTTATGC	CTGGTGATAA	800
	CACCAACCTG	ACCGTTAAAC	TGATCCAACC	GATCGCTATG	GAAAAAGGTC	850
35	TGAAATTTCG	GATCCGCGAA	GGTGGCCGTA	CCGTAGGTGC	AGGA	894

2) INFORMATION FOR SEQ ID NO: 1742

40

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 906 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 45 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 50 (A) ORGANISM: *Helicobacter pylori*
 (B) STRAIN: 26695
 (C) ACCESSION NUMBER: AE000626

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1742

	AACATGATCA	CCGGTGCGGC	GCAAATGGAC	GGAGCGATTT	TGGTTGTTTC	50
	TGCAGCTGAT	GGCCCTATGC	CTCAAAC TAG	GGAGCATATC	TTATTGTCTC	100
5	GTCAAGTAGG	CGTGCCTCAC	ATCGTTGTTT	TCTTAAACAA	ACAAGACATG	150
	GTAGATGACC	AAGAATTGTT	AGAACTTGTA	GAAATGGAAG	TGCGCGAATT	200
	GTTGAGCGCG	TATGAATTTT	CTGGCGATGA	CACTCCTATC	GTAGCGGGTT	250
	CAGCTTTAAG	AGCTTTAGAA	GAAGCAAAGG	CTGGTAATGT	GGGTGAATGG	300
	GGTGAAAAAG	TGCTTAAACT	TATGGCTGAA	GTGGATGCCT	ATATCCCTAC	350
10	TCCAGAAAGA	GAACTTAACT	AACTTTCTT	GATGCCGGTT	GAAGATGTGT	400
	TCTCTATTGC	GGGTAGAGGG	ACTGTGGTTA	CAGGTAGGAT	TGAAAGAGGC	450
	GTGGTGAAAG	TAGGCGATGA	AGTGGAATC	GTTGGTATCA	GACCTACACA	500
	AAAAACGACT	GTAACCGGTG	TAGAAATGTT	TAGGAAAGAG	TTGGAAAAAG	550
	GTGAAGCCGG	CGATAATGTG	GGCGTGCTTT	TGAGAGGAAC	TAAAAAAGAA	600
15	GAAGTGAAC	GCGGTATGGT	TCTATGCAAA	CCAGGTTCTA	TCACTCCGCA	650
	CAAGAAATTT	GAGGGAGAAA	TTTATGTCCT	TTCTAAAGAA	GAAGGCGGGA	700
	GACACACTCC	ATTCTTCACC	AATTACCGCC	CGCAATTCTA	TGTGCGCACA	750
	ACTGATGTGA	CTGGCTCTAT	CACCCCTCCT	GAAGGCGTAG	AAATGGTTAT	800
	GCCTGGCGAT	AATGTGAAAA	TCACTGTAGA	GTTGATTAGC	CCTGTTGCGT	850
20	TAGAGTTGGG	AACTAAATTT	GCGATTCGTG	AAGGCGGTAG	GACCGTTGGT	900
	GCTGGT					906

25 2) INFORMATION FOR SEQ ID NO: 1743

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 891 bases
 (B) TYPE: Nucleic acid
 30 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

35 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Micrococcus luteus*
 (B) STRAIN: IFO 3333
 (C) ACCESSION NUMBER: M17788

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1743

	AACATGATCA	CCGGCGCCGC	TCAGATGGAC	GGCGCGATCC	TCGTGGTCGC	50
	CGCTACCGAC	GGCCCGATGG	CCCAGACCCG	TGAGCACGTG	CTCCTGGCCC	100
	GCCAGGTCGG	CGTGCCGGCC	CTGCTCGTGG	CCCTGAACAA	GTCGGACATG	150
45	GTGGAGGACG	AGGAGCTCCT	CGAGCGTGTC	GAGATGGAGG	TCCGGCAGCT	200
	GCTGTCTCTC	AGGAGCTTCG	ACGTCGACGA	GGCCCCGGTC	ATCCGCACCT	250
	CCGCTCTGAA	GGCCCTCGAG	GGCGACCCCC	AGTGGGTCAA	GTCCGTCGAG	300
	GACCTCATGG	ATGCCGTGGA	CGAGTACATC	CCGGACCCGG	TGCGCGACAA	350
	GGACAAGCCG	TTCCTGATGC	CGATCGAGGA	CGTCTTCACG	ATCACC GGCC	400
50	GTGGCACCGT	GGTGACCGGT	CGCGCCGAGC	GCGGCACCCT	GAAGATCAAC	450
	TCCGAGGTCG	AGATCGTCGG	CATCCGCGAC	GTGCAGAAGA	CCACTGTCAC	500
	CGGCATCGAG	ATGTTCCACA	AGCAGCTCGA	CGAGGCCTGG	GCCGGCGAGA	550
	ACTGCGGTCT	GCTCGTGCGC	GGTCTGAAGC	GCGACGACGT	CGAGCGCGGC	600

	CAGGTGCTGG	TGGAGCCGGG	CTCCATCACC	CCGCACACCA	ACTTCGAGGC	650
	GAACGTCTAC	ATCCTGTCCA	AGGACGAGGG	TGGGCGTCAC	ACCCCGTTCT	700
	ACTCGAACTA	CCGCGCGCAG	TTCTACTTCC	GCACCACCGA	CGTCACCGGC	750
	GTCATCACGC	TGCCCCGAGG	CACCGAGATG	GTCATGCCCC	GCGACACCAC	800
5	CGAGATGTCG	GTCGAGCTCA	TCCAGCCGAT	CGCCATGGAG	GAGGGCCTCG	850
	GCTTCGCCAT	CCGCGAGGGT	GGCCGCACCG	TGGGCTCCGG	C	891

10 2) INFORMATION FOR SEQ ID NO: 1744 -

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 891 bases
 (B) TYPE: Nucleic acid
 15 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

20 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Mycobacterium tuberculosis*
 (B) STRAIN: Erdmann
 (C) ACCESSION NUMBER: X63539

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1744

	AACATGATCA	CCGGCGCCGC	GCAGATGGAC	GGTGCGATCC	TGGTGGTCCG	50
	CGCCACCGAC	GGCCCGATGC	CCCAGACCCG	CGAGCACGTT	CTGCTGGCGC	100
	GTCAAGTGGG	TGTGCCCTAC	ATCCTGGTAG	CGCTGAACAA	GGCCGACGCA	150
30	GTGGACGACG	AGGAGCTGCT	CGAACTCGTC	GAGATGGAGG	TCCGCGAGCT	200
	GCTGGCTGCC	CAGGAATTCG	ACGAGGACGC	CCCGGTTGTG	CGGGTCTCGG	250
	CGCTCAAGGC	GCTCGAGGGT	GACGCGAAGT	GGGTTGCCTC	TGTCGAGGAA	300
	CTGATGAACG	CGGTCGACGA	GTCGATTCCG	GACCCGGTCC	GCGAGACCGA	350
	CAAGCCGTTT	CTGATGCCGG	TCGAGGACGT	CTTCACCATT	ACCGGCCGCG	400
35	GAACCGTGGT	CACCGGACGT	GTGGAGCGCG	GCGTGATCAA	CGTGAACGAG	450
	GAAGTTGAGA	TCGTCGGCAT	TCGCCCATCG	ACCACCAAGA	CCACCGTCAC	500
	CGGTGTGGAG	ATGTTCCGCA	AGCTGCTCGA	CCAGGGCCAG	GCGGGCGACA	550
	ACGTTGGTTT	GCTGCTGCGG	GGCGTCAAGC	GCGAGGACGT	CGAGCGTGGC	600
	CAGGTTGTCA	CCAAGCCCGG	CACCACCACG	CCGCACACCG	AGTTCGAAGG	650
40	CCAGGTCTAC	ATCCTGTCCA	AGGACGAGGG	CGGCCGGCAC	ACGCCGTTCT	700
	TCAACAACCTA	CCGTCCGCAG	TTCTACTTCC	GCACCACCGA	CGTGACCGGT	750
	GTGGTGACAC	TGCCGGAGGG	CACCGAGATG	GTGATGCCCC	GTGACAACAC	800
	CAACATCTCG	GTGAAGTTGA	TCCAGCCCGT	CGCCATGGAC	GAAGGTCTGC	850
45	GTTTCGCGAT	CCGCGAGGGT	GGCCGCACCG	TGGGCGCCGG	C	891

2) INFORMATION FOR SEQ ID NO: 1745

50 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 891 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

5 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Mycoplasma genitalium*

(B) STRAIN: G37

(C) ACCESSION NUMBER: U39732

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1745

	AATATGATCA	CAGGTGCTGC	ACAAATGGAT	GGAGCTATTC	TAGTTGTTTC	50
	AGCAACTGAT	AGTGTGATGC	CCCAAACCCG	CGAGCACATC	TTACTTGCCC	100
	GCCAAGTAGG	GGTTCCTAAA	ATGGTAGTTT	TTCTAAACAA	GTGTGATATT	150
15	GCTAGTGATG	AAGAGGTACA	AGAACTTGTT	GCTGAAGAAG	TACGTGATCT	200
	GTAACTTCC	TATGGTTTTG	ATGGTAAGAA	CACTCCTATT	ATTTATGGCT	250
	CAGCTTTAAA	AGCATTGGAA	GGTGATCCAA	AGTGGGAGGC	TAAGATCCAT	300
	GATTTGATTA	AAGCAGTTGA	TGAATGGATT	CCAACTCCTA	CACGTGAAGT	350
	AGATAAACCT	TTCTTATTAG	CAATTGAAGA	TACGATGACC	ATTACTGGTA	400
20	GAGGTACAGT	TGTTACAGGA	AGAGTTGAAA	GAGGTGAACT	CAAAGTAGGT	450
	CAAGAAGTTG	AAATTGTTGG	TTTAAAACCA	ATTAGAAAAG	CAGTTGTTAC	500
	TGGAATTGAA	ATGTTCAAAA	AGGAACTTGA	TTCAGCAATG	GCTGGTGACA	550
	ATGCTGGGGT	ATTATTACGT	GGTGTGTAAC	GTAAAGAAGT	TGAAAGAGGT	600
	CAAGTTTTAG	CAAAACCAGG	CTCTATTAAA	CCGCACAAGA	AATTTAAAGC	650
25	TGAGATCTAT	GCTTTAAAGA	AAGAAGAAGG	TGGTAGACAC	ACTGGTTTTT	700
	TAAACGGTTA	CCGTCCTCAA	TTCTATTTC	GTACCACTGA	TGTAACGGT	750
	TCTATTGCTT	TAGCTGAAAA	TACTGAAATG	GTTCTACCTG	GTGATAATGC	800
	TTCTATTACT	GTTGAGTTAA	TTGCTCCTAT	CGCTTGTGAA	AAAGGTAGTA	850
	AGTTCTCAAT	TCGTGAAGGT	GGTAGAACTG	TAGGGGCAGG	C	891

2) INFORMATION FOR SEQ ID NO: 1746

35 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 891 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

40

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Neisseria gonorrhoeae*

45 (B) STRAIN: MS11

(C) ACCESSION NUMBER: L36380

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1746

50	AACATGATTA	CCGGCGCCGC	ACAAATGGAC	GGTGCAATCC	TGGTATGTTC	50
	TGCTGCCGAC	GGCCCTATGC	CGCAAACCCG	CGAACACATC	CTGCTGGCCC	100
	GTCAAGTAGG	CGTACCTTAC	ATCATCGTGT	TCATGAACAA	ATGCGACATG	150
	GTCGACGATG	CCGAGCTGTT	CCAAGTGGTT	GAAATGGAAA	TCCGCGACCT	200

	GCTGTCCAGC	TACGACTTCC	CCGGCGACGA	CTGCCCCGATC	GTACAAGGTT	250
	CCGCACTGAA	AGCCTTGGA	GGCGATGCCG	CTTACGAAGA	AAAAATCTTC	300
	GAAGTGGCTA	CCGCATTGGA	CAGATACATC	CCGACTCCCG	AGCGTGCCGT	350
	GGACAAACCA	TTCCTGCTGC	CTATCGAAGA	CGTGTTCTCC	ATTTCCGGCC	400
5	GCGGTACCGT	AGTCACCGGC	CGTGTAAGC	GAGGTATCAT	CCACGTTGGT	450
	GACGAGATTG	AAATCGTCGG	TCTGAAAGAA	ACCCAAAAAA	CCACCTGTAC	500
	CGGCGTTGAA	ATGTTCCGCA	AACTGCTGGA	CGAAGGTCAG	GCGGGCGACA	550
	ACGTAGGCGT	ATTGCTGCGC	GGTACCAAAC	GTGAAGACGT	AGAACGCGGT	600
	CAGGTATTGG	CCAAACGGGG	TACTATCACT	CCTCACACCA	AGTTCAAAGC	650
10	AGAAGTGTAC	GTATTGAGCA	AAGAAGAGGG	CGGCCCCCAT	ACCCCGTTTT	700
	TCGCCAACTA	CCGTCCCCAA	TTCTACTTCC	GTACCACTGA	CGTAACCGGC	750
	ACGATTACTT	TGGAAAAAGG	TGTGGAAATG	GTAATGCCGG	GTGAGAACGT	800
	AACCATTACT	GTAGAACTGA	TTGCGCCTAT	CGCTATGGAA	GAAGGTCTGC	850
	GCTTTGCGAT	TCGCGAAGGC	GGCCGTACCG	TGGGTGCCGG	C	891

15

2) INFORMATION FOR SEQ ID NO: 1747

20 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 891 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

25

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Rickettsia prowazekii*
 (B) STRAIN: Madrid E
 (C) ACCESSION NUMBER: Z54170

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1747

35	AATATGATAA	CTGGTGCCGC	TCAGATGGAT	GGTGCTATAT	TAGTAGTTTC	50
	TGCTGCTGAT	GGTCCTATGC	CTCAAACTAG	AGAACATATA	TTACTGGCAA	100
	AACAGGTAGG	TGTACCTGCT	ATGGTAGTAT	TTTTGAATAA	AGTAGATATG	150
	GTAGATGATC	CTGACCTATT	AGAATTAGTT	GAGATGGAAG	TAAGAGAATT	200
	ATTATCAAAA	TATGGTTTCC	CTGGTAATGA	AATACCTATT	ATTAAAGGTT	250
40	CTGCACTTCA	AGCTTTAGAA	GGAAAACCTG	AAGGTGAAAA	AGCTATTAAT	300
	GAGTTAATGA	ATGCAGTAGA	TACGTATATA	CCTCAGCCTA	TAGAGCTACA	350
	AGATAAACCT	TTTTTAATGC	CAATAGAGGA	TGTATTTTCT	ATTTTCAGGCA	400
	GAGGTACCGT	TGTAACCTGGT	AGAGTGAGGT	CAGGCATAAT	TAAGGTGGGT	450
	GAAGAAATTG	AAATAGTAGG	TCTAAAAAAT	ACGCAAAAAA	CGACTTGTAAC	500
45	AGGTGTAGAA	ATGTTTCAGAA	AATTACTTGA	TGAAGGACAA	TCTGGAGATA	550
	ATGTCGGTAT	ATTACTACGT	GGTACAAAAA	GAGAAGAAGT	AGAAAGAGGA	600
	CAAGTACTTG	CAAACCTGG	GAGCATAAAA	CCGCATGATA	AATTTGAAGC	650
	TGAAGTGTAT	GTGCTTAGTA	AAGAGGAAGG	TGGACGTCAT	ACCCCATTTA	700
	CTAATGATTA	TCGCCCACAG	TTCTATTTTA	GAACAACAGA	TGTTACCGGC	750
50	ACAATAAAAT	TGCCTTCTGA	TAAGCAGATG	GTTATGCCTG	GAGATAATGC	800
	TACTTTTTCA	GTAGAATTAA	TTAAGCCGAT	TGCTATGCAA	GAAGGGTTAA	850
	AATTCTCTAT	ACGTGAAGGT	GGTAGAACAG	TAGGAGCCGG	T	891

2) INFORMATION FOR SEQ ID NO: 1748

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 891 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

10

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Salmonella choleraesuis* subsp. *choleraesuis*
 serotype Typhimurium
 (B) STRAIN: LT2 trpE91
 15 (C) ACCESSION NUMBER: X55116

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1748

20	AACATGATCA	CCGGTGCTGC	TCAGATGGAC	GGCGCGATCC	TGGTTGTTGC	50
	TGCGACTGAC	GGCCCGATGC	CGCAGACCCG	TGAGCACATC	CTGCTGGGTC	100
	GTCAGGTAGG	CGTTCCGTAC	ATCATCGTGT	TCCTGAACAA	ATGCGACATG	150
	GTTGATGACG	AAGAGCTGCT	GGAAGTGGTT	GAGATGGAAG	TTCGCGAACT	200
	GCTGTCTCAG	TACGACTTCC	CGGGCGACGA	CACTCCGATC	GTTCGTGGTT	250
	CTGCTCTGAA	AGCGCTGGAA	GGCGACGCAG	AGTGGGAAGC	GAAAATCATC	300
25	GAAGTGGCTG	GCTTCCTGGA	TTCTTATATT	CCGGAACCAG	AGCGTGCGAT	350
	TGACAAGCCG	TTCCTGCTGC	CGATCGAAGA	CGTATTCTCC	ATCTCCGGTC	400
	GTGGTACCGT	TGTTACCGGT	CGTGTAGAGC	GCGGTATCAT	CAAAGTGGGC	450
	GAAGAAGTTG	AAATCGTTGG	TATCAAAGAG	ACTCAGAAGT	CTACCTGTAC	500
	TGGCGTTGAA	ATGTTCCGCA	AACTGCTGGA	CGAAGGCCGT	GCCGGTGAGA	550
30	ACGTAGGTGT	TCTGCTGCGT	GGTATCAAAC	GTGAAGAAAT	CGAACGTGGT	600
	CAGGTACTGG	CTAAGCCGGG	CACCATCAAG	CCGCACACCA	AGTTCGAATC	650
	TGAAGTGTAC	ATTCTGTCCA	AAGATGAAGG	CGGCCGTCAT	ACTCCGTTCT	700
	TCAAAGGCTA	CCGTCCGCAG	TTCTACTTCC	GTACTACTGA	CGTGACTGGT	750
	ACCATCGAAC	TGCCGGAAGG	CGTAGAGATG	GTAATGCCGG	GCGACAACAT	800
35	CAAAATGGTT	GTTACCCTGA	TCCACCCGAT	CGCGATGGAC	GACGGTCTGC	850
	GTTTCGCAAT	CCGTGAAGGC	GGCCGTACCG	TTGGCGCGGG	C	891

40 2) INFORMATION FOR SEQ ID NO: 1749

(i) SEQUENCE CHARACTERISTICS:

- 45 (A) LENGTH: 881 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

50 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Shewanella putrefaciens*
 (B) STRAIN: DSM 50426

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1749

	ATGATCACTG	GTGCTGCACA	GATGGACGGC	GCGATTCTGG	TAGTCGCTTC	50
	AACAGACGGT	CCAATGCCAC	AGACTCGTGA	GCACATCCTG	CTTTCTCGTC	100
5	AGGTTGGCGT	ACCATTTCATC	ATCGTATTCA	TGAACAAATG	TGACATGGTA	150
	GATGACGAAG	AGCTGTTAGA	GCTAGTTGAG	ATGGAAGTGC	GTGAACTGTT	200
	ATCAGAATAC	GATTTCCCAG	GTGATGACTT	ACCGGTAATC	CAAGGTTTCAG	250
	CTCTGAAAGC	GCTAGAAGGC	GAGCCAGAGT	GGGAAGCAAA	AATCCTTGAA	300
	TTAGCAGCGG	CGCTGGATTTC	TTACATTCCA	GAACCACAAC	GTGACATCGA	350
10	TAAGCCGTTTC	CTACTGCCAA	TCGAAGACGT	ATTCTCAATT	TCAGGCCGTG	400
	GTACAGTAGT	AACAGGTCGT	GTTGAGCGTG	GTATTGTACG	CGTAGGCGAC	450
	GAAGTTGAAA	TCGTTGGTGT	ACGTGCGACA	ACTAAGACAA	CGTGTACTGG	500
	TGTAGAAATG	TTCCGTAAAC	TGCTTGACGA	AGGTCGTGCA	GGTGAGAACT	550
	GTGGTATTTT	GTTACGTGGT	ACTAAGCGTG	ATGACGTAGA	ACGTGGTCAA	600
15	GTATTAGCGA	AGCCAGGTTTC	AATCAACCCA	CACACTACTT	TTGAATCAGA	650
	AGTTTACGTA	CTGTCAAAAG	AAGAAGGTGG	TCGTCACACG	CCATTCTTCA	700
	AAGGCTACCG	TCCACAGTTC	TACTTCCGTA	CAACTGACGT	AACCGGTACT	750
	ATCGAACTGC	CAGAAGGCGT	AGAGATGGTA	ATGCCAGGCG	ATAACATCAA	800
	GATGGTAGTG	ACACTGATTT	GCCCAATCGC	GATGGACGAA	GGTTTACGCT	850
20	TCGCAATCCG	TGAAGGCGGT	CGTACAGTGG	T		881

2) INFORMATION FOR SEQ ID NO: 1750

25

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 897 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

30

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

35

- (A) ORGANISM: *Stigmatella aurantiaca*
- (B) STRAIN: DW4
- (C) ACCESSION NUMBER: X82820

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1750

40

	AACATGATCA	CGGGCGCGGC	GCAGATGGAC	GGAGCGATTG	TGGTGGTGTC	50
	CGCGGCCGAC	GGCCCGATGC	CCCAGACGCG	TGAGCACATC	CTGCTGGCCA	100
	GGCAGGTGGG	CGTGCCCTAC	ATCGTCGTCT	TCCTGAACAA	GGTGGACATG	150
	CTGGACGATC	CGGAGCTGCG	CGAGCTGGTG	GAGATGGAGG	TGCGCGACCT	200
45	GCTCAAGAAG	TACGAGTTCC	CGGGCGACAG	CATCCCCATC	ATCCCTGGCA	250
	GCGCGCTCAA	GGCGCTGGAG	GGAGACACCA	GCGACATCGG	CGAGGGAGCG	300
	ATCCTGAAGC	TGATGGCGGC	GGTGGACGAG	TACATCCCGA	CGCCGCAGCG	350
	TGCGACGGAC	AAGCCGTTCC	TGATGCCGGT	GGAAGACGTG	TTCTCCATCG	400
	CAGGCCGAGG	AACGGTGGCG	ACGGGCCGAG	TGGAGCGCGG	CAAGATCAAG	450
50	GTGGGCGAGG	AAGTGGAGAT	CGTGGGGATC	CGTCCGACGC	AGAAGACGGT	500
	CATCACGGGG	GTGGAGATGT	TCCGCAAGCT	GCTGGACGAG	GGCATGGCGG	550
	GAGACAACAT	CGGAGCGCTG	CTGCGAGGCC	TGAAGCGCGA	GGACCTGGAG	600
	CGTGGGCAGG	TGCTGGCGAA	CTGGGGGAGC	ATCAACCCGC	ACACGAAGTT	650

	CAAGGCGCAG	GTGTACGTGC	TGTCGAAGGA	AGAGGGAGGG	CGGCACACGC	700
	CGTTCTTCAA	GGGATACCGG	CCGCAGTTCT	ACTTCCGGAC	GACGGACGTG	750
	ACCGGAACGG	TGAAGCTGCC	GGACAACGTG	GAGATGGTGA	TGCCGGGAGA	800
	CAACATCGCC	ATCGAGGTGG	AGCTCATTAC	TCCGGTCGCC	ATGGAGAAGG	850
5	AGCTGCCGTT	CGCCATCCGT	GAGGGTGGCC	GCACGGTGGG	CGCCGGC	897

2) INFORMATION FOR SEQ ID NO: 1751

10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 897 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 15 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 20 (A) ORGANISM: *Thiomonas cuprina*
 (B) STRAIN: Hoe5
 (C) ACCESSION NUMBER: x76871

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1751

25

	AACATGATCA	CCGGTGCGGC	CCAGATGGAC	GGCGCCATCC	TGGTCGTGTC	50
	CGCCGCCGAC	GGCCCCATGC	CCCAAACCCG	CGAGCACATC	CTGCTGGCGC	100
	GTCAGGTGGG	CGTGCCCTAC	ATCATCGTGT	TCCTCAACAA	GTGCGACATG	150
	GTCGACGACG	CCGAGCTGCT	CGAACTCGTC	GAGATGGAAG	TGCGCGAGCT	200
30	GCTGTCCAAG	TACGACTTCC	CCGGTGACGA	CACCCCCATC	ATCAAGGGCT	250
	CGGCCAAGCT	GGCCCTCGAA	GGCGACAAGG	GCGAACTGGG	CGAAGGCGCC	300
	ATTCTCAAGC	TGGCCGAGGC	CCTGGACACC	TACATCCCCA	CGCCCGAGCG	350
	GGCCGTCGAC	GGCGCGTTCC	TCATGCCCGT	GGAAGACGTG	TTCTCCATCT	400
	CCGGGCGCGG	CACGGTGGTC	ACCGGGCGTG	TGGAGCGCGG	CATCATCAAG	450
35	GTCGGCGAGG	AAATCGAGAT	TGTCGGCCTC	AAGCCCACCC	TCAAGACCAC	500
	CTGCACCGGC	GTGGAAATGT	TCAGGAAGCT	GCTCGACCAG	GGCCAGGCCG	550
	GCGACAACGT	CGGCATCTTG	CTGCGCGGCA	CCAAGCGCGA	GGAAGTCGAG	600
	CGCGGCCAGG	TGCTGTGCAA	ACCGGGCTCG	ATCAAGCCCC	ACACCCACTT	650
	CACCGCCGAG	GTGTACGTGC	TGAGCAAGGA	CGAGGGCGGC	CGCCACACCC	700
40	CCTTCTTCAA	CAACTACCGC	CCGCAGTTCT	ACTTCCGCAC	CACCGACGTC	750
	ACCGGCGCCA	TCGAACTGCC	CAAGGACAAG	GAAATGGTCA	TGCCCGGCGA	800
	TAATGTGAGC	ATCACCGTCA	AGCTCATCGC	CCCCATCGCC	ATGGAAGAAG	850
	GCCTGCGCTT	CGCCATCCGC	GAAGGCGGCC	GCACCGTCGG	CGCCGGC	897

15

2) INFORMATION FOR SEQ ID NO: 1752

(i) SEQUENCE CHARACTERISTICS:

- 50 (A) LENGTH: 894 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 5 (A) ORGANISM: *Treponema pallidum*
 (B) STRAIN: Nichols
 (C) ACCESSION NUMBER: AE001202

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1752

```

10 AATATGATCA CGGGTGCTGC GCAGATGGAC GGTGGTATTC TCGTCGTGTC 50
    TGC GCCTGAC GGC GTTATGC CACAGACGAA GGAGCATCTT CTGCTCGCCC 100
    GTCAGGTTGG TGTTCCCTCC ATCATTGTTT TTTTGAACAA GGT TGATTG 150
    GTTGATGATC CTGAGTTGCT AGAGCTGGTG GAAGAAGAGG TCGTGATGC 200
15 GCTTGCTGGA TATGGGTTTT CGCGTGAGAC GCCTATCGTC AAGGGGTCTG 250
    CGTTTAAAGC TCTGCAGGAT GGCGCTTCCC CGGAGGATGC AGCTTGATT 300
    GAGGAAGTGC TTGCGGCCAT GGATTCCTAC TTTGAAGACC CAGTGCCTGA 350
    CGACGCAAGA CCTTCTCTGC TCTCTATCGA GGATGTGTAC ACTATTCTG 400
    GGC GTGTAC CGTTGTCACG GGGCGCATCG AATGTGGGGT AATTAGTCTG 450
20 AATGAAGAGG TCGAGATCGT CGGGATTAAG CCCACTAAGA AAACAGTGGT 500
    TACTGGCATT GAGATGTTTA ATAAGTTGCT TGATCAGGGA ATTGCAGGTG 550
    ATAACGTGGG GCTGCTTTTG CGCGGGGTGG ATAAAAAAGA GGTTGAGCGC 600
    GGT CAGGTGC TTTCTAAGCC CGGTTCTATT AAGCCACACA CCAAGTTTGA 650
    GGC GCAGATC TACGTGCTCT CTAAGGAAGA GGGTGGCCGT CACAGTCCTT 700
25 TTTTTC AAGG TTATCGTCCG CAGTTTTATT TTAGAACTAC TGACATTACC 750
    GGTACGATTT CTCTTCTGA AGGGGTAGAC ATGGTGAAGC CGGGGGATAA 800
    CACCAAGATT ATAGGTGAGC TCATCCACCC GATAGCTATG GACAAGGGTC 850
    TGAAGCTTGC GATTCGTGAA GGGGGGCGCA CTATTGCTTC TGGT 894
  
```

30

2) INFORMATION FOR SEQ ID NO: 1753

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 891 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

40 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Ureaplasma urealyticum*
 (B) STRAIN: ATCC 33697
 45 (C) ACCESSION NUMBER: Z34275

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1753

```

50 AATATGATTA CAGGGGCAGC ACAAATGGAT GGAGCAATTT TAGTTATTGC 50
    TGCATCTGAT GGG GTTATGG CTCAAATAA AGAACATATT TTATTAGCAC 100
    GTCAAGTTGG TGTTCCAAAA ATCGTTGTTT TCTTAAACAA ATGTGATTTC 150
    ATGACAGATC CAGATATGCA AGATCTTGTT GAAATGGAAG TTCGTGAATT 200
    ATTATCTAAA TATGGATTG ATGGCGATAA CACACCAGTT ATTCGTGTT 250
  
```

	CAGGTCTTAA	GGCTTTAGAA	GGAGATCCAG	TTTGAGAAGC	AAAAATTGAT	300
	GAATTAATGG	ACGCAGTTGA	TTCATGAATT	CCATTACCAG	AACGTAGTAC	350
	TGACAAACCA	TTCTTATTAG	CAATTGAAGA	TGTATTCACA	ATTTCCAGGAC	400
	GTGGTACAGT	AGTAACTGGA	CGTGTGTAAC	GTGGTGTATT	AAAAGTTAAT	450
5	GATGAGGTTG	AAATTGTTGG	TCTAAAAGAC	ACTCAAAAAA	CTGTTGTGTTAC	500
	AGGAATTGAA	ATGTTTAGAA	AATCATTAGA	TCAAGCTGAA	GCTGGTGATA	550
	ATGCTGGTAT	TTTATTACGT	GGTATTAAAA	AAGAAGATGT	TGAACGTGGT	600
	CAAGTACTTG	TAAAACCAGG	ATCAATTAAA	CCTCACCGTA	CTTTTACTGC	650
	TAAAGTTTAT	ATTCTTAAAA	AAGAAGAAGG	TGGACGTCAT	ACACCTATTG	700
10	TTTCAGGATA	CCGTCCACAA	TTCTATTTTA	GAACAACAGA	TGTAACAGGT	750
	GCTATTTTCAT	TACCTGCTGG	TGTTGATTTG	GTTATGCCAG	GTGATGACGT	800
	TGAAATGACT	GTAAGAATTAA	TTGCTCCAGT	TGCGATTGAA	GATGGATCTA	850
	AATTCTCAAT	CCGTGAAGGT	GGTAAACTG	TAGGTCATGG	T	891

15

2) INFORMATION FOR SEQ ID NO: 1754

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 909 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

25 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Wolinella succinogenes*
 (B) STRAIN: DSM 1740
 30 (C) ACCESSION NUMBER: X76862

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1754

	AACATGATTA	CAGGTGCTGC	TCAAATGGAT	GGCGCGATTC	TTGTTGTTTC	50
35	TGCGGCGGAT	GGCCCCATGC	CCCAAACCTAG	GGAGCACATT	CTTCTTTCTC	100
	GACAAGTAGG	CGTTCCTTAC	ATCGTGTTT	TCTTGAACAA	AGAAGATATG	150
	GTTGATGACG	CTGAGCTTCT	TGAGCTTGTT	GAAATGGAAG	TTAGAGAACT	200
	TCTTAGCAAC	TACGACTTCC	CTGGAGATGA	CACTCCTATC	GTTGCAGGTT	250
	CCGCTCTTAA	AGCTCTTGAA	GAGGCTAACG	ACCAGGAAAA	TGTTGGCGAG	300
40	TGGGGCGAGA	AAGTATTGAA	GCTTATGGCT	GAGGTTGACC	GATATATTCC	350
	TACGCCTGAG	CGAGATGTGG	ATAAGCCTTT	CCTTATGCCT	GTTGAAGACG	400
	TATTCTCCAT	CGCGGGTCGT	GGAACCGTTG	TGACAGGAAG	AATTGAAAGA	450
	GGCGTGTTA	AAGTCGGTGA	CGAAGTAGAA	ATCGTTGGTA	TCCGAAACAC	500
	ACAAAAACA	ACCGTAACTG	GCGTTGAGAT	GTTCCGAAAA	GAGCTCGACA	550
45	AGGGTGAGGC	GGGTGACAAC	GTTGGTGTTC	TTTTGAGAGG	CACCAAGAAA	600
	GAAGATGTTG	AGAGAGGTAT	GGTTCTTTGT	AAAATAGGTT	CTATCACTCC	650
	TCACACTAAC	TTTGAAGGTG	AAGTTTACGT	TCTTTCCAAA	GAGGAAGGCG	700
	GACGACACAC	TCCATTCTTC	AATGGATACC	GACCTCAGTT	CTATGTTAGA	750
	ACTACAGACG	TTACCGGTTT	TATCTCTCTT	CCTGAGGGCG	TAGAGATGGT	800
50	TATGCCTGGT	GACAACGTTA	AGATCAATGT	TGAGCTTATC	GCTCCTGTAG	850
	CCCTCGAAGA	GGGAACACGA	TTCGCGATCC	GTGAAGGTGG	TCGAACCGTT	900
	GGTGCGGGT					909

2) INFORMATION FOR SEQ ID NO: 1755

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 888 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

10

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Burkholderia cepacia*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1755

15

ATGATCACGG	GCGCAGCGCA	GATGGACGGC	GCGATCCTGG	TTTGCTCGGC	50
AGCAGACGGC	CCGATGCCGC	AAACGCGTGA	GCACATCCTG	CTGGCGCGTC	100
AGGTTGGTGT	TCCGTACATC	ATCGTGTTCC	TGAACAAGTG	CGACAGTGTG	150
GACGACGCTG	AACTGCTCGA	GCTGGTCGAG	ATGGAAGTTC	GCGAACTCCT	200
20 GTCGAAGTAC	GACTTCCCGG	GCGACGACAC	GCCGATCGTG	AAGGGTTCGG	250
CCAAGCTGGC	GCTGGAAGGC	GACACGGGCG	AGCTGGGCGA	AGTGGCGATC	300
ATGAGCCTGG	CAGACGCGCT	GGACACGTAC	ATCCCGACGC	CGGAGCGTGC	350
AGTTGACGGC	GCGTTCCTGA	TGCCGGTGGA	AGACGTGTTC	TCGATCTCGG	400
GCCGTGGTAC	GGTGGTGACG	GGTCGTGTCG	AGCGCGGCAT	CGTGAAGGTC	450
25 GGC GAAGAAA	TCGAAATCGT	CGGTATCAAG	CCGACGGTGA	AGACGACCTG	500
CACGGGCGTT	GAAATGTTCC	GCAAGCTGCT	GGACCAAGGT	CAGGCAGGCG	550
ACAACGTCGG	TATCCTGCTG	CGCGGCACGA	AGCGTGAAGA	CGTGGAGCGT	600
GGCCAGGTTC	TGGCGAAGCC	GGGTTCGATC	ACGCCGCACA	CGCACTTCAC	650
GGCTGAAGTG	TACGTGCTGA	GCAAGGACGA	AGGCGGCCGT	CACACGCCGT	700
30 TCTTCAACAA	CTACCGTCCG	CAGTTCTACT	TCCGTACGAC	GGACGTGACG	750
GGCTCGATCG	AGCTGCCGAA	GGACAAGGAA	ATGGTGATGC	CGGGCGACAA	800
CGTGTCGATC	ACGGTGAAGC	TGATTGCTCC	GATCGCGATG	GAAGAAGGTC	850
TGCGCTTCGC	AATCCGTGAA	GGCGGCCGTA	CGGTCTGGC		888

35

2) INFORMATION FOR SEQ ID NO: 1756

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 388 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

45

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacillus anthracis*
 (B) STRAIN: CIP 9444

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1756

TGAAAGTTCA GGTA AAACAA CAGTTTCATT ACACGCAATT GCAGAAGTAC 50

AGCGTCAAGG TGGACAAGCA GCGTTCATTG ATGCTGAGCA TGCAATGGAT 100
 CCTGTATATG CACAAAAACT AGGTGTTAAC ATCGATGAAT TACTATTATC 150
 ACAACCTGAT ACAGGGGAGC AAGGTTTAGA AATCGCAGAA GCACTTGTAC 200
 GAAGTGGTGC GGTTGATATT ATCGTAATTG ACTCTGTAGC AGCTCTTGTA 250
 5 CCGAAAGCTG AAATTGAAGG AGACATGGGT GACTCACACG TAGGTTTACA 300
 AGCTCGTCTA ATGTCTCAAG CACTTCGTAA ACTTTCAGGT GCAATCAATA 350
 AATCAAAAAC AATCGCAATC TTTATTAACC AAATTCGT 388

10

2) INFORMATION FOR SEQ ID NO: 1757

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 388 bases
 15 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

20

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacillus anthracis*
 (B) STRAIN: ATCC 4229

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1757

TGAAAGTTCA GGTAACAACAA CAGTTTCATT ACACGCAATT GCAGAAGTAC 50
 AGCGTCAAGG TGGACAAGCA GCGTTCATTG ATGCTGAGCA TGCAATGGAT 100
 CCTGTATATG CACAAAAACT AGGTGTTAAC ATCGATGAAT TACTATTATC 150
 30 ACAACCTGAT ACAGGGGAGC AAGGTTTAGA AATCGCAGAA GCACTTGTAC 200
 GAAGTGGTGC GGTTGATATT ATCGTAATTG ACTCTGTAGC AGCTCTTGTA 250
 CCGAAAGCTG AAATTGAAGG AGACATGGGT GACTCACACG TAGGTTTACA 300
 AGCTCGTCTA ATGTCTCAAG CACTTCGTAA ACTTTCAGGT GCAATCAATA 350
 AATCAAAAAC AATCGCAATC TTTATTAACC AAATTCGT 388

35

2) INFORMATION FOR SEQ ID NO: 1758

40 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 388 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 45 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacillus cereus*
 50 (B) STRAIN: ATCC 7064
 (C) ACCESSION NUMBER:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1758

5 TGAAAGTTCA GGTAAAACAA CAGTTTCATT ACACGCAATT GCAGAAGTAC 50
 AGCGTCAAGG TGGACAAGCA GCGTTCATTG ATGCTGAGCA TGCAATGGAT 100
 CCTGTATATG CACAAAAACT AGGTGTTAAC ATCGATGAAT TACTATTATC 150
 5 ACAACCTGAT ACAGGGGAGC AAGGTTTAGA AATCGCAGAA GCACTTGATC 200
 GAAGTGGTGC GGTGATATT ATCGTAATTG ACTCTGTAGC AGCTCTTGTA 250
 CCGAAAGCTG AAATTGAAGG AGACATGGGT GACTCACACG TAGGTTTACA 300
 AGCTCGTCTA ATGTCTCAAG CACTTCGTAA ACTTTCAGGT GCAATCAATA 350
 10 AATCAAAAAC AATCGCAATC TTTATTAACC AAATTCGT 388

2) INFORMATION FOR SEQ ID NO: 1759

15 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 388 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacillus cereus*
 25 (B) STRAIN: ATCC 13472
 (C) ACCESSION NUMBER:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1759

30 TGAAAGTTCA GGTAAAACGA CAGTTTCATT ACATGCAATT GCAGAAGTAC 50
 AACGTCAAGG TGGACAAGCA GCATTCATCG ATGCGGAGCA CGCAATGGAT 100
 CCTGTATATG CACAAAAATT AGGCGTTAAC ATAGATGAAT TACTATTATC 150
 ACAGCCTGAT ACAGGGGAGC AAGGATTAGA AATCGCGGAA GCACTTGATC 200
 GAAGTGGTGC GGTGACATT ATCGTAATTG ACTCTGTAGC AGCTCTTGTA 250
 35 CCGAAAGCAG AGATTGAAGG TGACATGGGT GACTCACACG TAGGTTTACA 300
 AGCACGTTTA ATGTCACAAG CACTTCGTAA GCTTTCAGGA GCAATCAACA 350
 AATCAAAAAC AATTGCAATC TTTATTAACC AAATTCGT 388

40

2) INFORMATION FOR SEQ ID NO: 1760

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 374 bases
 45 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

50

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacillus mycoides*
 (B) STRAIN: ATCC 6462

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1760

	AAACGACAGT	TTCATTACAT	GCAATTGCAG	AAGTACAACG	TCAAGGTGGA	50
5	CAAGCAGCAT	TCATCGATGC	GGAGCACGCA	ATGGATCCTG	TATATGCACA	100
	AAAATTAGGC	GTTAACATAG	ATGAATTACT	ATTATCACAG	CCTGATACAG	150
	GGGAGCAAGG	ATTAGAAATC	GCAGAAGCAC	TTGTACGAAG	TGGTGCGGTT	200
	GACATTATCG	TAATTGACTC	TGTAGCAGCT	CTTGTACCGA	AAGCAGAGAT	250
	TGAAGGAGAC	ATGGGTGACT	CACACGTAGG	TTTACAAGCA	CGTTTAATGT	300
10	CACAAGCACT	TCGTAAGCTT	TCAGGAGCAA	TCAACAAATC	AAAAACAATT	350
	GCAATCTTTA	TTAACCAAAT	TCGT			374

15 2) INFORMATION FOR SEQ ID NO: 1761

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 381 bases
 (B) TYPE: Nucleic acid
 20 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

25 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacillus pseudomycoides*
 (B) STRAIN: NRRL BD-10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1761

30	GGAAAGTTCA	GGTAAAACAA	CGGTTTCCTT	ACATGCGATT	GCAGAAGTGC	50
	AACGTCAAGG	TGGACAAGCG	GCATTTATTG	ATGCGGAGCA	TGCGATGGAT	100
	CCTGTATATG	CACAAAAGTT	AGGTGTTAAT	ATTGATGAGT	TACTATTATC	150
	GCAGCCTGAT	ACAGGAGAAC	AAGGTTTAGA	AATCGCAGAA	GCATTAGTAC	200
35	GAAGCGGTGC	GATTGATATC	ATTGTAATTG	ACTCTGTAGC	AGCTCTTGTA	250
	CCAAAAGCAG	AAATCGAAGG	GGAAATGGGT	GACTCCCACG	TTGGTTTACA	300
	AGCGCGTTTA	ATGTCACAAG	CACTTCGTAA	GCTTTCTGGT	GCGATTAACA	350
	AATCAAAAAC	AATTGCAATC	TTCATTAACC	A		381

40

2) INFORMATION FOR SEQ ID NO: 1762

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 388 bases
 45 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

50 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacillus thuringiensis*

(B) STRAIN: HER 1410

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1762

```

5  TGAAAGTTCA GGTAAAACGA CAGTTTCATT ACATGCAATT GCAGAAGTAC      50
   AACGTCAAGG TGGACAAGCA GCATTCATCG ATGCGGAGCA CGCAATGGAT      100
   CCTGTATATG CACAAAAAATT AGGCGTTAAC ATAGATGAAT TACTATTATC      150
   ACAGCCTGAT ACAGGGGAGC AAGGATTAGA AATCGCGGAA GCACTTGTAC      200
   GAAGTGGTGC GGTTGACATT ATCGTAATTG ACTCTGTAGC AGCTCTTGTA      250
10  CCGAAAGCAG AGATTGAAGG CGAATATGGGT GACTCACACG TAGGTTTACA      300
   AGCACGTTTA ATGTCACAAG CACTTCGTAA GCTTTCAGGA GCAATCAACA      350
   AATCAAAAAC AATTGCAATC TTTATTAACC AAATTCGT      388

```

15

2) INFORMATION FOR SEQ ID NO: 1763.

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 388 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

25

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacillus thuringiensis*
 (B) STRAIN: HER 1418

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1763

```

   TGAAAGTTCA GGTAAAACGA CAGTTTCATT ACATGCAATT GCAGAAGTAC      50
   AACGTCAAGG TGGACAAGCA GCATTCATTG ATGCGGAGCA CGCAATGGAT      100
   CCTGTATATG CACAAAAAATT AGGCGTTAAC ATAGATGAAT TACTATTATC      150
35  ACAGCCTGAT ACAGGGGAGC AAGGATTGGA AATCGCGGAA GCACTTGTAC      200
   GAAGTGGTGC GGTTGACATT ATCGTAATTG ACTCTGTAGC AGCTCTTGTA      250
   CCGAAAGCAG AGATTGAAGG CGATATGGGT GACTCACACG TAGGTTTACA      300
   AGCACGTTTA ATGTCACAAG CACTTCGTAA GCTTTCAGGA GCAATCAACA      350
   AATCAAAAAC AATTGCAATC TTTATTAACC AAATTCGT      388

```

40

2) INFORMATION FOR SEQ ID NO: 1764

45 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 358 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Klebsiella oxytoca*

(B) STRAIN: ATCC 33496

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1764

5
 CTCCTATCTG GATTATGCGA TGTCGGTCAT TGTTGGCCGT GCGCTGCCGG 50
 ATGTCCGAGA TGGCCTGAAG CCGGTACACC GTCGCGTACT ATACGCCATG 100
 AACGTATTGG GCAATGACTG GAACAAAGCC TATAAAAAAT CTGCCCCTGT 150
 CGTGGGTGAC GTCATCGGTA AATACCACCC TCATGGTGAT ACTGCCGTAT 200
 10- ACGACACCAT TGTACGTATG GCGCAGCCCT TCTCCCTGCG TTACATGCTG 250
 GTAGATGGCC AGGGTAACTT TGGTTCGGTC GACGGCGACT CCGCCGCAGC 300
 GATGCGTTAT ACGGAAATCC GTATGTCGAA GATCGCCCAT GAACTGATGG 350
 CCGACCTC 358

15

2) INFORMATION FOR SEQ ID NO: 1765

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 365 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

25 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Klebsiella pneumoniae* subsp. *ozaenae*
 (B) STRAIN: ATCC 11296

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1765

TTAAGAACTC TTATCTGGAT TATGCGATGT CGGTCATTGT TGGCCGTGCG 50
 CTGCCGGATG TCCGAGATGG CCTGAAGCCG GTACACCGTC GCGTACTTTA 100
 35 CGCCATGAAC GTATTGGGCA ATGACTGGAA CAAAGCCTAT AAAAAATCAG 150
 CCCGTGTCGT TGGTGACGTA ATCGGTAAAT ACCACCCGCA CGGCGACTCC 200
 GCGGTATACG ACACCATCGT GCGTATGGCG CAGCCGTTCT CGCTGCGTTA 250
 CATGCTGGTG GACGGCCAGG GTAACCTTGG TTCCATCGAC GGCGACTCCG 300
 CCGCGGCGAT GCGTTATACC GAAATTCGTC TGGCGAAAAT CGCTCATGAG 350
 40 CTGATGGCCG ATCTT 365

2) INFORMATION FOR SEQ ID NO: 1766

45

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 344 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 50 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Klebsiella planticola*
 (B) STRAIN: ATCC 33531

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1766

```

AAGAGCTCGT ATCTGGATTA TGCATGTCG GTCATTGTTG GCCGTGCGCT      50
GCCGGATGTC CGAGATGGCC TGAAACCGGT ACACCGTCGC GTACTTTACG      100
CCATGAACGT ATTGGGCAAT GACTGGAACA AAGCCTATAA AAAATCCGCC      150
10 CGTGTCGTTG GTGACGTAAT CGGTAAATAC CACCCTCATG GTGATACCGC      200
CGTTTATGAC ACCATTGTAC GTATGGCACA GCCATTCTCC TTGCGTTATA      250
TGCTGGTCGA TGGCCAGGGT AACTTCGGTT CTGTCGATGG CGACTCCGCC      300
GCAGCGATGC GTTATACGGA AATCCGTATG TCGAAAATCG CCCA          344

```

15

2) INFORMATION FOR SEQ ID NO: 1767

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 345 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

25 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Klebsiella pneumoniae*
 (B) STRAIN: ATCC 27336

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1767

```

AACTCTTATC TGGATTATGC GATGTCGGTC ATTGTTGGCC GTGCGCTGCC      50
GGATGTCCGA GATGGCCTGA AGCCGGTACA CCGTCGCGTA CTTTACGCCA      100
35 TGAACGTATT GGGCAATGAC TGGAACAAAG CCTATAAAAA ATCAGCCCGT      150
GTCGTTGGTG ACGTAATCGG TAAATACCAC CCGCACGGCG ACTCCGCGGT      200
ATACGACACC ATCGTGCGTA TGGCGCAGCC GTTCTCGCTG CGTTACATGC      250
TGGTGGACGG CCAGGGTAAC TTTGGTTCCA TCGACGGCGA CTCCGCCGCG      300
GCGATGCGTT ATACCGAAAT TCGTCTGGCG AAAATCGCTC ATGAG          345

```

40

2) INFORMATION FOR SEQ ID NO: 1768

(i) SEQUENCE CHARACTERISTICS:

- 45 (A) LENGTH: 356 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Klebsiella pneumoniae* subsp. *pneumoniae*

(B) STRAIN: ATCC 13883

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1768

5

CTTATCTGGA	TTATGCGATG	TCGGTCATTG	TTGGCCGTGC	GCTGCCGGAT	50
GTCCGAGATG	GCCTGAAGCC	GGTACACCGT	CGCGTACTTT	ACGCCATGAA	100
CGTATTGGGC	AATGACTGGA	ACAAAGCCTA	TAAAAAATCA	GCCCGTGTCTG	150
TTGGTGACGT	AATCGGTAAA	TACCACCCGC	ACGGCGACTC	CGCGGTATAC	200
10 GACACCATCG	TGCGTATGGC	GCAGCCGTTT	TGCCTGCGTT	ACATGCTGGT	250
GGACGGCCAG	GGTAACTTTG	GTTCCATCGA	CGGCGACTCC	GCCGCGGCCA	300
TGCGTTATAC	CGAAATTCGT	CTGGCGAAAA	TCGCTCATGA	GCTGATGGCC	350
GATCTT					356

15

2) INFORMATION FOR SEQ ID NO: 1769

(i) SEQUENCE CHARACTERISTICS:

20

(A) LENGTH: 361 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

25

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Klebsiella pneumoniae* subsp. *pneumoniae*

(B) STRAIN: ATCC 29011

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1769

TAAGAACTCT	TATCTGGATT	ATGCGATGTC	GGTCATTGTT	GGCCGTGCGC	50
TGCCGGATGT	CCGAGATGGC	CTGAAGCCGG	TACACCGTCG	CGTACTTTAC	100
35 GCCATGAACG	TATTGGGCAA	TGACTGGAAC	AAAGCCTATA	AAAAATCAGC	150
CCGTGTCGTT	GGTGACGTAA	TCGGTAAATA	CCACCCGCAC	GGCGACTCCG	200
CGGTATACGA	CACCATCGTG	CGTATGGCGC	AGCCGTTCTC	GCTGCGTTAC	250
ATGCTGGTGG	ACGGCCAGGG	TAACCTTGGT	TCCATCGACG	GCGACTCCGC	300
CGCGGCGATG	CGTTATACCG	AAATTCGTCT	GGCGAAAATC	GCTCATGAGC	350
40 TGATGGCCGA	T				361

2) INFORMATION FOR SEQ ID NO: 1770

45

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 365 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

50

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Klebsiella pneumoniae* subsp.
rhinoscleromatis
 (B) STRAIN: ATCC 13824

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1770

```

-- TAAGAACTCT TATCTGGATT ATGCGATGTC GGTCATTGTT GGCCGTGCGC      50
-- TGCCGGATGT CCGAGATGGC CTGAAGCCGG TACACCGTCG CGTACTTTAC      100
10 GCCATGAACG TATTGGGCAA TGACTGGAAC AAAGCCTATA AAAAATCAGC      150
   CCGTGTCGTT GGTGACGTAA TCGGTAAATA CCACCCGCAC GGCGACTCCG      200
   CGGTATACGA CACCATCGTG CGTATGCGCG AGCCGTTCTC GCTGCGTTAC      250
   ATGCTGGTGG ACGGCCAGGG TAACTTTGGT TCCATCGACG GCGATTCCGC      300
   CGCGGCGATG CGTTATACCG AAATTCTGTCT GGCGAAAATC GCTCATGAGC      350
15 TGATGGCCGA TCTTG                                     365

```

2) INFORMATION FOR SEQ ID NO: 1771

20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 357 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 25 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 30 (A) ORGANISM: *Klebsiella terrigena*
 (B) STRAIN: ATCC 33257

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1771

```

35 TCGTATCTGG ATTATGCGAT GTCGGTCATT GTTGGCCGTG CGCTGCCGGA      50
   TGTCCGAGAT GGGTTGAAAC CGGTACACCG TCGCGTACTT TACGCCATGA      100
   ACGTATTGGG CAATGACTGG AACAAAGCCT ATAAAAAATC CGCCCGTGTC      150
   GTTGGTGACG TAATCGGTAA ATATCACCCCT CACGGTGATA CCGCCGTTTA      200
   TGACACCATT GTACGTATGG CGCAGCCATT CTCCTTGCGT TATATGCTGG      250
40 TCGATGGCCA GGGTAACTTC GGTTCGTGTCG ATGGCGACTC CGCCGCAGCG      300
   ATGCGTTATA CGGAAATCCG TATGTCGAAA ATCGCCCACG AGCTGATGGC      350
   CGACCTC                                     357

```

45

2) INFORMATION FOR SEQ ID NO: 1772

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 968 bases
 50 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Legionella pneumophila* subsp. *pneumophila*
 5 (B) STRAIN: ATCC 33152

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1772

```

10 CAGTACACAG GCGAGTTCTT TTTGCGATGA GTGAGTTAAG TAATGATTGG      50
   AATAAGCCGT ATAAAAAATC TGCTCGTGTA GTAGGGGATG TCATTGGTAA      100
   ATATCATCCT CATGGGGATA CAGCTGTTTA TGACACTATT GTTCGTATGG      150
   CTCAGCCCTT TTCCATGCGT TATATGCTGA TTGATGGGCA GGGTAATTTT      200
   GGCTCTGTAG ATGGAGATGC TCCAGCTGCC ATGCGTTACA CTGAAGTAAG      250
   AATGTCCAAA GTGGCGCATG CTTTACTGGC TGATTTGGAT AAGGAAACCG      300
15 TTGATTTTAG TCCTAACTAT GATGAAACAG AATTTGCTCC AGTGGTATTG      350
   CCATCGAGAA TTCCAATTT ACTAGTTAAT GGCTCTTCCG GTATTGCGGT      400
   AGGGATGGCT ACTAATATTC CACCACATAA TCTTACCGAA GTAATCAATG      450
   CATGTATTGC TTTAGTGGAT GAACCTGACA CGAGTCTTGA AGATTTAATG      500
   GAAATTATTC CTGGCCCTGA TTTTCCTACA GCCGCAATTA TTAATGGTCG      550
20 TGCTGGAATT ATTGAAGGTT ATCGTACTGG AAAAGGGCGG GTTGTTATCA      600
   GGGCACGCAC AGAAATTGAA ACGGATGAAA GTTCAGGCCG TCAGTCAATT      650
   ATTATTCAGG AATTACCCTA TCAGGTGAAT AAAGCGCGTT TGATCGAGCG      700
   TATTGCTGAA TTGGTAAGGG ACAAGAAAAT CGAAGGAATT TCCGGCTTGA      750
   GAGATGAGTC AGACAAGCAA GGAATGAGAG TAGTCATTGA ATTAAAACGC      800
25 AATGAAGTAG CAGATGTGGT ATTGAATAAC CTGTTTCGCTC ATACTCAAAT      850
   GCAAAATGTA TTCGGAATTA ATATGGTTGC TCTGGTGGAT GGCCAACCGC      900
   GTACTTTGAA TTTGAAGCAA ATACTGGAAT ATTTTATAAA ACATCGAAGA      950
   GAGGTTGTTA CCAGACGC                                     968

```

30

2) INFORMATION FOR SEQ ID NO: 1773

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 967 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

40 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Proteus mirabilis*
 45 (B) STRAIN: ATCC 25933

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1773

```

50 CACCGCCGAG TGCTATTTGC GATGAATGTA CTGGGAAACG ATTGGAATAA      50
   ACCTTATAAA AAATCAGCCC GTGTTGTTGG GGATGTAATC GGTAAATATC      100
   ACCCGCACGG TGACAGTGCT GTCTATGAAA CGATTGTTCG TTTAGCACAG      150
   CCTTTTCTA TGCGCTACAT GTTGTTGAC GGTGAGGGTA ACTTCGGGTC      200
   AGTTGATGGT GACTCCGCGG CGGCTATGCG TTATACCGAA GTTCGTATGG      250
   CGAAGATCGC CCATGAACGT CTGGCGGATT TGGAAAAAGA GACGGTCGAC      300

```

	TTTGTTCTTA	ACTATGATGG	AACAGAAAAT	ATACCGGCTG	TTATGCCAAC	350
	CCGTATTCCA	AACTTGTTAG	TTAATGGCTC	TTCAGGTATT	GCCGTTGGGA	400
	TGGCAACGAA	TATCCCTCCG	CATAACCTCG	GTGAAGTTAT	CGACGGTTGT	450
	CTTGCTATG	TTGATAATGA	AGACATCACC	ATAGAAGAAT	TAATGGAATA	500
5	TATTACCGGG	CCTGATTTTC	CGACTGCTGC	GATTATTAAT	GGTCGCAGAG	550
	GAATATTAGA	TGCTTATCGT	ACAGGGCGTG	GAAAGATTTA	TATCCGTGCT	600
	CAGGCTGATA	TTGAAACTGA	TGAGAAAACA	GGTCGCGAAA	CCATTATCGT	650
	GACAGAAATT	CCTTATCAGG	TGAATAAAGC	CCGTTTAATT	GAAAAAATTG	700
	CGGAGCTTGT	AAAAGATAAA	CGTATTGAAG	GTATCAGCGG	ATTACGTGAC	750
10	GAGTCTGATA	AAGACGGTAT	GCGTATTGTT	GTTGAGATCA	AACGTGATGC	800
	AGTCGGTGAA	GTAGTATTAA	ATCACCTCTT	TTCACAAACT	CAAATGCAAG	850
	TCTCTTTTGG	TATTAATATG	GTTGCGCTTC	ATCAAGGCCA	ACCAAAATTA	900
	TTGAACCTAA	AAGAAATTAT	CGCAGCCTTT	ATTGCGCATC	GTCGTGAAGT	950
	GGTGACTCGC	CGTACCA				967

15

2) INFORMATION FOR SEQ ID NO: 1774

20 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 978 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

25

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Providencia rettgeri*
 (B) STRAIN: ATCC 9250

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1774

	CCAGTACACC	GCAGAGTATT	GTATGCGATG	AATGTATTGG	GAAATGATTG	50
35	GAATAAACCC	TATAAAAAAT	CTGCCCCGAT	TGTTGGGGAC	GTCATCGGTA	100
	AATACCATCC	ACATGGTGAT	AGCGCTGTTT	ACGAGACAAT	CGTTCGTCTT	150
	GCTCAGCCTT	TCTCAATGCG	TTACATGCTG	GTTGATGGTC	AGGGAAACTT	200
	CGGTTCTGTT	GACGGAGACT	CCGCAGCGGC	AATGCGTTAT	ACGGAAATCC	250
	GTATGGCGAA	AATTGCCCAT	GAAGTACTTG	CTGACCTTGA	AAAAGAAACC	300
40	GTTGATTTTC	TTCCTAACTA	TGACGGAACA	GAGCACATTC	CTGAAGTTAT	350
	GCCAACGAAA	ATCCCAAACC	TTTTGGTTAA	TGGGTCGTCA	GGTATTGCTG	400
	TTGGGATGGC	AACCAATATC	CCACCTCACA	ATTTAGGGGA	GGTGATTAAT	450
	GGTTGTCTTG	CCTATATAGA	AGACGAAGAC	ATCAGCATTG	ATGGTTTAAT	500
	GGAACACATT	CCAGGGCCTG	ATTTCCCAAC	CGCAGCTATT	ATTAATGGCC	550
45	GTCGTGGGAT	TATTGATGCG	TATCGCACAG	GGCGTGGCAA	GGTCTATATC	600
	CGTGCAAGCG	CTGAAGTGGA	AGTCGATGAG	AAAAATGGTC	GCGAAACCAT	650
	TATTGTCAGC	GAAATTCCTT	ATCAAGTGAA	TAAAGCTCGC	TTGATTGAAA	700
	AAATTGCTGA	GTTAGTTAAA	GACAAGCGTG	TTGAAGGTAT	CAGTGCCTG	750
	CGTGACGAGT	CTGATAAAGA	CGGTATGCGT	ATTGTTATTG	AAATCAAACG	800
50	CGATGCGGTG	GGTGAAGTTG	TACTGAACAA	CTTATATTCC	CTGACCCAAT	850
	TGCAAGTTTC	TTTTGGTATC	AATATGGTAG	CTCTACACCA	AGGGCAGCCG	900
	AAAATACTGA	ATTTAAAAGA	TATCATTGCT	GCTTTTGTGC	GTCACCGCCG	950
	TGAAGTCGTC	ACTCGTCGTA	CGATTTTC			978

2) INFORMATION FOR SEQ ID NO: 1775

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 978 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

10

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Proteus vulgaris*
 (B) STRAIN: ATCC 13315

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1775

	CCAGTACACC	GTCGCGTTCT	TTTCGCGATG	AATGTATTAG	GAAACGATTG	50
	GAATAAACCT	TATAAAAAAT	CAGCCCGTGT	TGTTGGGGAT	GTTATCGGTA	100
	AATATCACCC	GCACGGTGAC	AGTGCTGTTT	ATGAAACGAT	AGTTTCGTTA	150
20	GCACAGCCTT	TTTCTATGCG	TTACATGTTG	GTTGACGGGC	AGGGTAACTT	200
	CGGGTCAGTT	GATGGTGACT	CGGCGGCTGC	AATGCGTTAT	ACCGAAGTTC	250
	GTATGGCGAA	AATCGCCCAT	GAAGTCTGCT	CGGATTTGGA	AAAAGAAACG	300
	GTTGATTTTG	TTCCTAACTA	TGATGGAACA	GAGCATATCC	CGGCAGTCAT	350
	GCCAACCCGT	ATTCCAAACT	TATTAGTCAA	TGGTTCTTCA	GGTATCGCAG	400
25	TCGGGATGGC	AACAAACATT	CCTCCGCATA	ACCTAGGTGA	AGTTATCGAC	450
	GGCTGTCTTG	CTTATGTTGA	TAACGAAGAC	ATCACTATTG	AAGAGTTGAT	500
	GGAGCATATC	ACGGGGCCTG	ATTTCCCAAC	TGCCGCTATT	ATTAATGGCC	550
	GCAGAGGAAT	TTTAGATGCT	TACCGTACTG	GGCGCGGAAA	AATTTATATT	600
	CGTGACACAAG	CTGATGTAGA	AACCGATGAG	AAAAGTGGTC	GCGAAACAAT	650
30	TATCGTGACG	GAAATTCCTT	ATCAGGTGAA	CAAAGCTCGC	TTAATTGAAA	700
	AAATTCGAGA	GCTTGTTAAA	GATAAACGTA	TTGAAGGCAT	TAGCGGATTA	750
	CGTGATGAGT	CAGATAAAGA	TGGTATGCGC	ATTGTTGTTG	AAATTAAGCG	800
	TGATGCTGTT	GGTGAAGTTG	TACTAAATCA	CTTATTTTCT	CAGACTCAGA	850
	TGCAGGTTTC	TTTGGGTATT	AACATGGTTG	CACTGCATCA	AGGTCAACCG	900
35	AAAGTGTTAA	ACCTGAAAGA	AATTATTTCA	GCCTTTATTC	GTCACCGTCG	950
	TGAAGTGGTG	ACTCGTCGTA	CTATTTTTT			978

40 2) INFORMATION FOR SEQ ID NO: 1776

(i) SEQUENCE CHARACTERISTICS:

- 45 (A) LENGTH: 940 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

50 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Yersinia enterocolitica*
 (B) STRAIN: ATCC 9610

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1776

	TGGGTAATGA	CTGGAATAAG	CCATACAAAA	AATCGGCCCG	TGTAGTCGGG	50
	GACGTTATCG	GTAAATATCA	CCCGCATGGT	GACAGCGCGG	TCTACGACAC	100
5	AATTGTGCGT	ATGGCCCAGC	CGTTCTCACT	GCGCTATATG	CTGGTGGATG	150
	GGCAGGGCAA	CTTCGGTTCC	GTTGATGGCG	ACTCCGCCGC	AGCGATGCGT	200
	TATACCGAAA	TCCGTATGTC	TAAAATTGCT	CACGAATTGT	TGGCGGACTT	250
	AGAAAAAGAT	ACCGTCGACT	TCGTGCCGAA	CTATGACGGT	ACGGAGCAAA	300
	TTCCTGCCGT	AATGCCAACC	CGAATCCCTA	ACTTGCTGGT	TAACGGCTCG	350
10	TCAGGTATTG	CTGTCGGTAT	GGCAACCAAT	ATTCCGCCGC	ATAACCTTTC	400
	TGAGGTTATT	GATGGCTGTC	TGGCCTATAT	CGAAGATGAA	AACATCACCA	450
	TTGAAGGGTT	GATGGAGTAC	ATCCCGGGGC	CAGATTTCCT	AACTGCTGCG	500
	ATTATCAATG	GTCGCCGTGG	TATTGAAGAA	GCTTATCGTA	CTGGCCGTGG	550
	CAAGGTGTAT	ATCCGTGCCC	GTGCTGAAGT	TGAGGCTGAC	GCTTAAACCG	600
15	GTCGCGAAAC	CATTATTGTT	CACGAGATCC	CGTATCAGGT	GAACAAGGCG	650
	CGGTTGATTG	AAAAAATCGC	CGAGCTGGTT	AAAGAAAAAC	GCGTAGAAGG	700
	CATCAGTGCG	TTGCGTGATG	AGTCTGATAA	AGACGGCATG	CGTATCGTGA	750
	TTGAAATCAA	ACGTGATGCT	GTCGGGGAAG	TGGTTCTGAA	CAACCTCTAT	800
	TCTCTGACGC	AATTGCAGGT	GACTTTCGGT	ATCAATATGG	TGGCTCTGTC	850
20	TCAAGGGCAG	CCTAAGTTGC	TTAACCTGAA	AGACATTTTG	GTTGCTTTTCG	900
	TGCGCCACCG	CCGTGAAGTG	GTGACTCGCC	GTACCATTTT		940

25 2) INFORMATION FOR SEQ ID NO: 1777

(i) SEQUENCE CHARACTERISTICS:

- | | |
|----|--------------------------|
| | (A) LENGTH: 668 bases |
| | (B) TYPE: Nucleic acid |
| 30 | (C) STRANDEDNESS: Double |
| | (D) TOPOLOGY: Linear |

(ii) MOLECULE TYPE: Genomic DNA

35 (vi) ORIGINAL SOURCE:

- | | |
|--|---|
| | (A) ORGANISM: <i>Klebsiella oxytoca</i> |
| | (B) STRAIN: ATCC 13182 |

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1777

40	CCGTTTATTG	GCGATGGCCT	GAAGCCGGTC	CAGCGTCGCA	TCGTCTATGC	50
	GATGTCTGAA	CTGGGTCTGA	ACGCCAGCGC	GAAGTTCAA	AAGTCCGCC	100
	GCACCGTCGG	TGACGTGCTG	GGTAAATACC	ATCCCCACGG	CGACAGCGCG	150
	TGCTATGAAG	CCATGGTGCT	GATGGCTCAG	CCCTTCTCCT	ACCGCTATCC	200
45	GCTGGTTGAC	GGTCAGGGAA	ACTGGGGGGC	GCCGGACGAT	CCTAAATCCT	250
	TCGCCGCAAT	GCGTTATACC	GAATCCCGTT	TGTCGAAGTA	TGCTGAACTG	300
	CTGCTGAGCG	AACTGGGGCA	AGGCACCGTT	GACTGGGTAC	CAAACCTCGA	350
	CGGCACTTTG	CAGGAGCCGA	AGATGCTGCC	TGCGCGCCTG	CCCAATATTC	400
	TGCTAAACGG	TACTACCGGC	ATTGCCGTTG	GGATGGCGAC	GGACATTCCG	450
50	CCGCACAACC	TGCGTGAAGT	GGCCCGGGCG	GCCATTACCC	TGATTGAAAA	500
	GCCGCAAACT	TCGCTGGATG	ACCTGCTGGA	TATCGTGCAG	GGGCCGGATT	550
	ATCCTACCGA	AGCGGAAATC	ATTACCCCCC	GTGCCGAAAT	CCGCAAAATC	600
	TACCAGAATG	GCCGCGGTTT	GGTGCGGATG	CGCGCGGTAT	GGGCCAAAGA	650

AGACGGCGCG GTGGTGAT

668

5 2) INFORMATION FOR SEQ ID NO: 1778

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 714 bases
(B) TYPE: Nucleic acid
10 (C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

15 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Klebsiella oxytoca*
(B) STRAIN: ATCC 33496

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1778

20 GTTTATTGGC GATGGCCTGA AGCCGGTCCA GCGTCGCATC GTCTATGCGA 50
TGTCTGAACT GGGTCTGAAC GCCAGCGCGA AGTTCAAAAA GTCCGCCCCG 100
ACCGTCGGTG ACGTGCTGGG TAAATACCAT CCCCACGGCG ACAGCGCGTG 150
CTATGAAGCC ATGGTGCTGA TGGCTCAGCC CTTCTCCTAC CGCTATCCGC 200
25 TGGTTGACGG TCAGGGAAAC TGGGGGGCGC CGGACGATCC TAAATCCTTC 250
GCCGCAATGC GTTATACCGA ATCCCGTTTG TCGAAGTATG CTGAACTGCT 300
GCTGAGCGAA CTGGGGCAAG GCACCGTTGA CTGGGTACCA AACTTCGACG 350
GCACTTTGCA GGAGCCGAAG ATGCTGCCTG CGCGCCTGCC CAATATTCTG 400
CTAAACGGTA CTACCGGCAT TGCCGTGGG ATGGCGACGG ACATTCCGCC 450
30 GCACAACCTG CGTGAAGTGG CCCGGGCGGC CATTACCCTG ATTGAAAAGC 500
CGCAAACCTC GCTGGATGAC CTGCTGGATA TCGTGCAGGG GCCGGATTAT 550
CCTACCGAAG CGGAAATCAT TACCCCCCGT GCCGAAATCC GCAAAATCTA 600
CCAGAATGGC CGCGGTTTCG TGC GGATGCG CGCGGTATGG GCCAAAGAAG 650
ACGGCGCGGT GGTGATTAGC GCGCTGCCGC ATCAGGTTTC CGGCGCCCCG 700
35 GTGCTTGAGC AGAT 714

2) INFORMATION FOR SEQ ID NO: 1779

40

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 722 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
45 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 50 (A) ORGANISM: *Klebsiella pneumoniae* subsp. *ozaenae*
(B) STRAIN: ATCC 11296

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1779

	TTGGCGATGG	CTTAAAACCG	GTCCAGCGTC	GCATCGTCTA	TGCGATGTCC	50
	GAGCTGGGGC	TGAACGCCAG	CGCGAAATTC	AAAAAGTCCG	CCCGCACCGT	100
	CGGCGACGTG	TTGGGTAAAT	ATCACCCGCA	CGGCGACAGC	GCCTGCTATG	150
5	AAGCGATGGT	GCTGATGGCG	CAGCCGTTCT	CTTACCGCTA	TCCGCTGGTG	200
	GATGGTCAGG	GAAACTGGGG	GGCGCCGGAC	GATCCCAAAT	CTTTCGCCGC	250
	CATGCGTTAC	ACCGAATCCC	GCCTGTCGAA	GTATGCCGAG	CTGCTGCTCA	300
	GCGAGCTGGG	GCAGGGGACG	GTCGACTGGG	TGCCAAACTT	TGACGGTACG	350
	CTGCAGGAGC	CGAAAATGCT	GCCAGCGCGT	TTGCCGAACA	TCCTGCTGAA	400
10	CGGCACCACC	GGCATCGCGG	TAGGTATGGC	GACCGATATT	CCTCCGCACA	450
	ACCTGCGGGA	AGTGGCCAAA	GCGGCGATTA	CGCTGATTGA	GCAGCCGAAA	500
	ACCACCCTCG	ACGAACTGCT	GGATATCGTA	CAGGGGCCGG	ATTTCCCAGC	550
	CGAGGCGGAG	ATCATCACCT	CGCGGCGGGA	AATTCGAAAA	ATCTACCAGA	600
	ACGGGCGCGG	CTCAGTGC GC	ATGCGCGCGG	TGTGGAGTAA	AGAGGACGGC	650
15	GCGGTGGTGA	TCAGCGCGCT	GCCGCATCAG	GTCTCCGGCG	CCAAAGTGCT	700
	GGAGCAGATT	GCGGCGCAGA	TG			722

20 2) INFORMATION FOR SEQ ID NO: 1780

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 692 bases
 (B) TYPE: Nucleic acid
 25 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

30 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Klebsiella planticola*
 (B) STRAIN: ATCC 33531

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1780

35	GTCCAGCGTC	GCATCGTTTA	TGCGATGTCT	GAGCTGGGGC	TGAACGCCAG	50
	CGCGAAGTTC	AAAAAGTCCG	CCCGCACCGT	GGGTGATGTG	CTGGGTAAAT	100
	ATCACCCGCA	CGGCGATAGC	GCATGCTATG	AAGCTATGGT	GCTGATGGCG	150
	CAGCCATTCT	CCTACCGCTA	CCCGCTGGTG	GATGGGCAGG	GGAAGTGGGG	200
40	GGCACCGGAC	GATCCTAAAT	CCTTCGCCGC	GATGCGTTAT	ACCGAATCCC	250
	GTTTGTGCGAA	GTATGCGGAA	CTGCTGCTGG	GCGAACTGGG	GCAGGGAACC	300
	GTCGACTGGG	TGCCGAACTT	CGACGGGACG	ATGCAGGAGC	CGAAAATGCT	350
	GCCTGCGCGT	CTGCCGAATA	TTCTGCTGAA	CGGCACTACC	GGCATCGCCG	400
	TCGGTATGGC	AACCGATATT	CCTCCGCACA	ACCTGCGTGA	AGTGGCGCAG	450
45	GCGGCGATTA	CCCTGATCGA	AAAACCGCAG	ACCTCGCTCG	ACGAACTGCT	500
	GGATATCGTT	CACGGACCCG	ACTACCCGAC	CGAAGCCGAA	ATCATTACTC	550
	CACGCGCGGA	GATCCGCAAA	ATCTACCAGA	ACGGCCGCGG	TTCGGTGC GG	600
	ATGCGCGCGG	TATGGAAAAA	AGAGGACGGC	GCGGTCTGTA	TTACGGCGTT	650
	GCCGCATCAG	GTTTCCGGCG	CCCGCGTGCT	GGAGCAAATT	GC	692
50						

2) INFORMATION FOR SEQ ID NO: 1781

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 700 bases
 (B) TYPE: Nucleic acid
 5 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

10 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Klebsiella pneumoniae*
 (B) STRAIN: ATCC 27336

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1781

15
 GTTTATTGGC GATGGCTTAA AACCGGTCCA GCGTCGCATC GTCTATGCGA 50
 TGTCCGAGCT GGGGCTGAAC GCCAGCGCGA AATTCAAAAA GTCCGCCCCG 100
 ACCGTCGGCG ACGTGTTGGG TAAATATCAC CCGCACGGCG ACAGCGCCTG 150
 CTATGAAGCG ATGGTGCTGA TGGCGCAGCC GTTCTCTTAC CGCTATCCGC 200
 20 TGGTGGATGG TCAGGGA AAC TGGGGGGCGC CGGACGATCC CAAATCTTTC 250
 GCCGCCATGC GTTACACCGA ATCCCGCCTG TCGAAGTATG CCGAGCTGCT 300
 GCTCAGCGAG CTGGGGCAGG GGACGGTCGA CTGGGTGCCA AACTTTGACG 350
 GCACGCTGCA GGAGCCGAAA ATGCTGCCAG CGCGTTTGCC GAACATCCTG 400
 CTGAACGGCA CCACCGGCAT CGCGGTAGGC ATGGCGACCG ATATTCCTCC 450
 25 GCACAACCTG CGGGAAGTGG CCAAAGCGGC GATTACGCTG ATTGAGCAGC 500
 CGAAAACCA CCGGACGAGG CGGAGATCAT CACCTCGCGG GCGGAAATTC GCAAAATCTA 600
 CCGGACGAGG CGGAGATCAT CACCTCGCGG GCGGAAATTC GCAAAATCTA 600
 CCAAAACGGG CGCGGCTCAG TGCGCATGCG CGCGGTGTGG AGTAAAGAGG 650
 ACGGCGCGGT GGTGATCAGC GCGCTGCCGC ATCAGGTCTC CGGCGCCAAA 700
 30

2) INFORMATION FOR SEQ ID NO: 1782

35 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 726 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 40 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Klebsiella pneumoniae* subsp. *pneumoniae*
 45 (B) STRAIN: ATCC 13883

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1782

ATTGGCGATG GCTTAAAACC GGTCCAGCGT CGCATCGTCT ATGCGATGTC 50
 50 CGAGCTGGGG CTGAACGCCA GCGCGAAATT CAAAAAGTCC GCCCGCACCG 100
 TCGGCGACGT GTTGGGTAAA TATCACCCGC ACGGCGACAG CGCCTGCTAT 150
 GAAGCGATGG TGCTGATGGC GCAGCCGTTT TCTTACCGCT ATCCGCTGGT 200
 GGATGGTCAG GGAAACTGGG GGGCGCCGGA CGATCCCAA TCTTTCGCCG 250

	CCATGCGTTA	CACCGAATCC	CGCCTGTCGA	AGTATGCCGA	GCTGCTGCTC	300
	AGCGAGCTGG	GGCAGGGGAC	GGTCGACTGG	GTGCCAAACT	TTGACGGCAC	350
	GCTGCAGGAG	CCGAAAATGC	TGCCAGCGCG	TCTGCCGAAC	ATCCTGCTGA	400
	ACGGCACCAC	CGGCATCGCG	GTAGGCATGG	CGACCGATAT	TCCTCCGCAC	450
5	AACCTGCGGG	AAGTGGCCAA	AGCGGCGATT	ACGCTGATTG	AGCAGCCGAA	500
	AACCACCCTC	GACGAACTGC	TGGATATCGT	ACAGGGGCCG	GATTTCCTGA	550
	CCGAGGCGGA	GATCATCACC	TCGCGGGCGG	AAATTGCGAA	AATCTACCAG	600
	AACGGGCGCG	GCTCAGTGCG	CATGCGCGCG	GTGTGGAGTA	AAGAGGACGG	650
	CGCGGTGGTG	ATCAGTGCGC	TGCCGCATCA	GGTCTCTGGC	GCCAAAGTGC	700
-10	TGGAGCAGAT	TGCGGCGCAG	ATGCGC			726

2) INFORMATION FOR SEQ ID NO: 1783

15

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 706 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

25

- (A) ORGANISM: *Klebsiella pneumoniae* subsp. *pneumoniae*
- (B) STRAIN: ATCC 29011

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1783

30	GGCTTAAAC	CGGTCCAGCG	TCGCATCGTC	TATGCGATGT	CCGAGCTGGG	50
	GCTGAACGCC	AGCGCGAAAT	TCAAAAAGTC	CGCCCGCACC	GTCGGCGACG	100
	TGTTGGGTAA	ATATCACCCG	CACGGCGACA	GCGCCTGCTA	TGAAGCGATG	150
	GTGCTGATGG	CGCAGCCGTT	CTCTTACCGC	TATCCGCTGG	TGGATGGTCA	200
	GGGAAACTGG	GGGGCGCCGG	ACGATCCCAA	ATCTTTTGCC	GCCATGCGTT	250
35	ACACCGAATC	CCGCCTGTCG	AAGTATGCCG	AGCTGCTGCT	CAGCGAGCTG	300
	GGGCAGGGGA	CGGTCGACTG	GGTGCCAAAC	TTTGACGGCA	CGCTGCAGGA	350
	GCCGAAAATG	CTGCCAGCGC	GTCTGCCGAA	CATCCTGCTG	AACGGCACCA	400
	CCGGCATCGC	GGTAGGCATG	GCGACCGATA	TTCCTCCGCA	CAACCTGCGG	450
	GAAGTGGCCA	AAGCGGCGAT	TACGCTGATT	GAGCAGCCGA	AAACCACCCT	500
40	CGACGAACTG	CTGGATATCG	TACAGGGGCC	GGATTTCCCG	ACCGAGGCGG	550
	AGATCATCAC	CTCGCGGGCG	GAAATTCGCA	AAATCTACCA	GAACGGGCGC	600
	GGCTCAGTGC	GCATGCGCGC	GGTGTGGAGT	AAAGAGGACG	GCGCGGTGGT	650
	GATCAGTGCG	CTGCCGCATC	AGGTCTCCGG	CGCCAAAGTG	CTGGAGCAGA	700
	TTGCGG					706

45

2) INFORMATION FOR SEQ ID NO: 1784

50

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 614 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

5 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Klebsiella pneumoniae* subsp.
rhinoscleromatis

(B) STRAIN: ATCC 13884

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1784

	TTGGCGATGG	CTTAAAACCG	GTCCAGCGTC	GCATCGTCTA	TGCGATGTCC	50
	GAGCTGGGGC	TGAACGCCAG	CGCGAAATTC	AAAAAGTCCG	CCCGCACCGT	100
	CGGCGACGTG	TTGGGTAAAT	ATCACCCGCA	CGGCGACAGC	GCCTGCTATG	150
15	AAGCGATGGT	GCTGATGGCG	CAGCCGTTCT	CTTACCGCTA	TCCGCTGGTG	200
	GATGGTCAGG	GAAACTGGGG	GGCGCCGGAC	GATCCCAAAT	CTTTCGCCGC	250
	CATGCGTTAC	ACCGAATCCC	GCCTGTCGAA	GTATGCCGAG	CTGCTGCTCA	300
	GCGAGCTGGG	GCAGGGGACG	GTCGACTGGG	TGCCAAACTT	TGACGGCACG	350
	CTGCAGGAGC	CGAAAATGCT	GCCAGCGCGT	CTGCCGAACA	TCCTGCTGAA	400
20	CGGCACCACC	GGCATCGCGG	TAGGCATGGC	GACCGATATT	CCTCCGCACA	450
	ACCTGCGGGA	AGTGGCCAAA	GCGGCGATTA	CGCTGATTGA	GCAGCCGAAA	500
	ACCACCCTCG	ACGAACTGCT	GGATATCGTA	CAGGGGCCGG	ATTTCCTGAC	550
	CGAGGCGGAG	ATCATCACCT	CGCGGGCGGA	AATTCGCAA	ATCTACCAGA	600
	ACGGGCGCGG	CTCA				614

25

2) INFORMATION FOR SEQ ID NO: 1785

30 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 668 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Klebsiella terrigena*

40 (B) STRAIN: ATCC 33257

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1785

	GCCTGAAACC	GGTCCAGCGG	CGCATCGTTT	ATGCGATGTC	CGAACTGGGT	50
45	CTGAACGCCA	CCGCTAAATT	CAAAAAATCC	GCGCGCACCG	TCGGCGACGT	100
	GCTGGGTAAA	TATCACCCGC	ACGGCGATAG	CGCCTGCTAT	GAGGCGATGG	150
	TGCTGATGGC	GCAGCCGTTC	TCTTACCGCT	ACCCGCTGGT	GGACGGTCAG	200
	GGCAACTGGG	GCGCCCCGGA	CGATCCCAAA	TCCTTCGCCG	CGATGCGTTA	250
	TACCGAATCC	CGCCTGTCAA	AGTATGCGGA	GCTGCTGCTG	GGCGAGCTGG	300
50	GTCAGGGAAC	CGTTGACTGG	GTACCTAACT	TTGACGGTAC	GATGCAGGAG	350
	CCGAAAATGC	TGCCTGCGCG	TTTGCCGAAT	ATTCTGCTCA	ACGGCACCAC	400
	CGGTATCGCC	GTGGGGATGG	CCACCGATAT	TCCGCCGCAC	AACCTGCGCG	450
	AAGTGGCCAA	AGCGGCCATC	ACCCTGATTG	AAAAGCCGCA	GACCTCGCTC	500

GACGAACTGC TGGATATCGT TCACGGGCCG GACTACCCCA CCGAAGCTGA 550
 AATCATCACC CCGCGCGCCG AGATCCGCAA AATCTATCAG AACGGTCGCG 600
 GCTCGGTTTC CATGCGTGCG GTGTGGAAAA AAGAGGACGG CGCGGTGGTG 650
 ATTAGCGCCC TGCCGCAT 668

5

2) INFORMATION FOR SEQ ID NO: 1786

10 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

15

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacillus cereus*
- (B) STRAIN: ATCC 7064

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1786

CATTACGTTC TAACACTCAA GGACGCGGAA CATTCTCTAT GGTGTTTGAC 50
 25 CACTATGAAG AAGTACCAAA GTCTGTTTCT GAAGAAATTA TCAAAAAAAA 100
 TAAAGGTGAA TAA 113

30 2) INFORMATION FOR SEQ ID NO: 1787

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 118 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: Genomic DNA

40 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacillus cereus*
- (B) STRAIN: ATCC 14579

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1787

45

AACGTCATTA CGTTCTAACA CTCAAGGACG CGGAACATTC TCTATGGTGT 50
 TTGACCACTA TGAAGAAGTA CCAAAGTCTG TTTCTGAAGA AATTATCAA 100
 AAAAATAAAG GTGAATAA 118

50

2) INFORMATION FOR SEQ ID NO: 1788

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 120 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
5 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

- (vi) ORIGINAL SOURCE:
10 (A) ORGANISM: *Bacillus anthracis*
(B) STRAIN: CIP 9444

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1788

15 GCAACGTCAT TACGTTCTAA CACTCAAGGA CGCGGAACAT TCTCTATGGT 50
GTTTGACCAC TATGAAGAAG TACCAAAGTC TGTCTGAA GAAATTATCA 100
AAAAAATAA AGGTGAATAA 120

20

2) INFORMATION FOR SEQ ID NO: 1789

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 118 bases
25 (B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

30

- (vi) ORIGINAL SOURCE:
(A) ORGANISM: *Bacillus cereus*
(B) STRAIN: ATCC 13472

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1789

AACGTCATTA CGTTCTAACA CTCAAGGACG CGGAACATTC TCTATGGTGT 50
TTGACCACTA TGAAGAAGTA CCAAAGTCTG TTTCTGAAGA AATTATCAAA 100
AAAAATAAAG GTGAATAA 118

40

2) INFORMATION FOR SEQ ID NO: 1790

- 45 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 120 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Bacillus anthracis*

(B) STRAIN: ATCC 4229

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1790

5

GCAACGTCAT TACGTTCTAA CACTCAAGGA CGCGGAACAT TCTCTATGGT 50
GTTTGACCAC TATGAAGAAG TACCAAAGTC TGTTTCTGAA GAAATTATCA 100
AAAAAATAA AGGTGAATAA 120

10

2) INFORMATION FOR SEQ ID NO: 1791

(i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 120 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacillus pseudomycoides*
- (B) STRAIN: NRRL B-617

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1791

GCAACGTCAT TACGTTCTAA CACGCAAGGA CGCGGAACAT TCTCAATGAC 50
ATTTGATCAT TATGAAGAAG TACCGAAGTC TGTTTCAGAA GAAATTATCA 100
30 AAAAAATAA AGGTGAATAA 120

2) INFORMATION FOR SEQ ID NO: 1792

35

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 116 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

40

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

45

- (A) ORGANISM: *Bacillus cereus*
- (B) STRAIN: ATCC 49064

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1792

CGTCATTACG TTCTAACACT CAAGGACGCG GAACATTCTC TATGGTGTTT 50
GACCACTATG AAGAAGTACC AAAGTCTGTT TCTGAAGAAA TTATCAAAAA 100
AAATAAAGGT GAATAA 116

2) INFORMATION FOR SEQ ID NO: 1793

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 120 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
(A) ORGANISM: *Bacillus anthracis*
(B) STRAIN: CIP 9440

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1793

GCAACGTCAT TACGTTCTAA CACTCAAGGA CGCGGAACAT TCTCTATGGT 50
GTTTGACCAC TATGAAGAAG TACCAAAGTC TGTTTCTGAA GAAATTATCA 100
AAAAAATAA AGGTGAATAA 120

2) INFORMATION FOR SEQ ID NO: 1794

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 100 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
(A) ORGANISM: *Bacillus cereus*
(B) STRAIN: ATCC 15816

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1794

CACTCAAGGA CGCGGAACAT TCTCTATGGT GTTTGATCAC TATGAAGAAG 50
40 TACCAAAGTC TGTTTCTGAA GAAATTATCA AAAAAAATAA AGGTGAATAA 100

2) INFORMATION FOR SEQ ID NO: 1795

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 120 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacillus weihenstephanensis*
(B) STRAIN: WSBC 10204

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1795

GCAACGGCAT TACGTTCTAA CACTCAAGGA CGCGGAACAT TCTCAATGAC 50
ATTTGATCAT TATGAAGAAG TACCGAAGTC TGTTTCTGAA GAAATTATTA 100
AAAAAATAA AGGTGAATAA 120

10

2) INFORMATION FOR SEQ ID NO: 1796

15 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 120 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacillus mycoides*
25 (B) STRAIN: ATCC 6462

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1796

GCGACAGCAT TACGTTCTAA CACTCAAGGA CGCGGAACAT TCTCAATGAC 50
30 ATTTGATCAT TATGAAGAAG TACCGAAGTC TGTTTCAGAA GAAATTATTA 100
AAAAAATAA AGGCGAATAA 120

35 2) INFORMATION FOR SEQ ID NO: 1797

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 120 bases
(B) TYPE: Nucleic acid
40 (C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

45 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacillus thuringiensis*
(B) STRAIN: ATCC 10792

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1797

50

GCAACGTCAT TACGTTCTAA CACTCAAGGA CGCGGAACAT TCTCTATGGT 50
GTTTGACCAC TATGAAGAAG TACCAAAGTC TGTTTCTGAA GAAATTATCA 100
AAAAAATAA AGGTGAATAA 120

2) INFORMATION FOR SEQ ID NO: 1798

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 117 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
(A) ORGANISM: *Bacillus weihenstephanensis*
(B) STRAIN: WSBC 10204

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1798

TTGATTTTTC TCGATTGTTC AAGTATAACT ACTTATGTAA GCTTAGAAAG 50
TGAGACGCAA GTTTCACCTT CTAGTCTAAA TATAAAATAA CCCATATAAA 100
CTAAGGAGGA ATTTAGA 117

2) INFORMATION FOR SEQ ID NO: 1799

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 117 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
(A) ORGANISM: *Bacillus thuringiensis*
(B) STRAIN: ATCC 10792

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1799

TTGATTTTTC TCGATTGTTC AAGTATAACT ACTTATGTAA GCTTAGAAAG 50
TGGGACGTAA GTTTCACCTT CTAGTCTAAA TATAAAATAA CCTATATAAA 100
CTAAGGAGGA ATTTAGA 117

45 2) INFORMATION FOR SEQ ID NO: 1800

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 117 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacillus anthracis*
(B) STRAIN: ATCC 4229

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1800

TTGATTTTTA TCGATTCTTC ACGTATAACT ACTTATGTAA GCTTAGAAAG 50
TGGGACGCAA GTTTCGCTTT CTAGCCTAAA TATAAAATAA CCTATATAAA 100
CTAAGGAGGA ATTTAGA 117

2) INFORMATION FOR SEQ ID NO: 1801

15

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 117 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

25

- (A) ORGANISM: *Bacillus pseudomyoides*
(B) STRAIN: NRRL B-617

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1801

TTGATTTTTA TCGATTGTTC AAGTATAACT ACTTATGTAA GCTTAGAAAG 50
TGGGACTTAA GTTTCACCTT CTAGTCTAAA TATAAAATAA CCTATATAAA 100
CTAAGGAGGA ATTTAGA 117

35

2) INFORMATION FOR SEQ ID NO: 1802

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 117 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

40

(ii) MOLECULE TYPE: Genomic DNA

45

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacillus anthracis*
(B) STRAIN: CIP 9444

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1802

TTGATTTTTA TCGATTCTTC ACGTATAACT ACTTATGTAA GCTTAGAAAG 50
TGGGACGCAA GTTTCGCTTT CTAGCCTAAA TATAAAATAA CCTATATAAA 100

CTAAGGAGGA ATTTAGA

117

5 2) INFORMATION FOR SEQ ID NO: 1803

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 117 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

15 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacillus cereus*
(B) STRAIN: ATCC 7064

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1803

TTGATTTTTA TCGATTCTTC ACGTATAACT ACTTATGTAA GCTTAGAAAG 50
TGAGACGCAA GTTTCGCTTT CTAGCCTAAA TATAAAATAA CCTATATAAA 100
CTAAGGAGGA ATTTAGA 117

25

2) INFORMATION FOR SEQ ID NO: 1804

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 117 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

35 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM *Bacillus cereus*
(B) STRAIN: ATCC 49064

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1804

TTGATTTTTA TCGATTCTTC ACGTATAACT ACTTATGTAA GCTTAGAAAG 50
TGGGACGCAA GTTTCACCTTT CTAGCCTAAA TATAAAATAA CCTATATAAA 100
45 CTAAGGAGGA ATTTAGA 117

50 2) INFORMATION FOR SEQ ID NO: 1805

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 117 bases
(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

5

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Bacillus mycoides*

(B) STRAIN: ATCC 6462

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1805

TTGATTTTTA TCAATTGTTT GAGTATAACT ACTTATGTAA GCTTAGAAAG 50
TGGGACGTAA GTTTCGCTTT CTAGTCTAAA TATAAAATAA CCTATATAAA 100
CTAAGGAGGA ATTTAGA 117

15

2) INFORMATION FOR SEQ ID NO: 1806

20 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 117 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

25

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Bacillus cereus*

30 (B) STRAIN: ATCC 14579

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1806

TTGATTTTTA TCGATTGTTT AAGTATAACT ACTTATGTAA GCTTAGAAAG 50
35 TGGGACGTAA GTTTCACCTT CTAGTCTAAA TATAAAATAA CCTATATAAA 100
CTAAGGAGGA ATTTAGA 117

40 2) INFORMATION FOR SEQ ID NO: 1807

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 117 bases

(B) TYPE: Nucleic acid

45 (C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

50 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Bacillus cereus*

(B) STRAIN: ATCC 15816

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1807

TTGATTTTTA TCGATTCTTC ACGTATAACT ACTTATGTAA GCTTAGAAAG 50
TGGGACGCAA GTTTCGCTTT CTAGCCTAAA TATAAAATAA CCTATATAAA 100
5 CTAAGGAGGA ATTTAGA 117

2) INFORMATION FOR SEQ ID NO: 1808

10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 117 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
15 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 20 (A) ORGANISM: *Bacillus cereus*
(B) STRAIN: ATCC 13472

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1808

25 TTGATTTTTA TCGATTGTTC AAGTATAACT ACTTATGTAA GCTTAGAAAG 50
TGGGACGTAA GTTTCACCTT CTAGTCTAAA TATAAAATAA CCTATATAAA 100
CTAAGGAGGA ATTTAGA 117

30

2) INFORMATION FOR SEQ ID NO: 1809

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 117 bases
35 (B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

40

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacillus anthracis*
(B) STRAIN: CIP 9440

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1809

TTGATTTTTA TCGATTCTTC ACGTATAACT ACTTATGTAA GCTTAGAAAG 50
TGGGACGCAA GTTTCGCTTT CTAGCCTAAA TATAAAATAA CCTATATAAA 100
CTAAGGAGGA ATTTAG 117

50

2) INFORMATION FOR SEQ ID NO: 1810

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 278 bases
 (B) TYPE: Nucleic acid
 5 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

10 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacillus mycoides*
 (B) STRAIN: ATCC 6462

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1810

15 ATGGCTAAAG CTAAATTCGA ACGTTCTAAA CCCCATGTTA ACATCGGTAC 50
 AATCGGCCAC GTTGACCATG GTAAACTAC ATTAAGTCT GCGATCACTA 100
 CAGTTCTTGC AAAAGCTGGT GGTGCTGAAG CACGCGGATA CGATCAAATC 150
 GACGCTGCTC CAGAAGAAAG AGAGCGCGGA ATCACAATCT CAACTGCACA 200
 20 CGTTGAGTAC GAAACTGAAA CTCGTCACCTA TGCACACGTT GACTGCCCAG 250
 GTCACGCTGA CTATGTTAAA AACATGAT 278

25 2) INFORMATION FOR SEQ ID NO: 1811

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 278 bases
 (B) TYPE: Nucleic acid
 30 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

35 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacillus thuringiensis*
 (B) STRAIN: ATCC 10792

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1811

40 ATGGCTAAAG CTAAATTCGA ACGTTCTAAA CCCCATGTTA ACATCGGTAC 50
 AATCGGCCAC GTTGACCATG GTAAACTAC ATTAAGTCT GCGATCACTA 100
 CAGTTCTTGC AAAAGCTGGT GGTGCTGAAG CACGCGGATA CGATCAAATC 150
 GATGCTGCTC CAGAAGAAAG AGAGCGCGGT ATCACAATCT CAACTGCACA 200
 45 CGTTGAGTAC GAAACTGAAA CTCGTCACCTA TGCACACGTT GACTGCCCAG 250
 GTCACGCTGA CTATGTTAAA AACATGAT 278

50 2) INFORMATION FOR SEQ ID NO: 1812

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 270 bases

- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

5 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacillus cereus*
- (B) STRAIN: ATCC 15816

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1812

ATGGCTAAAG	CTAAATTCGA	ACGTTCTAAA	CCCCATGTTA	ACATCGGTAC	50
AATCGGCCAC	GTTGACCATG	GTAAACTAC	ATTAAGTCT	GCGATCACTA	100
15 CAGTACTTGC	AAAAGCTGGT	GGTGCTGAAG	CACGCGGATA	CGATCAAATC	150
GATGCTGCTC	CAGAAGAAAG	AGAGCGCGGT	ATCACAATCT	CAACTGCACA	200
CGTTGAGTAC	GAAACTGAAA	CTCGTCACTA	TGCACACGTT	GACTGCCCAG	250
GTCACGCTGA	CTATGTTAAA				270

20

2) INFORMATION FOR SEQ ID NO: 1813

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 278 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

30 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacillus weihenstephanensis*
- (B) STRAIN: WSBC 10204

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1813

ATGGCTAAAG	CTAAATTCGA	ACGTTCTAAA	CCCCATGTTA	ACATCGGTAC	50
AATCGGCCAC	GTTGACCATG	GTAAACTAC	ATTAAGTCT	GCGATCACTA	100
40 CAGTTCTTGC	AAAAGCTGGT	GGTGCTGAAG	CACGCGGATA	CGATCAAATC	150
GACGCTGCTC	CAGAAGAAAG	AGAGCGCGGA	ATCACAATCT	CAACTGCACA	200
CGTTGAGTAC	GAAACTGAAA	CTCGTCACTA	TGCACACGTT	GACTGCCCAG	250
GTCATGCTGA	CTATGTTAAA	AACATGAT			278

45

2) INFORMATION FOR SEQ ID NO: 1814

(i) SEQUENCE CHARACTERISTICS:

- 50 (A) LENGTH: 266 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 5 (A) ORGANISM: *Bacillus anthracis*
(B) STRAIN: CIP 9440

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1814

```
10 ATGGCTAAAG CTAAATTCGA ACGTTCTAAA CCCCATGTTA ACATCGGTAC 50
   AATCGGCCAC GTTGACCATG GTAAAACTAC ATTAAGTCTGCT GCGATCACTA 100
   CAGTACTTGC AAAAGCTGGT GGTGCTGAAG CACGCGGATA CGATCAAATC 150
   GATGCTGCTC CAGAAGAAAG AGAGCGCGGT ATCACAATCT CAACTGCACA 200
   CGTTGAGTAC GAAACTGAAA CTCGTCACTA TGCACACGTT GACTGCCCAG 250
15 GTCACGCTGA CTATGT 266
```

2) INFORMATION FOR SEQ ID NO: 1815

20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 269 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
25 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 30 (A) ORGANISM: *Bacillus cereus*
(B) STRAIN: ATCC 7064

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1815

```
35 ATGGCTAAAG CTAAATTCGA ACGTTCTAAA CCCCATGTTA ACATCGGTAC 50
   AATCGGCCAC GTTGACCATG GTAAAACTAC ATTAAGTCTGCT GCGATCACTA 100
   CAGTACTTGC AAAAGCTGGT GGTGCTGAAG CACGCGGATA CGATCAAATC 150
   GATGCTGCTC CAGAAGAAAG AGAGCGCGGT ATCACAATCT CAACTGCACA 200
   CGTTGAGTAC GAAACTGAAA CTCGTCACTA TGCACACGTT GACTGCCCAG 250
40 GTCACGCTGA CTATGTTAA 269
```

2) INFORMATION FOR SEQ ID NO: 1816

45

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 268 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
50 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Bacillus cereus*

(B) STRAIN: ATCC 13472

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1816

	ATGGCTAAAG	CTAAATTCGA	ACGTTCTAAA	CCCCATGTTA	ACATCGGTAC	50
	AATCGGCCAC	GTTGACCATG	GTAAAACTAC	ATTAAGTCTG	GCGATCACTA	100
	CAGTTCTTGC	AAAAGCTGGT	GGTGCTGAAG	CACGCGGATA	CGATCAAATC	150
10	GATGCTGCTC	CAGAAGAAA	AGAGCGCGGT	ATCACAATCT	CAACTGCACA	200
	CGTTGAGTAC	GAAACTGAAA	CTCGTCACTA	TGCACACGTT	GACTGCCCAG	250
	GTCACGCTGA	CTATGTTA				268

15

2) INFORMATION FOR SEQ ID NO: 1817

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 278 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

25 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Bacillus anthracis*

(B) STRAIN: ATCC 4229

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1817

	ATGGCTAAAG	CTAAATTCGA	ACGTTCTAAA	CCCCATGTTA	ACATCGGTAC	50
	AATCGGCCAC	GTTGACCATG	GTAAAACTAC	ATTAAGTCTG	GCGATCACTA	100
	CAGTACTTGC	AAAAGCTGGT	GGTGCTGAAG	CACGCGGATA	CGATCAAATC	150
35	GATGCTGCTC	CAGAAGAAA	AGAGCGCGGT	ATCACAATCT	CAACTGCACA	200
	CGTTGAGTAC	GAAACTGAAA	CTCGTCACTA	TGCACACGTT	GACTGCCCAG	250
	GTCACGCTGA	CTATGTTAAA	AACATGAT			278

40

2) INFORMATION FOR SEQ ID NO: 1818

(i) SEQUENCE CHARACTERISTICS:

- 45 (A) LENGTH: 268 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

50 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Bacillus cereus*

(B) STRAIN: ATCC 14579

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1818

```

5  ATGGCTAAAG CTAAATTCGA ACGTTCTAAA CCCCATGTGA ACATCGGTAC      50
   AATCGGCCAC GTTGACCATG GTAAAACTAC ATTAAGTGCT GCGATCACTA      100
   CAGTTCTTGC AAAAGCTGGT GGTGCTGAAG CACGCGGATA CGATCAAATC      150
   GATGCTGCTC CAGAAGAAAG AGAGCGCGGT ATCACAATCT CAACTGCACA      200
   CGTTGAGTAC GAAACTGAAA CTCGTCACTA TGCACACGTT GACTGCCCAG      250
   GTCACGCTGA CTATGTGA                                     268
10

```

2) INFORMATION FOR SEQ ID NO: 1819

15 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 278 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacillus anthracis*
- (B) STRAIN: CIP 9444

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1819

```

30 ATGGCTAAAG CTAAATTCGA ACGTTCTAAA CCCCATGTGA ACATCGGTAC      50
   AATCGGCCAC GTTGACCATG GTAAAACTAC ATTAAGTGCT GCGATCACTA      100
   CAGTACTTGC AAAAGCTGGT GGTGCTGAAG CACGCGGATA CGATCAAATC      150
   GATGCTGCTC CAGAAGAAAG AGAGCGCGGT ATCACAATCT CAACTGCACA      200
   CGTTGAGTAC GAAACTGAAA CTCGTCACTA TGCACACGTT GACTGCCCAG      250
   GTCACGCTGA CTATGTAAA AACATGAT                                     278
35

```

2) INFORMATION FOR SEQ ID NO: 1820

40 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 278 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

45

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacillus pseudomycoides*
- (B) STRAIN: NRRL B-617

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1820

ATGGCTAAAG CTAAATTCGA ACGTTCTAAA CCCCATGTTA ACATCGGTAC 50
 AATCGGCCAC GTTGACCATG GTAAAACTAC ATTAAGTCT GCGATCACTA 100
 CAGTTCTTGC AAAAGCTGGT GGTGCTGAAG CACGCGGATA CGACCAAATC 150
 GATGCTGCTC CAGAAGAAAG AGAGCGCGGT ATCACAATCT CAACTGCACA 200
 5 CGTTGAGTAC GAAACTGAAA CTCGTCCTA TGCACACGTT GACTGCCCAG 250
 GTCACGCTGA CTATGTTAAA AACATGAT 278

10 2) INFORMATION FOR SEQ ID NO: 1821

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 263 bases
 (B) TYPE: Nucleic acid
 15 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

20 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacillus cereus*
 (B) STRAIN: ATCC 49064

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1821

25 ATGGCTAAAG CTAAATTCGA ACGTTCTAAA CCCCATGTTA ACATCGGTAC 50
 AATCGGCCAC GTTGACCATG GTAAAACTAC ATTAAGTCT GCGATCACTA 100
 CAGTACTTGC AAAAGCTGGT GGTGCTGAAG CACGCGGATA CGATCAAATC 150
 GATGCTGCTC CAGAAGAAAG AGAGCGCGGT ATCACAATCT CAACTGCACA 200
 30 CGTTGAGTAC GAAACTGAAA CTCGTCCTA TGCACACGTT GACTGCCCAG 250
 GTCACGCTGA CTA 263

35 2) INFORMATION FOR SEQ ID NO: 1822

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1668 bases
 (B) TYPE: Nucleic acid
 40 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

45 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus oralis*
 (B) STRAIN: ATCC 35037

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1822

50 CAATCGAAGT ACAACGTTCT CTTGCGGTAT TGGACGGTGC GGTTACTGTT 50
 CTTGACTCAC AATCAGGTGT TGAGCCTCAA ACTGAAACAG TTTGGCGTCA 100
 AGCAACTGAG TACGGAGTTC CACGTATCGT ATTTGCTAAC AAAATGGACA 150

	AAATCGGTGC	TGACTTCCTT	TACTCAGTAA	GCACACTTCA	CGACCGTCTT	200
	CAAGCAAACG	CACACCCAAT	CCAATTGCCA	ATCGGTGCTG	AAGATGACTT	250
	CCGTGGTATC	ATCGACTTGA	TCAAGATGAA	AGCTGAAATC	TATACTAACG	300
	ACCTTGGTAC	AGATATCCTT	GAAGAAGATA	TTCCAGCTGA	ATACCTTGAC	350
5	CAAGCTCAAG	AATACCGTGA	AAAATTGGTT	GAAGCAGTCG	CTGAAACTGA	400
	TGAAGACTTG	ATGATGAAAT	ACCTTGAAGG	TGAAGAAATC	ACTAACGAAG	450
	AATTGAAAGC	TGCTATCCGT	AAAGCAACTA	TCAACGTTGA	ATTCTTCCCA	500
	GTATTGTGTG	GTTCTGCCTT	CAAGAACAAG	GGTGTTC AAT	TGATGCTTGA	550
	TGCGGTTATC	GACTACCTTC	CAAGCCCACT	TGATATCCCA	GCGATCAAAG	600
10	GTATCAACCC	AGATWCAGAT	GAAGAAGAAA	CTCGTCCAGC	ATCTGACGAA	650
	GAGCCATTTC	CAGCTCTTGC	CTTCAAGATC	ATGACGGACC	CATTGTAGG	700
	TCGTTTGACA	TTCTTCCGTG	TATACTCARG	TGTTCTCCAA	TCARGKTCTT	750
	ACGTATTGAA	CACATCTAAA	GGTAAACGTG	AACGTATCGG	ACGTATCCTT	800
	CAAATGCACG	CTAACAGCCG	TCAAGAAATT	GACACTGTTT	ACTCAGGTGA	850
15	TATCGCTGCT	GCCGTTGGTT	TGAAAGATAC	TYCAACTGGT	GACTCATTGM	900
	CAGATGAAAA	AGCTAAAATC	ATCCTTGAGT	CAATCAACGT	TCCAGAMCCA	950
	GTTATCCAAT	TGATGGTTGA	GCCAAAATCT	AAAGCTGACC	AAGATAAGAT	1000
	GGGTATCGCC	CTTCAAAAAT	TGGCTGAAGA	AGATCCAACA	TTCCGCGTTG	1050
	AAMCAAACGT	TGAAACTGGT	GAAMCAGTTA	TCTCAGGTAT	GGGTGAGCTT	1100
20	CACTTGACG	TCCTTGTTGA	CCGTATGCGT	CGTGAGTTCA	AAGTGAAGC	1150
	GAACGTAGGT	GCTCCTCAAG	TATCTTACCG	TGAAACATTC	CGCGCTTCTA	1200
	CTCAAGCACG	TGGATTCTTC	AAACGTCAGT	CTGGTG GTAA	AGGTCAATTC	1250
	GGTGATGTAT	GGATTGAATT	TACTCCAAAC	GAAGAAGGTA	AAGGATTCGA	1300
	ATTCGAAAAC	GCAATCGTCG	GTGGTGTGGT	TCCTCGTGAA	TTTATCCAG	1350
25	CGGTTGAAAA	AGGTTTGGTA	GAATCTATGG	CTAACGGTGT	TCTTGCAGGT	1400
	TACCCAATGG	TTGACGTTAA	AGCTAAGCTT	TACGATGGTT	CATACCACGA	1450
	TGTCGACTCA	TCTGAAACTG	CCTTCAAGAT	CGCGGCTTCA	CTTGCCCTTA	1500
	AAGAAGCTGC	TAAGTCAGCA	CAACCAGCTA	TCCTTGAGCC	AATGATGCTT	1550
	GTAACCATCA	CTGTTCCAGA	AGAAAACCTT	GGTGATGTTA	TGGGTCACGT	1600
30	AACTGCTCGT	CGTGGACGTG	TAGATGGTAT	GGAAGCACWC	GGTAACAGCC	1650
	AAATCGTTTC	TGCTTACG				1668

35 2) INFORMATION FOR SEQ ID NO: 1823

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 115 bases
 (B) TYPE: Nucleic acid
 40 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

45 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Budvicia aquatica*
 (B) STRAIN: ATCC 35567

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1823

50	AGACCTGCGT	TCACAAACAC	AGGGTCGTGC	TTCTTACTCT	ATGGAGTTCT	50
	TGAAGTACAA	CGAAGCGCCA	AACAACGTTG	CTACAGCAAT	CATTGAAGCT	100
	CGTAAGGCTA	GATAA				115

2) INFORMATION FOR SEQ ID NO: 1824

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 107 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
(A) ORGANISM: *Buttiauxella agrestis*
(B) STRAIN: ATCC 33320
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1824

CTGCGTTCAC TGACCAAGGT CGTGCATCTT ACTCCATGGA ATTCCTGAAG 50
TATGATGACG CGCCAAACAA CGTAGCTCAG GCCGTAATCG AAGCTCGCGG 100
TAAATAA 107

2) INFORMATION FOR SEQ ID NO: 1825

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 79 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
(A) ORGANISM: *Klebsiella oxytoca*
(B) STRAIN: ATCC 13182
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1825

TTACTCCATG GAGTTCCTGA AGTATGATGA TGCGCCGAAC AACGTTGCTC 50
AGGCCGTAAT CGAAGCCCGT GGTAAATAA 79

2) INFORMATION FOR SEQ ID NO: 1826

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 111 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Plesiomonas shigelloides*
(B) STRAIN: ATCC 14029

5. (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1826

CAGCTGCGTT CTCTGACCAA AGGTCGTGCA TCATACACTA TGGAAATTCCT 50
GAAGTATGAT GATGCGCCAA ACAACGTTGC TCAGGCCGTT ATTGAAGCCC 100
GTGGTAAGTA A 111

10

2) INFORMATION FOR SEQ ID NO: 1827

15 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 108 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Shewanella putrefaciens*
25 (B) STRAIN: ATCC 8071

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1827

GATTTGCGCT CTGCAACTCA TGGGCGTGCT TCGTACTCCA TGGAGTTCTT 50
30 GAAGTACTCT GATGCACCGC AAAACATTGC GAAAGCGATT ATTGAATCTC 100
GTAGCTAA 108

35 2) INFORMATION FOR SEQ ID NO: 1828

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 bases
(B) TYPE: Nucleic acid
40 (C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

45 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Obesumbacterium proteus*
(B) STRAIN: ATCC 12841

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1828

50

CTCAGCTGCG TTCTCTGACC AAAGGTCGTG CATCTTACTC CATGGAATTC 50
CTGAAGTATG ATGATGCGCC TAACAACGTT GCTCAGGCCG TTATTGAAGC 100
TCGTGGCAAA TAA 113

2) INFORMATION FOR SEQ ID NO: 1829

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 70 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

- (vi) ORIGINAL SOURCE:
(A) ORGANISM: *Klebsiella oxytoca*
(B) STRAIN: ATCC 13182

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1829

GCCGCAGGGT TAAAACCAAA GTCCCGTGCT CTCTCCTGAA GGGGAGAGCA 50
CTATAGTAAG GAATATAGCC 70

20

2) INFORMATION FOR SEQ ID NO: 1830

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 66 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

- (vi) ORIGINAL SOURCE:
(A) ORGANISM: *Budvicia aquatica*
(B) STRAIN: ATCC 35567

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1830

GCCTCGGGTA AAACCTTATAT CCCAGTCCCC CTCGTATAGA GGGGGATAGA 50
GTAAAGGAAG ATAATC 66

40

2) INFORMATION FOR SEQ ID NO: 1831

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 81 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Plesiomonas shigelloides*

(B) STRAIN: ATCC 14029

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1831

5

TCCACAGGAT TAAAACCCAG GTTTAAACCT AAGTCCCGTG CTCTCTCCTC 50
AGGGGAGAGC ACAATAGTAA GGAATATAGC C 81

10

2) INFORMATION FOR SEQ ID NO: 1832

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 70 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

20

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Obesumbacterium proteus*

(B) STRAIN: ATCC 12841

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1832

GCTACTAGTT TAAAACATTG ATCCCGTGCT CTCTCTATGA AGGGAGAGCA 50
CAAGAGTAAG GAATAAAGCC 70

30

2) INFORMATION FOR SEQ ID NO: 1833

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 72 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

40 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Shewanella putrefaciens*

(B) STRAIN: ATCC 8071

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1833

TTTCCAGTTA CGACATAAAT GTTATTATGG TCCAGCTTTG ACTGGACTAT 50
TCTGAAAAGA AAGGAATATA TC 72

50

2) INFORMATION FOR SEQ ID NO: 1834

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 73 bases
 (B) TYPE: Nucleic acid
 5 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

10 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Buttiauxella agrestis*
 (B) STRAIN: ATCC 33320

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1834

15 GCCCCGGGTT TTAAAAACA TTGATCCCGT GCTCTCTCCA GAAGGGGAGA 50
 GCGCAACAGT AAGGAATATA GCC 73

20 2) INFORMATION FOR SEQ ID NO: 1835

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 795 bases
 25 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

30 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Campylobacter coli*
 (B) STRAIN: ATCC 43479

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1835

CTGCAGCTGA TGGTCCTATG CCACAACTA GAGAGCACAT CCTTCTATCA 50
 CGCCAAGTAG GTGTTCCATA TATCGTTGTA TTTATGAATA AAGCAGATAT 100
 GGTGTATGAT GCTGAACTTT TAGAATTGGT TGAAATGGAA ATTAGAGAAT 150
 40 TATTAAGCTC TTATGATTTC CCAGGTGATG ACACACCTAT TATTTAGGT 200
 TCTGCTTTAA AAGCTCTTGA AGAAGCAAAA GCTGGACAAG ATGGCGAATG 250
 GTCAGCGAAA ATTATGGATC TTATGGCTGC TGTTGATAGC TATATTCCAA 300
 CTCCAACCTCG TGACACTGAA AAAGATTTCT TAATGCCAAT TGAAGATGTT 350
 TTCTCAATTT CAGGTCGTGG TACTGTTGTT ACAGGTAGAA TTGAAAAAGG 400
 45 TATTGTAAAA GTTGGTGATA CTATAGAAAT CGTTGGTATT AAAGATACTC 450
 AAACAACAAC TGTAACCTGC GTTGAAATGT TTAGAAAAGA AATGGACCAA 500
 GGTGAAGCAG GGGATAATGT TGGTGTCTT CTTCGTGGTA CAAAAAAGA 550
 AGAAGTTATC CGCGGTATGG TTCTTGCTAA ACCAAAATCA ATTACTCCAC 600
 ATACTGATTT CGAAGCTGAA GTTTATATCC TAAATAAAGA TGAGGGTGGT 650
 50 AGACATACTC CATTCTTTAA TAACTATAGA CCGCAATTCT ATGTAAGAAC 700
 AACAGATGTA ACAGGTTCTA TTAAATTAGC TGATGGCGTT GAAATGGTTA 750
 TGCCTGGTGA AAATGTAAGA ATTACTGTAA GCTTGATTGC ACCAG 795

2) INFORMATION FOR SEQ ID NO: 1836

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 817 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

10

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Campylobacter fetus* subsp. *fetus*
 (B) STRAIN: ATCC 25936

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1836

GCCATACTAG TTGTTTCTGC AGCTGATGGC CCAATGCCAC AAAC TAGAGA 50
 GCACATTTTG CTATCTCGTC AAGTTGGTGT TCCATATATA GTTGTTTTTA 100
 TGAACAAAGC TGATATGGTA GATGACGCAG AGTTGCTAGA ATTAGTTGAA 150
 20 ATGGAGATCA GAGAGTTATT AAGCGAATAT GACTTCCCTG GTGATGATAC 200
 TCCTATTATA AGCGGATCAG CACTTCAAGC TCTTGAAGAA GCTAAAGCTG 250
 GTAATGATGG CGAATGGTCA GCTAAGATTA TGGATCTTAT GGCTGCTGTT 300
 GATAGCTACA TACCAACTCC AGTTCGTGCT ACTGATAAAG ATTTCTTAAT 350
 GCCGATTGAA GACGTATTCT CAATTTCTGG CCGTGGTACT GTTGTTACTG 400
 25 GTAGAATTGA AAAAGGTATA GTTAAAGTTG GTGATACTAT CGAAATCGTA 450
 GGTATTAGAG ATACACAAAC TACAACAGTT ACCGGCGTTG AAATGTTTAG 500
 AAAAGAAATG GATCAAGGCG AGGCTGGTGA TAACGTTGGT GTTCTTTTAC 550
 GCGGTACAAA GAAAGAAGAC GTTGAAAGAG GTATGGTTCT TTGTAAGCCA 600
 AAATCAATTA CTCCTCATA TAAATTTGAG GGAGAAGTTT ATATCTTGAC 650
 30 TAAGGAAGAG GCGGTTAGAC ATACTCCATT CTTCAACAAC TATAGACCAC 700
 AATTTTATGT AAGAACAACA GATGTTACTG GATCAATCAC TCTTCCAGAG 750
 GGTACTGAGA TGGTTATGCC TGGTGATAAC TTAAAAATCA CTGTTGAGTT 800
 AATCAACCCA GTTGCTC 817

35

2) INFORMATION FOR SEQ ID NO: 1837

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 798 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

45

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Campylobacter fetus* subsp. *venerealis*
 (B) STRAIN: ATCC 33561

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1837

CCATACTAGT TGTTTCTGCA GCTGATGGCC CAATGCCACA AACTAGAGAG 50

	CACATTTTGC	TATCTCGTCA	AGTTGGTGTT	CCATATATAG	TTGTTTTTAT	100
	GAACAAAGCT	GATATGGTAG	ATGACGCAGA	GTTGCTAGAA	TTAGTTGAAA	150
	TGGAGATCAG	AGAGTTATTA	AGCGAATATG	ACTTCCCTGG	TGATGATACT	200
	CCTATTATAA	GCGGATCAGC	ACTTCAAGCT	CTTGAAGAAG	CTAAAGCTGG	250
5	TAATGATGGC	GAATGGTCAG	CTAAGATTAT	GGATCTTATG	GCTGCTGTTG	300
	ATAGCTACAT	ACCAACTCCA	GTTCTGTGCTA	CTGATAAAGA	TTTCTTAATG	350
	CCGATTGAAG	ACGTATTCTC	GATTTCTGGC	CGTGGTACTG	TTGTTACTGG	400
	TAGAATTGAA	AAAGGTATAG	TTAAAGTTGG	TGATACTATC	GAAATCGTAG	450
	GTATTAGAGA	TACACAAACT	ACAACAGTTA	CCGGCGTTGA	AATGTTTAGA	500
10	AAAGAAATGG	ATCAAGGCGA	GGCTGGTGAT	AACGTTGGTG	TTCTTTTACG	550
	CGGTACAAAG	AAAGAAGACG	TTGAAAGAGG	TATGGTTCTT	TGTAAGCCAA	600
	AATCAATTAC	TCCTCATACT	AAATTTGAGG	GAGAAGTTTA	TATCTTGACT	650
	AAGGAAGAGG	GCGGTAGACA	TACTCCATTC	TTCAACAACT	ATAGACCACA	700
	ATTTTATGTA	AGAACAACAG	ATGTTACTGG	ATCAATCACT	CTTCCAGAGG	750
15	GTA CTGAGAT	GGTTATGCCT	GGTGATAACT	TAAAATCAC	TGTTAGTT	798

2) INFORMATION FOR SEQ ID NO: 1838

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1116 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 25 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 30 (A) ORGANISM: *Buttiauxella agrestis*
 (B) STRAIN: ATCC 33320

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1838

35	GTGTCTAAAG	AAAAATTTGA	ACGTACAAAA	CCGCACGTCA	ACGTCGGTAC	50
	TATCGGCCAC	GTTGACCATG	GTA AACTAC	TCTGACTGCA	GCAATCACTA	100
	CCGTTCTGGC	TAAACCTAC	GGCGTTCTG	CACGCGCATT	CGACCAGATC	150
	GATAACGCAC	CAGAAGAAAA	AGCTCGTGGT	ATCACCATCA	ACACTTCCCA	200
	CGTTGAATAT	GACACCCCGA	CTCGTCACTA	CGCGCACGTT	GACTGCCCAG	250
40	GGCACGCCGA	CTACGTTAAA	AACATGATCA	CCGGTGCTGC	TCAGATGGAC	300
	GGCGCTATCC	TGGTTGTTGC	TGCGACTGAT	GGCCCGATGC	CACAGACTCG	350
	TGAGCACATC	CTGCTGGGTC	GCCAGGTTGG	CGTTCCATTC	ATGATCGTGT	400
	TCATGAACAA	ATGTGACATG	GTTGATGACG	AAGAGCTGCT	GGA ACTGGTA	450
	GAAATGGAAG	TTCGTGAACT	TCTGTCTGCT	TATGATTTCC	CGGGCGACGA	500
45	CATCCAGTG	GTTCTGGT	CAGCTCTGAA	AGCGCTGGAA	GGCGAAGCAG	550
	AGTGGAAGC	TAAATCATC	GAGCTGGCTG	GTCACCTGGA	TA ACTACATC	600
	CCAGAACCAG	AGCGTGCTAT	CGACAAGCCA	TTCCTGCTGC	CAATCGAAGA	650
	CGTATTCTCC	ATCTCCGGCC	GTGGTACTGT	TGTTACTGGT	CGTGTAGAGC	700
	GTGGTATCAT	TAAAGTTGGT	GAAGAAGTAG	AAATCGTTGG	TATCAAAGAT	750
50	ACCGTGAAAT	CTACCTGTAC	TGGCGTTGAA	ATGTTCCGCA	AACTGCTGGA	800
	CGAAGGCCGT	GCTGGTGAGA	ACGTTGGTGT	TCTGCTGCGT	GGTATTAAAC	850
	GTGAAGATAT	CGAACGTGGT	CAGGTTCTGG	CTAAGCCAGG	CTCTATCAAG	900
	CCGCACACTC	AGTTCGAATC	AGAAGTTTAT	ATCCTGTCCA	AAGATGAAGG	950

CGGCCGTCAT	ACTCCGTTCT	TCAAAGGCTA	CCGTCCACAG	TTCTACTTCC	1000
GTACAACTGA	CGTGACTGGC	ACCATCGAAC	TGCCAGAAGG	CGTTGAGATG	1050
GTAATGCCGG	GCGACAACAT	TCAAATGGTT	GTTACCCTGA	TCCACCCAAT	1100
CGCAATGGAC	GACGGT				1116

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2) INFORMATION FOR SEQ ID NO: 1839

- 10 (i) SEQUENCE CHARACTERISTICS: - - - - -
- (A) LENGTH: 1109 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear
- 15 (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Klebsiella oxytoca*
- 20 (B) STRAIN: ATCC 13182
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1839

GTGTCTAAAG	AAAAATTTGA	ACGTACAAAA	CCGCACGTCA	ACGTCGGTAC	50
25 TATCGGCCAC	GTTGACCATG	GTAAACTAC	TCTGACCGCT	GCAATCACTA	100
CCGTTCTGGC	TAAACCTAC	GGTGGTGCTG	CTCGCGCATT	CGACCAGATC	150
GATAACGCGC	CGGAAGAAAA	AGCTCGTGGT	ATCACCATCA	ACACTTCCCA	200
CGTTGAATAT	GACACCCCGA	CTCGCCACTA	CGCGCACGTA	GA CTGCCCCG	250
GCCACGCCGA	CTATGTTAAA	AACATGATCA	CCGGTGCTGC	GCAGATGGAC	300
30 GGC GCGATCC	TGGTTGTTGC	TGCGACTGAC	GGCCCGATGC	CGCAGACTCG	350
TGAGCACATC	CTGCTGGGTC	GTCAGGTAGG	CGTTCCGTAC	ATCATCGTGT	400
TCCTGAACAA	GTGCGACATG	GTTGATGACG	AAGAGCTGCT	GGA ACTGGTT	450
GAAATGGAAG	TTCGTGAACT	TCTGTCTCAG	TACGATTTC	CGGGCGACGA	500
CACTCCGATC	GTTCTGTGGT	CTGCTCTGAA	AGCTCTGGAA	GGCGACGCTG	550
35 AGTGGGAATC	TAAATCATC	GA ACTGGCTG	GCTTCCTGGA	TTCTTATATT	600
CCGGAACCAG	AGCGTGCGAT	TGACAAGCCG	TTCCTGCTGC	CGATCGAAGA	650
CGTATTCTCC	ATCTCCGGTC	GTGGTACCGT	TGTTACCGGT	CGTG TAGAGC	700
GCGGTATCAT	CAAAGTTGGC	GAAGAAGTTG	AAATCGTTGG	TATCAAAGAC	750
ACTGCTAAGT	CTACCTGTAC	TGGCGTTGAA	ATGTTCCGCA	AACTGCTGGA	800
40 CGAAGGCCGT	GCTGGTGAGA	ACGTTGGTGT	TCTGCTGCGT	GGTATCAAAC	850
GTGAAGAAAT	CGAACGTGGT	CAGGTACTGG	CTAAGCCGGG	CTCTATCAAG	900
CCGCACACCA	AGTTCGAATC	TGAAGTTTAT	ATCCTGTCCA	AAGACGAAGG	950
CGGCCGTCAC	ACTCCGTTCT	TCAAAGGCTA	CCGTCCGCAG	TTCTACTTCC	1000
GTACAACTGA	CGTGACTGGC	ACCATCGAAC	TGCCGGAAGG	CGTAGAGATG	1050
45 GTTATGCCGG	GCGACAACAT	CAAAATGGTT	GTTACCCTGA	TCCACCCGAT	1100
CGCGATGGA					1109

50 2) INFORMATION FOR SEQ ID NO: 1840

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1108 bases

- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

5 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Plesiomonas shigelloides*
- (B) STRAIN: ATCC 14029

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1840

	GTGTCTAAAG	AAAAATTTGA	ACGTACTAAA	CCGCACGTTA	ACGTTGGTAC	50
	TATCGGCCAC	GTTGACCACG	GTAAACTAC	CCTGACTGCA	GCTATCACTA	100
15	CCGTACTGTC	TAAAGTATAC	GGTGGTCAGG	CTCGTGCATT	CGATCAGATC	150
	GATAACGCGC	CAGAAGAAAA	AGCTCGTGGT	ATCACCATCA	ACACTTCTCA	200
	CGTAGAGTAC	GACACCCCAA	CTCGTCACTA	CGCGCACGTT	GACTGCCCAG	250
	GTCACGCCGA	CTACGTGAAG	AACATGATCA	CTGGTGCTGC	TCAGATGGAC	300
	GGCGCTATCC	TGGTAGTAGC	TGCGACTGAC	GGCCCAATGC	CTCAGACTCG	350
20	TGAGCACATC	CTGCTGGGTC	GTCAGGTAGG	CGTTCCTTAC	ATCATCGTGT	400
	TCCTGAACAA	GTGTGACATG	GTTGATGACG	AAGAGCTGCT	GGAAGTGGTA	450
	GAAATGGAAG	TACGTGAGCT	GCTGTCTCAG	TACGACTTCC	CAGGCGACGA	500
	TACTCCAGTT	GTTGCGGGTT	CTGCACTGAA	AGCGCTGGAA	GGCGATGCTC	550
	AGTGGGAAGA	GAAGATTGTT	GAAGTGGCAG	GCTACCTGGA	CAGCTACATC	600
25	CCTGAGCCAG	AGCGTGCTAT	CGACAAGCCA	TTCCTGCTGC	CAATCGAAGA	650
	CGTATTCTCT	ATCTCCGGCC	GTGGTACTGT	AGTAACTGGT	CGTGTAGAGC	700
	GCGGTATCAT	CAAAGTTGGT	GAAGAAGTAG	AAATCGTTGG	TATCAAAGAG	750
	ACTACCAAGA	CTACTTGATC	TGGCGTTGAA	ATGTTCCGTA	AGCTGCTGGA	800
	CGAAGGTCGT	GCGGGCGAGA	ACGTAGGTGT	TCTGCTGCGT	GGTACCAAGC	850
30	GTGATGACGT	AGAGCGTGGT	CAGGTTCTGG	CTAAGCCAGG	CTCAATCAAC	900
	CCACACACCA	ACTTTGTAGC	AGAAGTTTAT	ATTCTGTCCA	AAGATGAAGG	950
	TGGTCGTCAC	ACTCCATTCT	TCAAAGGCTA	CCGTCCACAG	TTCTACTTCC	1000
	GTACAACTGA	CGTGACCGGT	ACCATCGAAC	TGCCAGAAGG	CGTAGAGATG	1050
	GTAATGCCAG	GTGACAACAT	TCAAATGGTT	GTTACCCTGA	TTGCACCAAT	1100
35	CGCGATGG					1108

2) INFORMATION FOR SEQ ID NO: 1841

10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1107 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

15

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

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- (A) ORGANISM: *Shewanella putrefaciens*
- (B) STRAIN: ATCC 8071

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1841

	TGGCAAAAGC	TAAATTTGAA	CGTATTAAGC	CTCACGTAAA	CGTGGGCACC	50
	ATTGGTCACG	TTGACCATGG	TAAAACCACT	CTGACTGCAG	CTATCTCTCA	100
	CGTACTGGCT	AAGACCTACG	GTGGCGAAGC	TAAAGACTTC	TCTCAAATCG	150
5	ATAACGCTCC	AGAAGAGCGT	GAGCGCGGTA	TTACCATCAA	TACCTCTCAC	200
	ATCGAATATG	ACACGCCATC	ACGCCACTAC	GCCCACGTAG	ACTGCCCAGG	250
	CCACGCTGAC	TATGTTAAAA	ACATGATCAC	TGGTGCTGCA	CAGATGGACG	300
	GCGCGATTCT	GGTAGTCGCT	TCAACAGACG	GTCCAATGCC	ACAGACTCGT	350
	GAGCACATCC	TGCTTTCTCG	TCAGGTGGC	GTACCATTCA	TCATCGTATT	400
10	CATGAACAAA	TGTGACATGG	TAGATGACGA	AGAGCTGTTA	GAGCTAGTTG	450
	AGATGGAAGT	GCGTGAACTG	TTATCAGAAT	ACGATTTCCT	AGGTGATGAC	500
	TTACCGGTAA	TCCAAGGTTT	AGCTCTGAAA	GCGCTAGAAG	GCGAGCCAGA	550
	GTGGGAAGCA	AAAATCCTTG	AATTAGCAGC	GGCGCTGGAT	TCTTACATTC	600
	CAGAACCACA	ACGTGACATC	GATAAGCCGT	TCCTACTGCC	AATCGAAGAC	650
15	GTATTCTCAA	TTTCAGGCCG	TGGTACAGTA	GTAACAGGTC	GTGTTGAGCG	700
	TGGTATTGTA	CGCGTAGGCG	ACGAAGTTGA	AATCGTTGGT	GTACGTGCGA	750
	CAACTAAGAC	AACGTGTACT	GGTGTAGAAA	TGTTCCGTAA	ACTGCTTGAC	800
	GAAGGTCGTG	CAGGTGAGAA	CTGTGGTATT	TTGTTACGTG	GTACTAAGCG	850
	TGATGACGTA	GAACGTGGTC	AAGTATTAGC	GAAGCCAGGT	TCAATCAACC	900
20	CACACACTAC	TTTTGAATCA	GAAGTTTACG	TACTGTCAAA	AGAAGAAGGT	950
	GGTCGTCACA	CGCCATTCTT	CAAAGGCTAC	CGTCCACAGT	TCTACTTCCG	1000
	TACAACTGAC	GTAACCGGTA	CTATCGAACT	GCCAGAAGGC	GTAGAGATGG	1050
	TAATGCCAGG	CGATAACATC	AAGATGGTAG	TGACACTGAT	TTGCCCCAATC	1100
	GCGATGG					1107
25						

2) INFORMATION FOR SEQ ID NO: 1842

- 30 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1116 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Double
 - (D) TOPOLOGY: Linear
- 35 (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Obesumbacterium proteus*
 - 40 (B) STRAIN: ATCC 12841
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1842

	GTGTCTAAAG	AAAAATTTGA	ACGTACAAAA	CCGCACGTTA	ACGTTGGTAC	50
45	AATCGGCCAC	GTTGACCACG	GTAAACTAC	CCTGACTGCT	GCAATCACTA	100
	CCGTTCTGGC	TAAAACCTAC	GGTGGTTCTG	CACGTGCATT	CGACCAGATC	150
	GATAACGCGC	CAGAAGAAAA	AGCTCGTGGT	ATCACCATCA	ACACTTCTCA	200
	CGTTGAATAT	GACACCCCGA	CTCGCCACTA	CGCACACGTA	GACTGCCCAG	250
	GCCACGCCGA	CTATGTTAAA	AACATGATCA	CCGGTGCTGC	GCAGATGGAC	300
50	GGCGCGATCC	TGGTTGTTGC	TGCGACTGAC	GGCCCTATGC	CTCAGACTCG	350
	TGAGCACATC	CTGCTGGGTC	GTCAGGTTGG	CGTTCCTTAC	ATCATCGTAT	400
	TCCTGAACAA	ATGCGACATG	GTTGATGATG	AAGAGCTGCT	GGAGCTGGTA	450
	GAAATGGAAG	TTCGTGAACT	TCTGTCTCAG	TACGACTTCC	CAGGCAATGA	500

	TACTCCAATC	ATCCGTGGTT	CTGCTCTGAA	AGCGCTGGAA	GGCGAAGCTG	550
	AGTGGGAAGC	TAAGATCGTA	GAAGTGGCTG	AAACTCTGGA	TTCTTACATC	600
	CCAGAACCAG	AACGTGCTAT	CGACAAGCCA	TTCCTGCTGC	CAATCGAAGA	650
	CGTATTCTCA	ATCTCTGGCC	GTGGTACTGT	TGTTACCGGT	CGTGTAGAGC	700
5	GCGGTATCGT	TAAAGTTGGT	GAAGAAGTTG	AGATTGTTGG	TATCAAAGAT	750
	ACCGTTAAAT	CAACTTGTAC	CGGCGTTGAA	ATGTTCCGTA	AACTGCTGGA	800
	CGAAGGTCGT	GCAGGCGAGA	ACGTTGGTGT	TCTGCTGCGT	GGTATCAAGC	850
	GTGAAGACAT	CGAACGTGGT	CAGGTTCTGG	CTAAACCAGG	TTCTATCAAA	900
	CCACACACCA	AGTTCGAATC	AGAAGTTTAT	ATTCTGAGCA	AAGATGAAGG	950
10	CGGCCGTCAT	ACTCCGTTCT	TCAAAGGCTA	CCGTCCACAG	TTCTACTTCC	1000
	GTACAACCTGA	CGTGACCGGT	ACCATCGAAC	TGCCAGAAGG	CGTGGAATG	1050
	GTAATGCCAG	GCGATAACAT	CAAATGATC	GTTACCCTGA	TCCACCCAAT	1100
	CGCAATGGAC	GATGGT				1116

15

2) INFORMATION FOR SEQ ID NO: 1843

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 1129 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

25 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Budvicia aquatica*
 (B) STRAIN: ATCC 35567

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1843

	GTGTCTAAAG	AAAAATTTGA	ACGTACAAAA	CCGCACGTTA	ACGTTGGTAC	50
	TATCGGCCAC	GTTGACCACG	GTAAACAAC	TCTGACTGCT	GCTATACCA	100
35	GCGTTTTAGC	TAAACTTAT	GGCGGTAACG	CTCGTGCAAT	CGATCAAATC	150
	GATAATGCAC	CAGAAGAAAA	AGCACGTGGT	ATCACCATCA	ACACTTCTCA	200
	CGTTGAGTAT	GATACTCCTG	CTCGCCACTA	CGCACACGTA	GACTGCCCAG	250
	GACACGCCGA	CTATGTGAAA	AACATGATCA	CCGGTGCTGC	TCAAATGGAC	300
	GGCGCGATCT	TAGTTGTTGC	GGCAACTGAT	GGTCCTATGC	CACAGACTCG	350
40	TGAGCACATC	CTGTTAGGTC	GTCAGGTTGG	CGTTCCTTAC	ATCATCGTGT	400
	TCCTGAACAA	GTGTGACATG	GTTGATGACG	AAGAACTGTT	AGAATTAGTT	450
	GAAATGGAAG	TTCGTGAGCT	TCTTTCTGCT	TATGATTTCC	CTGGTGACGA	500
	TACTCCAGTT	GTTCGTGGTT	CTGCGCTGAA	AGCGTTAGAA	GGCGAAGCTG	550
	AGTGGGAAGC	TAAGATCATT	GAATTAGCCG	GATATCTGGA	TAGCTACATC	600
45	CCAGAGCCAG	AGCGTGCGAT	TGACCGTCCG	TTCCTGCTGC	CAATCGAAGA	650
	CGTATTCTCT	ATTTACAGCC	GTGGTACAGT	TGTTACCGGT	CGTGTAGAGC	700
	GCGGAATCGT	TAAAGTCGGT	GAAGCCGTTG	AGATTGTTGG	TATCAAAGAT	750
	ACCGTACAAA	CTACCTGTAC	TGGCGTTGAA	ATGTTCCGTA	AGTTACTTGA	800
	CGAAGGCCGT	GCTGGTGAGA	ACGTTGGTGT	TCTGCTGCGT	GGTACTAAGC	850
50	GTGAAGAAAT	CGAACGCGGT	CAAGTACTGG	CTAAGCCAGG	TTCAATCAAC	900
	CCGCACACCA	ACTTTGTATC	AGAAGTTTAT	ATTCTGAGCA	AAGATGAAGG	950
	TGGTCGTCAT	ACTCCATTCT	TCAAAGGCTA	CCGTCCACAG	TTCTACTTCC	1000
	GTACAACCTGA	CGTGACCGGT	ACTATCGAAC	TGCCAGAAGG	CGTAGAGATG	1050

GTGATGCCTG GTGACAACAT TCAGATGACT GTAACCTCTGA TTGCACCAAT 1100
CGCGATGGAC GAAGGTTTAC GCTTCGCTA 1129

5

2) INFORMATION FOR SEQ ID NO: 1844

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 810 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear.

15 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Abiotrophia adiacens*
(B) STRAIN: ATCC 49175

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1844

ATATTCATAA TGCATTACAA GTTGTGAAAA CAACAAGTGA CGGAAGTGAA 50
AAGACTGTTA CATTGGAAAC TGCTGTAGAA TTAGGGGATG GTGCAGTTCG 100
TACGATTGCC ATGGAATCTA CAGATGGTTT GCAACGTGGC ATGAAAGTAG 150
25 TGGACTTAGG ACGCACAATT AGCGTTCCTG TGGGACCTGA AACATTAGGT 200
CGTGTATTCA ACGTTTTAGG AGATACAATC GACTTGAAAG AACCATTCCC 250
AGAAGACTTT ACAAGACATG AAATCCATAA ACCAGCACCA AAATTTGAAG 300
AATTAAACAG TCAATATGAA ATTCTACAAA CAGGGATTAA AGTTATTGAC 350
CTTTTAGCAC CTTATCTTAA AGGTGGTAAA ATCGGTTTAT TCGGTGGTGC 400
30 CGGTGTAGGG AAAACCGTAT TAATTCAAGA ATTAATTCAT AATATCGCTG 450
AAGAACTTGG TGGTATTTCA GTATTTACAG GGGTAGGGGA ACGTACTCGT 500
GAAGGGAATG ACCTTTACCA TGAAATGCAA GAATCAGGCG TATCTGCTAA 550
AACAGCGATG GTGTTTGGGC AAATGAACGA ACCACCAGGA GCTCGTATGC 600
GTGTAGCACT AACAGGGTTA ACTATTGCGG AATACTTCCG TGATATGGAA 650
35 AAACAAGACG TGCTTTTATT CATCGATAAC ATTTATCGTT TCACGCAAGC 700
AGGTTTCAGAA GTGTCAGCGT TACTTGGTCG TATGCCTTCT GCCGTAGGGT 750
ATCAACCAAC ATTAGCGACA GAAATGGGTC AATTACAAGA ACGTATCAGT 800
TCAACTAAAG 810

40

2) INFORMATION FOR SEQ ID NO: 1845

(i) SEQUENCE CHARACTERISTICS:

- 45 (A) LENGTH: 815 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

50 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Arcanobacterium haemolyticum*

(B) STRAIN: ATCC 9345

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1845

5	TGCTCTGCCA	GAAATTAACA	ACGCCCTCCT	CACCGAAGTA	GACCTCTCCG	50
	GCCAAGGCGA	AGGCGAAAGC	GTTCTCAAGA	TGACTCTTGA	GGTTGCTCAG	100
	CACCTCGGCG	ATAACATCGT	CCGTACCATC	GCCATGAAGC	CAACCGACGG	150
	TCTGGTTTCG	GGCGCCACCG	TTATCGATAC	CGGCGCCCCA	ATCACCGTGC	200
	CAGTTGGCGA	CGCAACTAAA	GGTCATGTTT	TCAACGTGAC	CGGTGATGTC	250
10	CTAAACTTGG	GCGAAGGCGA	AACCCTTGAC	GTCAAGGAAC	GGTGGCCAAT	300
	CCACCGCAAG	GCTCCACAGT	TCGACGAACT	CGAACCGGAA	ACCAAGATGT	350
	TCGAAACAGG	CATCAAGGTG	ATCGATCTCC	TCACCCCATATA	CGTACAGGGC	400
	GGCAAGATCG	GTCTGTTTGG	CGGTGCTGGT	GTTGGTAAGA	CCGTTCTTAT	450
	CCAGGAAATG	ATCCAGCGTG	TTGCACAGGA	TCATGGCGGT	GTGTCCGTGT	500
15	TCGCGGGTGT	GGGTGAACGT	ACCCGTGAAG	GTAACGATCT	TATCCACGAA	550
	ATGGAAGATG	CGGGCGTTCT	TGATAAGACC	GCGCTTGTGT	TCGGCCAGAT	600
	GGATGAACCG	CCAGGGGTTC	GTTTGCGTAT	TGCACTTTCC	GGCCTGACCA	650
	TGGCGGAATA	CTTCCGTGAC	GTGCAAAACC	AGGACGTGCT	TTTGTTTCATC	700
	GATAACATCT	TCCGCTTCAC	CCAGGCAGGT	TCGGAAAGTGT	CCACGTTGCT	750
20	TGGCCGTATG	CCATCAGCAG	TGGGCTACCA	GCCGACCTTG	GCAGATKAAA	800
	TGGGCGCATT	GCAGG				815

25 2) INFORMATION FOR SEQ ID NO: 1846

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1073 bases
 (B) TYPE: Nucleic acid
 30 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

35 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Basidiobolus ranarum*
 (B) STRAIN: ATCC 24670

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1846

40	ACCTTCCTCC	TATCTTGAAG	GCCCTGGAGG	TCCAAAACCA	CAGCTCTCGY	50
	TTAGTTTTAG	AGGTGTCCCA	GCATTTGGGT	GAAAACACCG	TTCGTACTAT	100
	TGCTATGGAC	GGTACTGAAG	GATTGGTTCG	TGGTCAAAAT	GTCGTAGATA	150
	CCGGATATCC	TATTAGAGTT	CCTGTCGGTC	CTGAATGTTT	GGGTCGTATC	200
45	ATGAACGTTA	TTGGCGAGCC	TGTTGATGAG	CGCGGYCCTA	TCAAGACCAA	250
	GAAGCTTGCA	CCCATCCACG	CTTCTCCCCC	CGAGTTCGTY	GACCAATCCA	300
	CCACCCCGA	AATCTTGAG	ACTGGTATTA	AGGTTGTCGA	TTTGTTGGCC	350
	CCTTACGCTC	GTGGTGGTAA	GATCGGTCTT	TTCGGTGGTG	CCGGTGTCGG	400
	TAAGACTGTG	TTTATCCAGG	AGTTGATYAA	CAACGTTGCC	AAGGCCACG	450
50	GTGGTTACTC	CGTGTTGCT	GGTGTTGGTG	AGCGTACTCG	TGAGGGTAAC	500
	GATTTGTACC	ACGAGATGAT	TCAAACCTGGT	GTCATCAAGC	TTGATGGCCA	550
	ATCCAAGGCT	GCCCTTGCT	ACGGMCAAAT	GAACGAGCCC	CCAGGTGCTC	600
	GTGCCCGMGT	CGCTTTGACC	GGTCTTACCG	TTGCTGAATA	CTTCCGTGAT	650

GAGGAAGGHC AAGATGTGTT GCTCTTCATT GACAACATTT TCCGTTTCAC 700
 CCAAGCTGGT TCTGAAGTGT CYGCCTTGTT GGGTCGTATC CCCTCCGCTG 750
 TCGGTTACCA ACCCACCTTG GCCACCGATA TGGGTGTCAT GCAAGAGCGT 800
 ATTACCACCA CCAAGAAGGG TTCCATTACC TCTGTCCAGG CCATTTACGT 850
 5 CCCTGCTGAT GATTTGACCG ATCCCGCTCC TGCCACTACT TTTGCCCATC 900
 TTGACGCCAC CACCGTGTTG TCTCGTTCCA TCTCTGAGTT GGGTATTTAC 950
 CCCGCTGTCG ATCCCCTCGA CTCCAAGTCT CGTATGTTGG ATCCYCGTAT 1000
 TGTCGGTGAA GAGCACTACG ACATCGCCAC TGGTGTTTCAG AAGATTCTCC 1050
 ARTCTTACAA GTCTCTCCAG GAT 1073
 10

2) INFORMATION FOR SEQ ID NO: 1847

15 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 480 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Blastomyces dermatitidis*
 25 (B) STRAIN: ATCC 56220

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1847

TGTCTTTATC CAGGAGTTGA TTGTACGTCT TGCCTCACCC TTTGGGTATT 50
 30 TTGCGAATAC TAATTATAGT AGAACAACAT TGCCAAGGCT CACGGTGGGT 100
 ACTCTGTCTT CACTGGTGTC GGTGAACGTA CTCGTGAGGG TAACGATTTG 150
 TACCACGAAA TGCAGGAAAC TGGTGTTCATT CAGCTCGAGG GTGAATCCAA 200
 GGTCGCCCTC GTGTTCCGTC AGATGAACGA GCCCCCTGGT GCCCGTGCCC 250
 GTGTCGCTCT TACTGGTTTG ACCATTGCCG AGTACTTCCG TGACGAGGAG 300
 35 GGTCAAGATG TGCTTCTCTT CATTGACAAC ATTTTCCGTT TCACTCAGGC 350
 CGGTTCTGAG GTGTCTGCCC TTTTGGGTGCG TATCCCCTCT GCCGTCGGTT 400
 ACCAGCCAC TCTCGCCGTC GACATGGGTG TCATGCAGGA GCGTATTACC 450
 ACCACCACCA AGGGTTCCAT CACCTCCGTC 480

40

2) INFORMATION FOR SEQ ID NO: 1848

45 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 566 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

50 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Blastomyces dermatitidis*

(B) STRAIN: ATCC 14112

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1848

5	TGTCTTCATT	CAGGAGTTGA	TTGTACGTCC	CTTCCTCTCT	ACAAATGACG	50
	GGCGAGGAAA	ATTTTGGCT	TTTTCTAATA	GCTCGTTATA	GAACAACATT	100
	GCCAAAGCCC	ACGGTGGTTA	CTCCGTTTTC	ACTGGTGTCTG	GCGAGCGGAC	150
	CCGTGAAGGA	AACGATTTGT	ACCACGAGAT	GCAGGAAACC	CGTGTTATCC	200
	AGCTCGATGG	CGAGTCTAAG	GTCGCACTCG	TCTTCGGTCA	GATGAACGAG	250
10	CCCCCGGAG	CCCGTGCCCG	TGTTGCCCTC	ACTGGCCTGA	GCATTGCTGA	300
	ATATTTCCGT	GACGAGGAAG	GTCAAGACGG	TATGTATTCA	TATAAATTAC	350
	TCCGGGCAAA	TTGACTCAGA	ACCGCACTCA	CTCACACATA	TATTAGTGCT	400
	TCTCTTTATC	GACAACATTT	TCCGCTTCAC	CCAGGCCGGT	TCCGAAGTGT	450
	CCGCCCTGCT	TGGTCGTATT	CCCTCCGCCG	TCGGTTACCA	ACCCACTCTC	500
15	GCCGTCGACA	TGGGTGGTAT	GCAGGAACGT	ATCACAACCA	CCACCAAGGG	550
	CTCCATTACC	TYCGTG				566

20 2) INFORMATION FOR SEQ ID NO: 1849

(i) SEQUENCE CHARACTERISTICS:

	(A) LENGTH: 817 bases
	(B) TYPE: Nucleic acid
25	(C) STRANDEDNESS: Double
	(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

30 (vi) ORIGINAL SOURCE:

	(A) ORGANISM: <i>Campylobacter coli</i>
	(B) STRAIN: ATCC 43479

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1849

35	AATGAAGCCA	TTGTTGTAAA	TTTTGAAAGT	GAAGGCAAAA	AACAAAAACT	50
	TGTTTTAGAA	GTAGCAGCAC	ACTTGGGCGA	TAATAGAGTT	AGAACTATTG	100
	CTATGGATAT	GACAGATGGC	TTGGTAAGAG	GACTTAAAGC	AGAAGCTTTG	150
	GGTGCTCCTA	TTAGCGTTCC	TGTGGGTGAA	AAAGTTT TAG	GAAGAATTTT	200
40	TAATGTTACG	GGAGATTTGA	TCGATGAAGG	TGAAGAAATT	TCTTTTGATA	250
	AAAAATGGGC	AATTCATAGA	GATCCACCAG	CTTTTGAAGA	TCAAAGCACA	300
	AAAAGTGAGA	TTTTTGAAAC	AGGGATTAAA	GTTGTGGATT	TACTTGCTCC	350
	TTATGCAAAA	GGTGGTAAAG	TAGGTCTTTT	TGGTGGTGCA	GGTGTGGTA	400
	AAACTGTTAT	TATTATGGAG	CTTATTCACA	ATGTTGCATT	TAAACATAGC	450
45	GGCTATTCTG	TATTTGCAGG	TGTAGGTGAG	AGAACTCGTG	AAGGAAATGA	500
	CCTTTATAAT	GAAATGAAAG	AAAGTAATGT	TTTAGACAAA	GTTGCTCTAT	550
	GTTATGGACA	AATGAATGAA	CCACCAGGGG	CAAGAAATCG	TATTGCTTTA	600
	ACAGGTTTAA	CAATGGCTGA	GTATTTTAGA	GATGAAATGG	GTCTTGATGT	650
	GCTTATGTTT	ATTGATAATA	TCTTTAGATT	TTCACAATCA	GGTTCTGAAA	700
50	TGTCAGCACT	TTTAGGAAGA	ATTCCATCAG	CTGTGGGTTA	TCAACCAACC	750
	CTAGCAAGTG	AAATGGGTAA	ATTCCAAGAA	AGAATTACTT	CAACTAAAAA	800
	AGGATCAATT	ACTTCAG				817

2) INFORMATION FOR SEQ ID NO: 1850

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 775 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

10

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Campylobacter fetus* subsp. *fetus*
(B) STRAIN: ATCC 25936

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1850

AAGGCAACAC GCATAAACTT ATTTTAGAGA CTGCTGCACA CCTTGGAGAT 50
AATCGTGTA AACTATCGC TATGGATATG AGCGAAGGAC TTACAAGAGG 100
GTTAGATGCT ATAGCGCTTG GGTGCGCTAT CAGTGTTCTT GTTGGAGAAA 150
20 AAGTTTTAGG AAGAATATTC AACGTAATTG GTGATCTTAT AGACGAAGGC 200
GAAGAAGAAA AATTTGATAA AAAATGGTCG ATTCATAGAG ATCCGCCGGC 250
ATTTGAAGAT CAAAGCACAA AAAGTGAAAT TTTTGAAACA GGTATAAAAG 300
TCGTAGATCT TTTGGCTCCT TATGCAAAAG GCGGTAAAGT TGGACTATTT 350
GGCGGTGCCG GCGTTGGTAA AACAGTTATC ATTATGGAAC TTATCCACAA 400
25 CGTTGCATTC AAACACAGCG GCTATTCGGT ATTTGCCGGT GTCGGTGAAA 450
GAACAAGAGA GGGTAACGAT CTTTATAATG AAATGAAAGA ATCCGGCGTT 500
TTGGATAAAG TTGCCTTATG TTATGGACAA ATGAATGAAC CGCCGGGTGC 550
AAGAAACCGT ATAGCGCTTA CTGGTCTTAC AATGGCTGAG TATTTTCGTG 600
ACGAGATGGG ACTAGATGTT CTTATGTTTA TCGATAACAT CTTCCGTTTC 650
30 TCACAATCAG GCTCAGAGAT GTCGGCTCTT CTTGGACGTA TCCAAGTGC 700
GGTTGGTTAT CAACCAACGT TAGCTAGCGA AATGGGAAGA CTTCAAGAAA 750
GAATCACATC AACTAAAAA GGTTC 775

35

2) INFORMATION FOR SEQ ID NO: 1851

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 793 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

45

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Campylobacter fetus* subsp. *venerealis*
(B) STRAIN: ATCC 33561

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1851

CGAAGCTATT GAAGTAAATT TTACAGTAGA AGGCAACACG CATAAACTTA 50
TTTTAGAGAC TGCTGCACAC CTTGGAGATA ATCGTGTAAG AACTATCGCT 100

	ATGGATATGA	GCGAAGGACT	TACAAGAGGG	TTAGATGCTA	TAGCGCTTGG	150
	GTCGCCTATC	AGTGTTCCCTG	TTGGAGAAAA	AGTTTTAGGA	AGAATATTCA	200
	ACGTAATTGG	TGATCTTATA	GACGAAGGCG	AAGAAGAAAA	ATTTGATAAA	250
	AAATGGTCGA	TTCATAGAGA	TCCGCCGGCA	TTTGAAGATC	AAAGCACAAA	300
5	AAGTGAAATT	TTTGAAACAG	GTATAAAAGT	CGTAGATCTT	TTGGCTCCTT	350
	ATGCAAAGG	CGGTAAAGTT	GGACTATTTG	GCGGTGCCGG	CGTTGGTAA	400
	ACAGTTATCA	TTATGGAAC	TATCCACAAC	GTTGCATTCA	AACACAGCGG	450
	CTATTCGGTA	TTTGCCGGTG	TCGGTGAAAG	AACAAGAGAG	GGTAACGATC	500
	TTTATAATGA	AATGAAAGAA	TCCGGCGTTT	TGGATAAAGT	TGCCTTATGT	550
10	TATGGACAAA	TGAATGAACC	GCCGGGTGCA	AGAAACCGTA	TAGCGCTTAC	600
	TGGTCTTACA	ATGGCTGAGT	ATTTTCGTGA	CGAGATGGGA	CTAGATGTTC	650
	TTATGTTTAT	CGATAACATC	TTCCGTTTCT	CACAATCAGG	CTCAGAGATG	700
	TCGGCTCTTC	TTGGACGTAT	CCCAAGTGCG	GTTGGTTATC	AACCAACGTT	750
	AGCTAGCGAA	ATGGGAAGAC	TTCAAGAAAG	AATCACATCA	ACT	793

2) INFORMATION FOR SEQ ID NO: 1852

- 20 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 825 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Double
 - (D) TOPOLOGY: Linear
- 25 (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Campylobacter gracilis*
 - 30 (B) STRAIN: ATCC 33236

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1852

	GGACTATTTA	CCGAAGATTA	ACGAAGCTAT	CGAGGTTAAA	TTTGACGTCG	50
35	AGGGCGCTCA	TCGCAGGCTG	ATCCTAGAGG	TAGCCGCGCA	CCTTGAGAGAC	100
	AATCGCGTCC	GCACGATCGC	TATGGATATG	AGCGATGGAC	TTAGGCGAGG	150
	GCTTGAGGCC	GTCGCTTTGG	GCGCGCCTAT	TACGGTGCCT	GTGGGCGAGA	200
	AAGTTTTGGG	TAGAATTTTT	AATGTTACGG	GCGATCTGAT	CGACGAAGGC	250
	GAGGATGAAA	AATTTGAAAC	CCGCTGGTCG	ATCCACAGAG	ATCCGCCTAG	300
40	CTTTGAAAAT	CAAAGCACGA	AGAGTGAAAT	TTTTGAAACC	GGCATTAAGG	350
	TAGTCGATCT	GCTCGCCCCT	TATGCAAAGG	GCGGTAAGGT	AGGACTATTC	400
	GGCGGTGCTG	GCGTCGGTAA	GACCGTCATC	ATCATGGAAC	TGATTCACAA	450
	CGTCGCTTTC	AAACACAGCG	GCTACTCCGT	ATTTGCGGGT	GTCGGCGAGC	500
	GAACGAGAGA	GGGAAACGAC	CTTTATAACG	AGATGAAAGA	ATCGGGCGTT	550
45	TTGGATAAAG	TCGCCTTGAC	CTATGGTCAG	ATGAACGAAC	CGCCGGGAGC	600
	GAGAAACCGT	ATCGCGCTAA	CCGGTCTTAC	GATGGCCGAG	TATTTCCGCG	650
	ACGAGCTAGG	GCTTGACGTT	TTGATGTTTA	TTGATAATAT	CTTCCGCTTC	700
	TCGCAGTCGG	GTTCCGAGAT	GTCCGCGCTT	TTAGGACGAA	TTCCGTCCGC	750
	GGTCGGTTAT	CAGCCTACGC	TTGCCAGCGA	AATGGGTAAA	TTACAGGAGC	800
50	GCATTACTTC	TACTAAGAAG	GGCTC			825

2) INFORMATION FOR SEQ ID NO: 1853

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 818 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

10

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Campylobacter jejuni* subsp. *jejuni*
 (B) STRAIN: ATCC 33560

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1853

TTTACCTCAA ATTAATGAAG CAATTGTTGT AAATTTTGAA AGCGAAGGAA 50
 AAAAACATAA ACTTGTTTGA GAAGTAGCAG CTCATTTAGG AGATAATAGA 100
 GTTAGAACTA TTGCTATGGA TATGACAGAT GGT TTGGTAA GGGGCTTAA 150
 20 AGCTGAGGCT TTAGGTGCTC CTATTAGTGT TCCTGTTGGT GAGAAAGTTT 200
 TAGGAAGAAT TTTCAATGTT ACTGGAGATT TGATCGATGA AGGTGAAGAA 250
 ATTTCTTTTG ATAAAAAATG GGCAATTCAT AGAGATCCGC CAGCTTTTGA 300
 AGATCAAAGC ACAAAAAGTG AGATTTTGA AACAGGGATT AAAGTTGTAG 350
 ATTTGCTTGC TCCTTATGCA AAAGGTGGTA AAGTAGGTCT TTTTGGTGGT 400
 25 GCAGGTGTTG GTAAACTGT TATTATTATG GAGCTTATTC ACAATGTTGC 450
 ATTTAAGCAT AGCGGCTATT CTGTATTTGC AGGTGTGGGT GAGAGAAGTC 500
 GTGAAGGAAA TGACCTTTAT AATGAAATGA AAGAAAGTAA TGTTTTAGAC 550
 AAAGTTGCTC TATGTTATGG ACAAATGAAT GAACCACCAG GAGCAAGAAA 600
 TCGTATTGCT TTAACAGGTT TAACAATGGC TGAGTATTTT AGAGATGAAA 650
 30 TGGGTCTTGA TGTGCTTATG TTTATTGATA ATATCTTTAG ATTTTCACAA 700
 TCAGGTTCAG AAATGTCAGC ACTTTTAGGA AGAATTCCAT CAGCTGTGGG 750
 TTATCAACCA ACCCTAGCAA GTGAAATGGG TAAATTCCAA GAAAGAATTA 800
 CTTCAACTAA AAAAGGCT 818

35

2) INFORMATION FOR SEQ ID NO: 1854

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 830 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

45

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus cecorum*
 (B) STRAIN: ATCC 43198

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1854

ATTACCTGAT ATCAACAACG CCTTATTGGT CTATAAAAAT GATGAACAAA 50

	AAAGTAAAAT	TGTGCTAGAA	GCTGCCTTAG	AATTAGGTGA	TGGCATCATT	100
	CGTACAATTG	CCATGGAATC	AACGGATGGT	TTACAACGTG	GGATGGAAGT	150
	TGTCGATACT	GGTAAACCAA	TTTCAGTTCC	AGTTGGTAAA	GAAACGCTAG	200
	GACGTGTCTT	TAACGTTTTA	GGGGATACGA	TTGATATGCA	AGAACCATT	250
5	GCACAAGATG	CAGATCGTTC	TGCAATTCAT	AAAGCTGCAC	CAAAATTTGA	300
	AGACTTAAGT	ACAAGTACTG	AAATTTTAGA	AACAGGGATT	AAAGTTATCG	350
	ACTTATTAGC	ACCATATTTA	AAAGGTGGTA	AAGTCGGTCT	ATTCGGGGGT	400
	GCCGGAGTAG	GTAAAACCGT	TTTAATCCAA	GAATTAATCC	ATAATATTGC	450
	ACAAGAACAT	GGTGGGATTT	CTGTATTTAC	CGGTGTTGGT	GAACGTACAC	500
10	GTGAAGGAAA	TGACTTGTTAT	CATGAAATGC	GTGATTCAGG	AGTTATTGAA	550
	AAAACCTGCCA	TGGTGTTTGG	TCAAATGAAC	GAACCACCTG	GAGCTCGTAT	600
	GCGTGTTGCT	TTAACTGGGT	TAACGATTGC	TGAATATTTT	CGTGATGTAG	650
	AAGGACAAGA	TGTGTTGCTA	TTTATTGATA	ACATCTTCCG	TTTCACTCAA	700
	GCGGGTTCTG	AAGTATCAGC	CTTGCTTGGT	CGTATGCCAT	CTGCCGTGGG	750
15	TTATCAACCT	ACATTGGCTA	CAGAAATGGG	TCAATTACAA	GAACGTATCA	800
	CTTCAACTAA	GAAGGGCTCT	ATCACTTCTA			830

20 2) INFORMATION FOR SEQ ID NO: 1855

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 823 bases
 (B) TYPE: Nucleic acid
 25 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

30 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus columbae*
 (B) STRAIN: ATCC 51263

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1855

35	TCTTTACCAG	ATATCAATAA	TGCGCTTATT	GTCTATAAAA	ATGATGAACA	50
	AAAAAGTAAA	ATCGTGCTTG	AAGCTGCTTT	AGAGCTAGGA	GATGGCATT	100
	TTCGTACGAT	TGCAATGGAA	TCAACTGATG	GATTGCAACG	TGGAATGGAA	150
	GTTTTTCGATA	CAGGTAAGCC	AATTTTCAGTA	CCAGTAGGTC	GTGAAACATT	200
40	AGGTCGTGTA	TTTAATGTTT	TAGGTGATAC	CATTGATACG	CAAGAAGCTT	250
	TTCCTGCTGA	TGCGAATCGT	GATGCGATTC	ATAAATCAGC	TCCAGCTTTT	300
	GAAGAATTAA	GTACAAGTAC	TGAAATCCTA	GAAACAGGGA	TTAAAGTTAT	350
	CGACTTACTA	GCACCATACT	TAAAAGGTGG	GAAAGTTGGT	CTATTCGGTG	400
	GTGCCGGTGT	AGGTAAAACC	GTATTAATTC	AAGAATTAAT	TCATAATATC	450
45	GCCCAAGAAC	ATGGGGGTAT	TTCAGTATTT	ACCGGTGTTG	GTGAACGTAC	500
	ACGTGAAGGA	AATGACTTGT	ATCACGAAAT	GCGTGATTCA	GGCGTTATCG	550
	AAAAAAGTGC	TATGGTGTTT	GGGCAAATGA	ACGAACCACC	TGGAGCACGT	600
	ATGCGTGTTG	CGCTAACTGG	ACTAACTATT	GCGGAATACT	TCCGTGATGT	650
	TGAAGGCCAA	GACGTATTGC	TATTTATTGA	TAATATCTTC	CGTTTACTC	700
50	AAGCAGGTTT	TGAAGTTTCT	GCCTTACTTG	GTCGTATGCC	TTCTGCGGTA	750
	GGTTATCAAC	CTACTTTGGC	TACTGAAATG	GGTCAATTGC	AAGAACGGAT	800
	TACATCAACG	AAGAAAGGTT	CGA			823

2) INFORMATION FOR SEQ ID NO: 1856

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 826 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Enterococcus dispar*
 (B) STRAIN: ATCC 51266
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1856

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TTACCAGACA TTAATAATGC CTTGGTTGTC TATAAAAATG ACGAACAAAA    50
AACCAAGATT GTATTAGAAG CTGCCTTAGA ACTAGGAGAT GGTGTGATTC    100
GAACTATCGC CATGGAATCT ACTGATGGCT TACAACGGGG AATGGAAGTT    150
20  GTCGATACTG GCAGTTCCAT TTCTGTACCG GTAGGAAAAG AAACATTGGG    200
TCGTGTATTT AACGTTTTAG GAAATACAAT TGACTTAGAA GAACCTTTTC    250
CAGCGGATGC TAAACGTAGT GGTATCCATA AAAAAGCGCC TGATTTTGAT    300
GAATTAAGCA CTAGTACAGA AATTTTAGAA ACAGGGATTA AAGTTATTGA    350
CCTATTAGCC CTTATTTTAA AAGGTGGTAA AGTCGGATTA TTCGGTGGTG    400
25  CCGGAGTTGG TAAAACCGTT TTAATTCAAG AATTAATTCA TAATATTGCC    450
CAAGAACATG GTGGGATTTC TGTTTTTACT GGTGTTGGTG AAAGAACACG    500
TGAAGGTAAT GACTTGATT ATGAAATGAA AGAATCTGGC GTTATCGAAA    550
AAACTGCCAT GGTATTTGGT CAAATGAATG AGCCACCTGG TGCCCGGATG    600
CGGGTTGCTT TAACCGGACT TACCATTGCG GAATACTTCC GGGACGTTGA    650
30  AGGACAAGAT GTATTGCTCT TTATCGATAA TATTTTCCGT TTTACCCAAG    700
CTGGTTCAGA AGTATCTGCC TTATTAGGAC GGATGCCCTC TGCCGTTGGT    750
TATCAACCAA CTTTGGCTAC TGAAATGGGA CAACTTCAAG AACGGATTAC    800
CTCAACGAAA AAAGGTCTA TTACAT                                826

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2) INFORMATION FOR SEQ ID NO: 1857

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 814 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Enterococcus malodoratus*
 (B) STRAIN: ATCC 43197
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1857

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TCCTTACCAG ACATCAACAA TGCGTTGATT GTTTACAAAA AAAATAAAAC    50

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	AAAAGTTGTT	CTTGAAGCTG	CTTTGGAAC	TGGTGATGGT	GTTATCCGCA	100
	CGATCTCTAT	GGAATCAACA	GATGGCTTGC	AACGTGGAAT	GGAAGTTGTC	150
	GATACAGGCA	AACCAATCTC	AGTTCCCGTT	GGTAAAGAAA	CTTTAGGTCG	200
	TGTGTTTAAC	GTATTAGGTG	AAACAATCGA	CAAAGAAGCG	CCTTTTCCAG	250
5	AAGATGCAGT	AAAAAGCGGT	ATTCATAAAA	AAGCGCCGGC	TTTTGAAGAA	300
	CTTAGTACCA	GTAATGAAAT	TTTAGAAACA	GGGATCAAAG	TTATCGACTT	350
	ATTAGCTCCT	TACTTAAAGG	GTGGTAAAGT	CGGACTATTT	GGTGGTGCCG	400
	GTGTTGGTAA	AACCGTCTTG	ATCCAAGAAT	TGATTTCATA	TATCGCCCCA	450
	GAACACGGTG	GTATTTTCAGT	GTTTACGGGT	GTTGGTGAAC	GTAATCGTGA	500
10	AGGGAACGAC	CTTTATTATG	AAATGAAGGA	ATCAGGCGTT	ATTGAGAAAA	550
	CTGCCATGGT	GTTTGGACAA	ATGAACGAGC	CGCCAGGTGC	GCGTATGCGT	600
	GTTGCCTTGA	CTGGTTTGAC	ATTGGCTGAA	TATTTCCGAG	ATGAAGAAGG	650
	ACAAGATGTG	CTGTTGTTTA	TCGACAACAT	CTTCCGTTTC	ACTCAAGCCG	700
	GTTCTGAAGT	TTCTGCCTTG	CTTGCCCGGA	TGCCTTCAGC	CGTTGGCTAC	750
15	CAACCAACTT	TGGCAACTGA	AATGGGTCAA	TTGCAAGAAC	GAATCACTTC	800
	AACGAAGAAG	GGCT				814

20 2) INFORMATION FOR SEQ ID NO: 1858

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 791 bases
 (B) TYPE: Nucleic acid
 25 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

30 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus mundtii*
 (B) STRAIN: ATCC 43186

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1858

35	CGCATTAGTT	GTTTATAAAA	ATGATGAGCA	AAAATCAAAA	GTTGTTCTTG	50
	AAGCAGCATT	AGAATTAGGT	GACGGTGTGA	TCCGTACGAT	CGCAATGGAA	100
	TCGACGGATG	GACTACAACG	TGGAATGGAA	GTCATCGACA	CAAGCAAAGC	150
	GATCTCTGTA	CCAGTTGGAA	CAGAAACATT	AGGTCGTGTG	TTCAACGTGT	200
40	TAGGTGAAAC	AATCGATTG	GAAGCACCAT	TTCCAGAGGA	TGCCCAAAGA	250
	AGCGAGATCC	ACAAGAAAGC	ACCAAATTTT	GATGAATTAA	GCACAAGTAC	300
	AGAGATTCTT	GAAACTGGGA	TCAAAGTCAT	TGACTTATTA	GCACCTTATT	350
	TAAAAGGTGG	GAAAGTTGGA	TTGTTTGGGG	GTGCCGGTGT	TGGTAAAACC	400
	GTAATGATCC	AAGAATTGAT	CCATAATATC	GCCCAAGAAC	ATGGGGGAAT	450
45	CTCAGTGTGTT	ACCGGTGTAG	GGGAACGTAC	CCGTGAAGGA	AACGATCTGT	500
	ATTACGAAAT	GAAAGATTCA	GGCGTAATCG	AAAAAACAGC	GATGGTGTTT	550
	GGACAAATGA	ATGAGCCACC	AGGTGCTCGT	ATGCGTGTCG	CACTAACTGG	600
	ATTGACGATT	GCGGAATATT	TCCGTGATGT	CGAAGGACAA	GACGTGCTCT	650
	TATTTATTGA	TAATATTTTC	CGTTTCACCC	AAGCAGGTTC	AGAAGTATCT	700
50	GCCTTACTAG	GACGTATGCC	ATCAGCGGTT	GGTTATCAAC	CAACCTTAGC	750
	GACTGAAATG	GGACAACCTC	AAGAACGGAT	CACTTCAACG	A	791

2) INFORMATION FOR SEQ ID NO: 1859

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 817 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Enterococcus raffinosus*
 (B) STRAIN: ATCC 49427
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1859

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TCCTTACCAG ACATCAACAA TGC GTTGATT GTTTATAAAA AAGATAAAAC      50
AAAAGTTGTT CTTGAAGCTG CTTTGGAACT TGGTGATGGT GTTATTCGCA      100
CAATCGCCAT GGAATCAACG GATGGATTAC AACGTGGAAT GGAAGTTGTC      150
20 GATACTGGCA AGCCTATTTT TGTTCAGTA GGAAAAGAAA CTCTAGGTCTG      200
TGTATTTAAT GTATTAGGTG AAACAATCGA CAAGGAAGCG CCTTTTCCAG      250
AAGATGCAGA AAAAAGTGGT ATTCACAAGA AAGCACCAAC TTTCGAAGAA      300
CTTAGCACAA GTAATGAGAT CTTAGAAACA GGAATCAAAG TTATTGACTT      350
GTTAGCTCCT TACTTAAAAG GTGGTAAAGT TGGATTATTT GGTGGTGCCG      400
25 GTGTTGGTAA AACAGTCTTG ATTCAAGAGC TAATTCATAA TATCGCTCAA      450
GAACATGGTG GTATTTCTGT GTTTACTGGT GTTGGTGAAC GTACTCGTGA      500
AGGGAACGAC CTTTATTATG AAATGAAAGA TTCTGGTGTT ATTGAGAAAA      550
CTGCTATGGT GTTCGGTCAA ATGAACGAGC CGCCAGGTGC ACGTATGCGT      600
GTTGCCTTAA CTGGTTTAAC CTTAGCCGAA TACTTCCGTG ATGAAGAAGG      650
30 ACAAGATGTG TTGCTATTTA TTGACAACAT TTTCCGTTTC ACTCAAGCCG      700
GATCAGAAGT TTCTGCCTTA CTTGGCCGTA TGCCGTCAGC AGTTGGTTAC      750
CAACCGACTT TAGCAACTGA AATGGGTCAA TTACAAGAAC GTATTACGTC      800
GACGAAAAAA GGTTCAA                                           817
35

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2) INFORMATION FOR SEQ ID NO: 1860

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 852 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Globicatella sanguis*
 (B) STRAIN: ATCC 51173
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1860

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CCTGACATTC ATAATGCATT AATTGTAACG AACGCTGATA TGGCGGATGT      50

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	AATGCAAGAA	AATATTTTCGG	ATGAAGAAAA	ATTATTAACC	TTAGAAGTTG	100
	CACTGGATTT	AGGTCATGGA	ATGGTCCGGA	CAATTGCGAT	GGAATCAACC	150
	GATGGTTTGG	AACGCGGCAT	GACAGTTGTG	GATTATTTAA	CACCGATTAA	200
	AGTGCCAGTA	GGCGAAGCCA	CTTTAGGTAG	AGTATTCAAT	GTTTGTAGGTG	250
5	AGACAATTGA	TGAACTAGAA	CCGGTTGGCG	ACGATGTTGA	ACTCAAAAGT	300
	ATTCATCGTG	AAGCCCCTAA	ATATGAGGAC	TTAGATAATA	GTTTTCATGT	350
	TTTAGAAACC	GGAATTAAGG	TCATCGATTT	ATTAGCTCCT	TATATTAAAG	400
	GGGGAAAAAT	CGGTTTATTC	GGTGGTGCCG	GAGTGGGTAA	AACGGTCTTA	450
	ATTCAAGAAT	TAATTCATAA	TATTGCAGAA	CAATTAGGAG	GTATCTCAGT	500
10	TTTCACTGGG	GTTGGAGAAC	GTACCCGTGA	AGGGAATGAC	CTCGTTTTTG	550
	AAATGCGAGA	GTCAGGTGTA	AGCAAGAAGA	CGGCCATGGT	TTTCGGTCAA	600
	ATGAATGAAC	CACCTGGAGC	ACGTATGCGT	GTTGTCTTAA	CAGGACTTAC	650
	AATGGCGGAA	TATTTCCGTG	ACGAATTGAA	ACAAGACGTC	TTATTATTTA	700
	TTGATAATAT	TTATCGTTTT	ACTCAAGCAG	GTTCCGAAGT	GTCAGCCTTA	750
15	TTAGGTCGTA	TGCCTTCAGC	AGTAGGGTAT	CAACCAACTT	TAGCAAGTGA	800
	AATGGGACAA	ATGCAAGAAC	GTATTACGTC	WACGAAGCRC	GGTTCATTA	850
	CA					852

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2) INFORMATION FOR SEQ ID NO: 1861

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 828 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Lactococcus garvieae*
 (B) STRAIN: ATCC 49156

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1861

	GCGCGACTCT	TCCTGAGATT	AATAACGCAC	TCATCGTTTA	CAAAGATGTA	50
	GACGGCGTTA	AAACTAAAAT	CGTCCTTGAA	GTGGCGTTGG	AACTTGGTGA	100
	TGGTGCCGTA	CGTACCATCG	CTATGGAATC	AACTGATGGC	TTGACACGTG	150
40	GACTTGAAGT	TCTCGATACA	GGTAAAGCAA	TCAGCGTACC	TGTTGGTCAA	200
	GAAACACTTG	GACGTGTCTT	CAATGTACTT	GGAGATGCTA	TTGATGGAGG	250
	GGAAGCATTT	GCTGAAAATG	CAGAACGCAG	CCCTATCCAT	AAAAAAGCCC	300
	CATCTTTTGA	TGAACTTTCA	ACAGCAAATG	AAATTCTGGT	GACAGGGATT	350
	AAAGTTATTG	ACTTGCTTGC	CCCATACCTT	AAAGGTGGTA	AGATTGGGTT	400
45	GTTCGGTGGT	GCCGGAGTTG	GTAAACCGT	CCTTATCCAA	GAGTTGATTC	450
	ACAATATTGC	CCAAGAACAC	GGTGGTATTT	CCGTATTTAC	TGGTGTGGG	500
	GAACGTACAC	GTGAAGGGAA	TGACCTTTAC	TGGGAAATGA	AAGAATCAGG	550
	CGTTATCGAA	AAAACAGCCA	TGGTCTTCGG	TCAAATGAAT	GAACCACCTG	600
	GAGCACGTAT	GCGTGTTGCT	CTTACTGGTT	TGACAAATTGC	TGAATATTTT	650
50	CGTGATGTAG	AAAAACAAGA	CGTTTTGCTT	TTCATTGATA	ATATCTTCCG	700
	TTTCACCCAA	GCCGGTTCAG	AAGTATCTGC	CCTCTTAGGA	CGTATGCCAT	750
	CAGCCGTTGG	TTACCAACCT	ACGCTTGCAA	CTGAAATGGG	TCAACTTCAA	800
	GAACGTATCA	CTTCAACAAA	ACAAGGTT			828

2) INFORMATION FOR SEQ ID NO: 1862

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 828 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

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(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Lactococcus lactis*
(B) STRAIN: ATCC 11454

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1862

AATTGCCTGA RATTAACAAT GCCTTGATTG TCTACAAAGA TGTCAATGGC 50
CTAAAAACAA AAATTACTCT TGAAGTTGCT TTGGAAGTTG GTGATGGTGC 100
AGTTCGTACA ATCGCTATGG AATCTACTGA TGGCTTGACT CGTGGACTTG 150
20 AAGTCCTTGA TACAGGTAAA GCAGTCAGCG TTCCTGTTGG GGAAGCCACT 200
CTTGGTCGTG TTTTAAACGT TCTTGGTGAT GTTATTGACG GTGGGGAAGA 250
ATTTGCTGCT GATGCAGAAC GTAATCCTAT CCATAAAAAA GCTCCAACAT 300
TTGACGAATT GTCAACTGCA AACGAAGTTC TCGTAACTGG GATTAAAGTT 350
GTCGATTTGC TTGCACCTTA CCTTAAAGGT GGTAAAGTTG GACTTTTCGG 400
25 TGGTGCCGGA GTTGGTAAAA CCGTCCTTAT TCAAGAATTG ATTCACAACA 450
TCGCCCAAGA ACACGGAGGT ATTTCTGTGT TTACCGGTGT TGGGGAACGT 500
ACTCGTGAAG GGAATGACCT TTAAGTGGAA ATGAAAGAAT CAGGCGTTAT 550
TGAAAAAACT GCCATGGTCT TTGGTCAAAT GAATGAACCA CCAGGAGCAC 600
GTATGCGTGT TGCCCTTACT GGTTTGACAA TTGCTGAATA TTTCCGTGAT 650
30 GTTCAAGGTC AAGACGTACT GCTTTTCATT GACAACATCT TCCGTTTCAC 700
ACAAGCTGGT TCAGAAGTTT CTGCCCTTTT GGGACGTATG CCTTCTGCCG 750
TTGGTTACCA ACCAACACTT GCTACTGAAA TGGGGCAATT GCAAGAACGT 800
ATCACTTCTA CTAAGAAGGG TTCTGTTA 828

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2) INFORMATION FOR SEQ ID NO: 1863

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 825 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

45 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Listeria ivanovii*
(B) STRAIN: ATCC 19119

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1863

CTTACCTGAA ATCTACAACG CCCTAGTTAT TGAATATAAA TCTGATGCAG 50

	AAGAAGCACC	AACTAGCCAA	CTTACTTTAG	AAGTAGCCAT	TCAATTAGGT	100
	GATGACGTTG	TTCGTACAAT	TGCAATGGCA	TCAACTGATG	GTGTTCAAAG	150
	AGGTATGGAA	GTTATTGATA	CTGGGAGCCC	AATCACAGTT	CCAGTTGGTA	200
	CAGTAACACT	TGGTCGTGTA	TTTAACGTAT	TAGGAAACAC	TATCGATTTG	250
5	GATGAGCCAC	TTCCAAGCGA	TATCAAGCGT	AATAAAATTC	ACCGTGAAGC	300
	ACCAACATTT	GACCAATTAG	CAACAACACT	TGAAATTCTT	GAAACAGGAA	350
	TAAAAGTTGT	AGACTTGCTA	GCCCCATATT	TAAAAGGTGG	TAAAATTGGT	400
	TTGTTCCGGC	GAGCGGGTGT	TGGTAAACC	GTTTTAATCC	AAGAACTTAT	450
	TCATAATATC	GCTCAAGAAC	ATGGTGGTAT	TTCTGTGTTT	GCTGGTGTG	500
10	GAGAACGTAC	TCGTGAAGGG	AACGATCTTT	ACTTTGAAAT	GAAAGACTCT	550
	GGTGTAAATTG	AAAAAACTGC	CATGGTATTC	GGTCAAATGA	ACGAACCACC	600
	AGGTGCTCGT	ATGCGTGTAG	CTTTAACAGG	TCTTACAATC	GCTGAATATT	650
	TCCGTGATGA	AGAACACCAA	GATGTACTTC	TATTCATTGA	TAATATTTTC	700
	CGCTTTACTC	AAGCTGGTTC	AGAGGTTTCG	GCTTTACTAG	GTCGTATGCC	750
15	ATCTGCAGTA	GGTTATCAAC	CAACTCTAGC	TACCGAAATG	GGACAATTAC	800
	AAGAACGTAT	TACTTCTACT	AATGT			825

20 2) INFORMATION FOR SEQ ID NO: 1864

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 821 bases
- (B) TYPE: Nucleic acid
- 25 (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- 30 (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Succinivibrio dextrinosolvens*
- (B) STRAIN: ATCC 19716

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1864

	GTCATATTCC	AGAGCTTTAT	GACGCTCTGG	AGGTAAAGGG	CGATGGTAAG	50
	CATCGTTTCA	ACCTAGTTCT	TGAGGTTCAA	CAGCAGATTG	GCGGTGGTGT	100
	GGTACGCTGC	ATTGCCATGG	GTTCTTCTGA	CGGTTTGAGC	AGAGGAATTG	150
	AGGCTGTAAA	TACTGGTGCC	GGTGTTAAGG	TTCCAGTTGG	TCGTGAGACC	200
40	CTAGGACGTA	TTATGAACGT	TTTAGGTCAG	CCTGTAGATG	AGAGAGGTCC	250
	TATCGGACAG	AAAGAGGATT	GGGAAATTCA	CCGTCCAGCT	CCTACCTATG	300
	CTGAGCAGTC	ATCAACTACA	GAAATTCTAG	AAACCGGTAT	TAAGGTTATG	350
	GACCTTATCT	GCCCATTTCG	TAAGGGTGGT	AAAGTTGGTC	TGTTCCGGTGG	400
	TGCCGGTGTG	GGTAAGACAG	TTAACATGAT	GGAGCTTATC	AATAACATTG	450
45	CTAAGGCTCA	CTCAGGTCTA	TCTGTATTTA	CCGGTGTGTT	TGAGCGTACT	500
	CGTGAGGGTA	ACGACTTCTA	CCACGAAATG	CAGGAATCAA	AGGTTATCGA	550
	TAAGGTATCA	ATGATTTACG	GTCAGATGAA	CGAGCCTCCA	GGGAACCGTC	600
	TACGTGTTGC	TCTGACAGGT	CTGACTGTTG	CTGAGAAGTT	CCGTGACGAA	650
	GGTCTGGATG	TGCTTCTGTT	CATCGATAAC	ATCTATCGTT	ATACACTGGC	700
50	TGGTACAGAG	GTATCTGCTC	TGTTAGGCCG	TATGCCCTCA	GCTGTGGGTT	750
	ACCAGCCTAC	ACTGGCTGAG	GAAATGGGTG	TATTACAGGA	GCGTATTGCT	800
	TCAACTAAGA	AAGGTTCTAT	T			821

2) INFORMATION FOR SEQ ID NO: 1865

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 822 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Tetragenococcus halophilus*
 (B) STRAIN: ATCC 33315

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1865

	TGATACTTTA	CCAGATATCA	ATAATGCATT	AGCCGTATAT	AAAAATGATG	50
	AGAACAAGAC	GCGTGTTGTA	TTGGAAGCTA	CTTTAGAACT	TGGAGATGGG	100
	GTAATTCGTG	CCATTTCTAT	GGGGTCTACT	GACGGCTTGC	AACGTGGCAT	150
20	GGAAGTTGTG	GATACACAAG	AACCTATTTT	TGTTCCGGTA	GGAAATGATA	200
	CTTTAGGTCG	TGTATTTAAT	GTGTTAGGAG	AAACAATAGA	TAATCAGGAG	250
	CCATTTCTCTG	AAGATGCTGA	AAAAAGTGGT	ATTCACAAAA	AAGCCCCCTAG	300
	TTTTGATGAA	TTAAGTACTA	GTTTCGGAAAT	ATTAGAAACA	GGGATCAAAG	350
	TGATTGATTT	ATTAGAACCT	TATCTAAGAG	GCGGTAAAGT	CGGATTGTTT	400
25	GGAGGCGCCG	GTGTTGGAAA	AACGGTGCTA	ATTCAAGAAT	TGATCAATAA	450
	TGTTGCCCAA	GAACACGGGG	GTATTTCCGT	GTTTAATGGT	GTAGGTGAAC	500
	GTAATCGTGA	AGGTAATGAC	TTGTATTATG	AAATGCAGGA	TTCAGGCGTT	550
	ATCGAAAAAA	CAGCCATGGT	GTTTGGTCAA	ATGAACGAAC	CACCAGGTGC	600
	TCGTATGCGT	GTTGCTTTAA	CTGGCCTAAC	ACTGGCAGAA	TATTTTCGAG	650
30	ATGTTGAAGG	TCAAGACGTA	TTATTATTTA	TTGATAATAT	TTTCCGTTTT	700
	ACACAAGCAG	GTACCGAAGT	TTCCGCTTTA	CTTGGTAGAA	TGCCATCTGC	750
	TGTTGGCTAT	CAACCCACAC	TAGCAACTGA	AATGGGGCAA	CTGCAAGAAC	800
	GGATTACGTC	AACGGATAAG	GG			822

35

2) INFORMATION FOR SEQ ID NO: 1866

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 818 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Campylobacter fetus* subsp. *fetus*
 (B) STRAIN: ATCC 25936

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1866

ATCTCCTCAG	GATCKATAGG	ACTTGATATA	GCTCTTGGA	TAGGCGGCGT	50
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	ACCAAAAGGA	AGAATAGTCG	AAATTTATGG	GCCAGAAAGC	TCTGGTAAAA	100
	CAACTCTTAC	TTTGCATTTA	ATAGCAGAAT	CTCAAAAAGT	CGGCGGAGTT	150
	TGCGCGTTTG	TAGATGCAGA	GCATGCACTT	GATGTTAAAT	ATGCTAAAAA	200
	TTTAGGCGTT	GATACGGATA	ACTTATATAT	TTCTCAACCG	GACTTCGGAG	250
5	AGCAAGCTCT	TGATATAGTA	GAAACTCTAG	CTAGAAGCGG	CGCCGTTGAT	300
	CTTATAGTAA	TAGATAGCGT	AGCAGCTYTA	ACACCAAAAA	GCGAAATAGA	350
	AGGCGATATG	GGAGATCAGC	ACGTAGGGCT	GCAAGCAAGA	CTCATGAGTC	400
	AAGCACTTAG	AAAATTAACC	GGAGTTGTCC	ATAAAATGGG	AACTACAGTT	450
	GTATTTATAA	ACCAAATTCG	TATGAAAATC	GGCGCTATGG	GCTATGGCAC	500
10	TCCTGAAACT	ACTACTGGCG	GAAATGCGCT	TAAATTTTAC	GCTTCAGTTA	550
	GACTTGACGT	ACGTAAAATA	GCTACTTTAA	AACAGAGCGA	TGAGCCAATC	600
	GGAAACCGCG	TAAAAGTAAA	AGTAGTAAAA	AACAAAGTCG	CTCCTCCTTT	650
	TAGACAAGCC	GAATTTGATA	TCATGTTTGG	AGAAGGTATC	AGCAAAGAAG	700
	GAGAGATAAT	AGATTACGGC	GTAAAACCTG	ATATTATCGA	TAAAAGCGGC	750
15	GCTTGGTTTA	GCTATGATAA	TTCAAAATTA	GGTCAAGGCA	GAGAAAATC	800
	AAAAGCGTTT	TTAAAAGA				818

20 2) INFORMATION FOR SEQ ID NO: 1867

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 814 bases
 (B) TYPE: Nucleic acid
 25 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

30 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Campylobacter fetus* subsp. *venerealis*
 (B) STRAIN: ATCC 33561

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1867

35	TCTCCTCAGG	ATCKATAGGA	CTTGATATAG	CTCTTGGTAT	AGGCGGCGTA	50
	CCAAAAGGAA	GAATAGTCGA	AATTTATGGG	CCAGAAAGCT	CTGGTAAAC	100
	AACTCTTACT	TTGCATTTAA	TAGCAGAATC	TCAAAAAGTC	GGCGGAGTTT	150
	GCGCGTTTGT	AGATGCAGAG	CATGCACTTG	ATGTTAAATA	TGCTAAAAAT	200
40	TTAGGCGTTG	ATACGGATAA	CTTATATATT	TCTCAACCGG	ACTTCGGAGA	250
	GCAAGCTCTT	GATATAGTAG	AAACTCTAGC	TAGAAGCGGC	GCCGTTGATC	300
	TTATAGTAAT	AGATAGCGTA	GCAGCTYTAA	CACCAAAAAG	CGAAATAGAA	350
	GGCGATATGG	GAGATCAGCA	CGTAGGGCTG	CAAGCAAGAC	TCATGAGTCA	400
	AGCACTTAGA	AAATTAACCG	GAGTTGTCCA	TAAAATGGGA	ACTACAGTTG	450
45	TATTTATAAA	CCAAATTCGT	ATGAAAATCG	GCGCTATGGG	CTATGGCACT	500
	CCTGAAACTA	CTACTGGCGG	AAATGCGCTT	AAATTTTACG	CTTCAGTTAG	550
	ACTTGACGTA	CGTAAAATAG	CTACTTTAAA	ACAGAGCGAT	GAGCCAATCG	600
	GAAACCGCGT	AAAAGTAAAA	GTAGTAAAAA	ACAAAGTCGC	TCCTCCTTTT	650
	AGACAAGCCG	AATTTGATAT	CATGTTTGGG	GAAGGTATCA	GCAAAGAAGG	700
50	AGAGATAATA	GATTACGGCG	TAAAACCTGA	TATTATCGAT	AAAAGCGGCG	750
	CTTGGTTTAG	CTATGATAAT	TCAAAATTAG	GTCAAGGCAG	AGAAAATCA	800
	AAAGCGTTTT	TAAA				814

2) INFORMATION FOR SEQ ID NO: 1868

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 824 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

10

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Campylobacter jejuni jejuni*
 (B) STRAIN: ATCC 33560

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1868

GATAGCATAG GCWCAGGTTT AGTTGGACTT GATCTTGCTT TAGGTATAGG 50
 CGGTGTTCCA AAAGGAAGAA TTATAGAAAT TTATGGGCCT GAAAGTTCAG 100
 GTAAACTAC TCTAACTCTA CACATTATCG CAGAATGCCA AAAAGCAGGT 150
 20 GGGGTTTGTG CTTTATCGA TGCAGAACAT GCACTTGATG TGAAATATGC 200
 TAAAAATTTA GGTGTAAATA CAGATGATTT GTATGTTTCT CAACCTGATT 250
 TTGGAGAGCA AGCCTTAGAA ATTGTAGAAA CTATAGCWAG AAGTGGTGCA 300
 GTAGATCTTA TWGTAGTAGA TAGCGTTGCA GCWCTTACCC CAAAAGCAGA 350
 AATTGAAGGC GATATGGGCG ATCARCATGT AGGACTTCAA GCAAGACTTA 400
 25 TGTCTCAAGC TCTAAGAAAA CTTACAGGTA TAGTTCATAA AATGAATACC 450
 ACAGTAATTT TCATCAACCA AATTCGTATG AAAATCGGTG CTATGGGTTA 500
 TGGTACTCCT GAAACCACAA CAGGTGGAAG TGCATTAAAA TTTTATGCTT 550
 CTGTGCGTTT AGATGTTAGA AAAGTAGCAA CCTTAAAMCA AAACGWAGAM 600
 CCTATAGGAA ACCGCGTTAA AGTAAAAGTA GTTAAAAATA AAGTTGCTCC 650
 30 TCCATTCAGM CAAGCTGAAT TTGATGTGAT GTTTGGAGAG GGTTTAAGCC 700
 GTGAAGGTGA ATTGATCGAT TATGGTGTAA AACTTGATAT CGTAGATAAA 750
 AGTGGTGCGT GGTTTTCTTA TAAAGATAAA AACTTGGAC AAGGTAGAGA 800
 AAATTCAAAA GCTTTCTTAA AAGA 824

35

2) INFORMATION FOR SEQ ID NO: 1869

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 388 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

45 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus avium*
 (B) STRAIN: ATCC 14025

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1869

AGAAAGTTCT GGTAACACAA CGGTTGCACT GCATGCGATT GCAGAAAGTTC 50

AAAAACATGG CGGGACGGCA GCCTTTATTG ATGCCGAGCA CGCGTTGGAC 100
 CCTCAATACG CACAACGTCT AGGTGTAAAC ATTGATGAAT TGCTGCTATC 150
 ACAACCAGAT ACTGGGGAAC AAGGCTTAGA AATTGCAGAT GCTTTAGTTT 200
 CAAGTGGCGC AGTCGATATT ATCGTTATTG ACTCGGTGGC CGCGCTAGTC 250
 5 CCCC GTGCTG AAATCGATGG CGAGATGGGT GATGCGCACG TTGGTCTGCA 300
 GGCTCGTTTG ATGTCACAAG CATTGCGCAA GCTGTCAGGC TCTATCAACA 350
 AAACAAAGAC TATCGCCGTC TTTATTAACC AAATTCGT 388

10

2) INFORMATION FOR SEQ ID NO: 1870

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 388 bases
 15 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

20

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus faecium*
 (B) STRAIN: ATCC 19434

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1870

TGAAAGTTCA GGTAAAACAA CAGTTGCACT ACACGCTATT GCAGAAGTAC 50
 AAAAAAATGG CGGAACGGCC GCTTTCATTG ATGCTGAGCA TGCGTTAGAT 100
 CCGCAATATG CACAAAAATT AGGTGTGAAT ATCGATGAAC TACTTCTTTC 150
 30 ACAGCCTGAC ACAGGAGAAC AAGGTCTAGA GATCGCTGAT GCTTTAGTAT 200
 CAAGTGGGGC TGTAGATATC GTAGTAGTCG ATTCAGTTGC TGCTTTAGTT 250
 CCACGAGCAG AAATCGACGG CGAAATGGGT GACTCACATG TCGGGTTACA 300
 AGCACGTTTG ATGTCTCAAG CATTGCGTAA ACTCTCTGGT TCGATCAACA 350
 AAACAAAAC AATCGCTATT TTCATCAACC AAATCCGT 388
 35

2) INFORMATION FOR SEQ ID NO: 1871

10 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 388 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 15 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Listeria monocytogenes*
 50 (B) STRAIN: ATCC 15313

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1871

AGAGAGTTCC GGTAAAACAA CTGTTGCGCT TCATGCAATT GCGGAAGTAC 50
 AAGCACAAGG CGGAACAGCA GCATTTATCG ATGCTGAGCA TCGGTTGGAT 100
 CCGGCTTATG CTAAAAACCT AGGTGTAAAT ATTGATGAAT TATTACTATC 150
 TCAACCAGAT ACAGGAGAAC AAGCTTTAGA GATTGCTGAA GCTTTAGTTA 200
 5 GAAGTGGTGC AGTTGATATG TTAGTAATTG ACTCCGTTGC AGCACTTGTA 250
 CCACGTGCTG AAATCGAAGG CGAGATGGGC GATGCTCATG TTGGATTACA 300
 AGCACGTTTA ATGTCCCAAG CATTGCGTAA ACTTTCTGGT GTTATTAATA 350
 AATCAAAAAC CATTGCTATT TTCATTAACC AAATTCGT 388

10

2) INFORMATION FOR SEQ ID NO: 1872

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 388 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

20 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus mitis*
 (B) STRAIN: ATCC 49456

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1872

AGAGTCATCT GGTAAGACAA CGGTTGCCCT TCATGCAGTT GCGCAAGCAC 50
 AAAAAGAAGG TGGTATTGCT GCCTTTATCG ATGCGGAACA TGCCCTTGAT 100
 30 CCAGCTTATG CTGCGGCCCT TGGTGTCAAC ATTGACGAAT TGCTCTTGTC 150
 ACAACCAGAC TCAGGAGAGC AAGGTCTTGA GATTGCAGGA AAATTGATTG 200
 ACTCAGGAGC CGTGGATCTT GTCGTAGTCG ACTCAGTTGC GGCCCTTGTC 250
 CCTCGTGCGG AAATTGATGG AGATATCGGT GATAGCCACG TTGGTTTGCA 300
 GGCTCGTATG ATGAGCCAGG CTATGCGTAA ACTTGGTGCT TCTATCAATA 350
 35 AAACCAAAAAC AATTGCCATC TTTATCAACC AATTGCGT 388

2) INFORMATION FOR SEQ ID NO: 1873

40

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 430 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 45 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 50 (A) ORGANISM: *Streptococcus oralis*
 (B) STRAIN: ATCC 35037

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1873

```

GAACATGACG CCGACTTTTT CACGCAATTG GTTGATAAAG ATGGCAATTG      50
TTTTGGTTTT ATTGATAGAA GCTCCGAGTT TACGCATGGC CTGGCTCATC      100
ATTCGAGCCT GCAAACCAAC GTGACTGTCT CCAATATCCC CATCAATTTT      150
5  CGCACGAGGT ACAAGGGCCG CAACTGAGTC GATAACGACA AGGTCAACTG      200
CACCTGAGTC AATCAATTTT CCAGCAATTT CAAGACCTTG TTCACCTGAG      250
TCTGGTTGTG ACAAGAGCAA TTCGTCAATA TTCACACCAA GGGCTGCAGC      300
ATAGGCTGGG TCAAGAGCAT GTTCCGCATC GATAAAGGCT GCAATACCAC      350
CTTCTTTCTG TGCTTGCGCA ACAGCGTGAA GGGCAACCGT TGTCTTACCA      400
10 GATGATTCTG GCGCRTACAY TTCGATGATA      430

```

2) INFORMATION FOR SEQ ID NO: 1874

15

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 947 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 20 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 25 (A) ORGANISM: *Aspergillus fumigatus*
 (B) STRAIN: ATCC 64746

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1874

```

30 TTGTCGTTGT TGCTGCCTCC GACGGTCAGA TGTAGGTGGA ACATCTTGGG      50
AAATACGTCG TAAAACACGT CGCTTACGTT TTCGCGAATA GGCCCCAGAC      100
TCGTGAGCAT TTGCTGCTCG CCCGCCAGGT TGGTGTCCAG AAGATCGTTG      150
TCTTCGTCAA CAAATCGAT GCTATTGATG ATCCGGAGAT GCTGGAAGTG      200
GTCGAACTCG AGATGCGTGA GCTGCTGAAC AGCTACGGTT TCGAGGGTGA      250
35 AGAGACTCCG ATCATTTTCG GTTCCGCTCT CTGTGCTCTC GAAGGACGCC      300
GTGACGACAT CGGTAAAGAC AGAATTGAGC AGCTTATGAA CGCTGTGCGAC      350
ACCTGGATCC CCACTCCTCA GCGTGACCTC GACAAACCTT TCTTGATGTC      400
TGTCGAGGAA GTGTTCTCTA TCGCCGGCCG TGGTACCGTG GCTTCTGGTC      450
GTGTCGAGCG TGGTATCTTG AAGAAGGACT CTGAGGTTGA GATTGTTGGA      500
10 GGCTCCTTCG AACCCAAGAA GACCAAAGTC ACCGACATTG AAACCTTCAA      550
GAAGAGCTGT GATGAATCGC GTGCTGGTGA CAACTCTGGT CTCCTCCTGC      600
GTGGTATCCG ACGTGAAGAC GTCAAGCGTG GTATGGTCAT TGCTGTTCCC      650
GGCAGCACCA AGGCTCACGA CAAGTTCCTC GTCTCCATGT ACGTCCTGAC      700
CGAGGCGGAG GGTGGTCGTC GTACTGGCTT CGGTGCCAAC TACCGTCCCC      750
15 AAGTCTTCAT CCGTACTGCA GGTAAGTTCC CGCACACCGT GTCCAGATCT      800
TCCGAGAGAT TAGCGATATA TGCTAATGAT TCATCAGACG AGGCTGCTGA      850
CCTCAGCTTC CCTGACGGCG ACCAATCTCG CAGAGTTATG CCTGGTGACA      900
ACGTCGAGAT GATCCTGAAG ACCCACCACC CTGTTGCTGC TGAGGCT      947

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30

2) INFORMATION FOR SEQ ID NO: 1875

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 923 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Aspergillus versicolor*
 (B) STRAIN: WSA-175

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1875

```

15  GCTGCTTCCG ATGGTCAAAT GTACGTCAAC CTTATATACA CCCTCTGATA      50
    TGACAGAATG TCGCCTAACA GCACGCGTGA ACTAGGCCCC AAACCCGTGA      100
    GCACTTGCTG CTTGCCCCGC AGGTCGGTGT CCAGAAGATT GTTGTGTTCTG      150
    TCAACAAGGT TGATGCCGTC GATGACCTTG AGATGTTGGA ACTTGTTGAG      200
    CTGGAAATGC GTGAGCTTCT CAGCACTTAC GGCTTCGAAG GCGAGGAGAC      250
20  CCCTATCATC TTCGGTTCCG CCCTATGCGC CCTCGAGGGT CGCCGCCCCG      300
    ATATCGGTAC TGAGCGAATT GACAGCCTTC TTGAGGCCGT TGACACCTGG      350
    ATCCCTACCC CTCAGCGTGA CCTGGACAAG CCTTTCCTGA TGTCTGTCGA      400
    GGAGGTCTTC TCCATTGCCG GTCGTGGTAC CGTTGCCTCT GGCCGTGTTG      450
    AGCGTGGTCT CCTTAAGAAG GACAGCGAGG TCGAGATTCT CGGAGGTGGT      500
25  CAGGTCATGA AGACCAAGGT CACTGACATT GAGACATTCA AGAAGCACTG      550
    TGACGAATCC CGTGCTGGTG ACAACTCCGG TCTTCTTCTC CGTGGTATCC      600
    GCCGTGAGGA TGTCAAGCGC GGTATGGTTA TTGCTGCTCC CGCCTCTATC      650
    AAGGCCCAACA AGAAGTTCAT GGTCTCCATG TACGTCCTCA CTGAGGCAGA      700
    AGGTGGCCGT CGCAGTGGCT TCGGTGTCAA CTATCGTCCC CAGGCTTACA      750
30  TTCGCACTGC TGGTAAGTTT TCAAACATT CGACCTCTCG CCTTAGAAGA      800
    AGAATACCTC TAACTTGAT TTAGACGAGG CTTGCGACCT TTCTTTCCCC      850
    GATGGCGACA TGAGCCGCCG TGTCATGCCT GGTGACAACG TGGAAATGAT      900
    CCTCAACCTC AACAACCCTG TCG                                923
  
```

35

2) INFORMATION FOR SEQ ID NO: 1876

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 807 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Basidiobolus ranarum*
 (B) STRAIN: ATCC 24670

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1876

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CATCATTGTT GTGTCCGCCA CTGATGGTCA AATGCCTCAA ACTCGTGAGC      50
  
```

	ATTTGTTGTT	GGCTCGCCAA	GTTGGTGTCC	AACACTTGGT	TGTCTTCATC	100
	AACAAGGTTG	ATGCCGTTGA	TGATCCTGAA	ATGTTGGAGT	TGGTCGAGAT	150
	GGAAATGCGT	GATTTGCTTT	CCCAATACGG	TTTCCCCGGA	GACAACGTCC	200
	CCATTATCCA	GGGTTCCGCT	CTCTGCGCTC	TTGAGGACCG	CAACCCCGAG	250
5	ATCGGCCGTA	ACGCCATCAT	GAAGTTGATG	GAGGCTGTTG	ATAGCAGCAT	300
	CCCCACCCCT	GCCCGTGATT	TGGACAAACC	TTTCCTCATG	CCCGTTGAAG	350
	ATGTGTTCTC	CATCTCTGGC	CGTGGTACTG	TTGCCACTGG	ACGTGTTGAG	400
	CGTGGTATGG	TCACCAAGGG	TACTGAAGTT	GAAATCGTCG	GTATGGGCGA	450
	GCACTTCAAG	ACCACCTTGA	CCGGTATTGA	AATGTTCCAC	AAGGAATTGG	500
10	ACAAGGGTAT	GGCTGGTGAC	AACATGGGTT	GCTTGCTTCG	TGGTGTCAAG	550
	CGTGAGCAAG	TCCGTCGTGG	TATGGTTATC	TGTGCCCCCG	GATCCGTCAA	600
	GCCACATAAG	AAGTTCATGG	CTCAGCTCTA	CATTCTCACC	AAGGATGAGG	650
	GAGGCCGCCA	CACTCCCTTC	GTCAACAAC	ACCGCCCACA	AATGTTCTTC	700
	AGAACTGTTG	ATGTTACCGC	CATCCTTAAG	CACCCCCCTG	GTACCCCCGA	750
15	TGCTGATGAG	AAGATGGTCA	TGCCCCGAGA	CAACGTTCAA	CTCGAGTGCG	800
	AGCTCTT					807

20 2) INFORMATION FOR SEQ ID NO: 1877

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 806 bases
 (B) TYPE: Nucleic acid
 25 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

30 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Campylobacter gracilis*
 (B) STRAIN: ATCC 33236

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1877

35	AGTTGTTTCT	GCTGCGGATG	GTCCTATGCC	TCAAACTCGC	GAGCATATCT	50
	TGCTTTCCTCG	TCAAGTAGGC	GTTCCATACA	TCGTAGTTTT	CCTAAACAAA	100
	ACCGATATGG	TCGATGATCC	GGATCTTTTA	GAGTTAGTTG	AAGAGGAAGT	150
	TAGAGATCTT	TTAAAAGAGT	ATAAATTCCC	TGGCGACGAA	ACCCCAATCA	200
10	TTAAGGGTTC	TGCTCTTAAG	GCTCTTGAGG	AAGCTAAGGC	CGGACAAGAC	250
	GGCGAATGGT	CTGCAAAGAT	TATGGAGCTT	ATGGACGCGG	TTGATAGCTA	300
	TATTCCAACT	CCTGTTCGCG	ATACTGATAA	AGATTTCCCT	CTTCCGATCG	350
	AAGATATTTT	CTCGATTTCC	GGTCGCGGTA	CCGTTGTAAC	CGGTAGAATC	400
	GAAAAAGGTA	TCGTTAAAGT	TGGTGATACT	ATCGAGATCG	TAGGTATTAA	450
15	ACCTACTCAG	ACTACTACCG	TCACTGGCGT	TGAGATGTTT	AGAAAAGAGA	500
	TGGATCAAGG	TGAAGCCGGC	GATAATGTAG	GTGTTTTATT	GCGCGGTACT	550
	AAGAAAGAGG	AAGTAGAGCG	CGGTATGGTT	TTATGCAAAC	CAAATCGAT	600
	CACTCCTCAT	ACTAAATTG	AGGGCGAGGT	TTATATCCTA	ACTAAAGAAG	650
	AAGGCGGACG	CCATACTCCA	TTCTTTAATA	ATTATAGACC	GCAGTTTTAC	700
30	GTTCGTACGA	CAGATGTTAC	CGGTTTCGATT	ACTCTTCCTG	AAGGAACCGA	750
	GATGGTTATG	CCGGGCGACA	ACGTTAAAAT	CACCGTTGAG	CTAATCGCTC	800
	CGATCG					806

2) INFORMATION FOR SEQ ID NO: 1878

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 806 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

10 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Campylobacter jejuni jejuni*
 (B) STRAIN: ATCC 33292

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1878

	GCTGCAGATG	GCCCTATGCC	ACAAACTAGA	GAGCACATTC	TTCTTTCTCG	50
	TCAAGTAGGC	GTTCCATATA	TTGTTGTTTT	TATGAATAAA	GCAGATATGG	100
	TTGATGATGC	TGAACTTTTA	GAGTTAGTTG	AAATGGAAAT	TAGAGAATTA	150
20	TTAAGCTCTT	ATGATTTCCC	AGGCGATGAT	ACACCTATTA	TTTCTGGTTC	200
	TGCTTTAAAA	GCTCTTGAAG	AAGCTAAAGC	TGGACAAGAT	GGTGAATGGT	250
	CAGCAAAAAT	TATGGATCTT	ATGGCTGCAG	TTGATAGCTA	TATTCCAAC	300
	CCAACCTCGT	G	ATACTGAAAA	AGACTTCTTG	ATGCCAATTG	350
	CTCAATTTCA	GGTCGTGGTA	CTGTTGTTAC	AGGTAGAATT	GAAAAAGGTG	400
25	TTGTAAAAGT	AGGTGATACT	ATCGAAATCG	TTGGTATTAA	AGATACTCAA	450
	ACAACAAC	TAACAGGTGT	TGAAATGTTC	AGAAAAGAAA	TGGATCAAGG	500
	CGAAGCAGGA	GATAACGTAG	GTGTTCTTCT	TCGTGGTACT	AAAAAAGAAG	550
	AAGTTATCCG	TGGTATGGTT	CTTGCTAAAC	CAAAATCAAT	TACTCCACAC	600
	ACTGACTTCG	AAGCTGAAGT	TTATATCTTA	AATAAAGATG	AAGGTGGTAG	650
30	ACATACTCCA	TTCTTTAACA	ACTATAGACC	ACAGTTTTAT	GTAAGAACAA	700
	CTGATGTTAC	AGGTTTCGATT	AAATTAGCTG	ATGGTGTTGA	AATGGTTATG	750
	CCAGGTGAAA	ATGTGAGAAT	TACTGTAAGC	TTGATCGCTC	CAGTAGCACT	800
	TGAAGA					806

35

2) INFORMATION FOR SEQ ID NO: 1879

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 896 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

45 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Coccidioides immitis*
 (B) STRAIN: WSA-222

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1879

ATGTATGCAA	CCGAGAGCAC	TCCCGGATCT	TGGTTTAAAT	GGCACTAATA	50
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	TAAGACAGGC	CTCAAAC TCG	AGAGCATTTA	CTTCTCGCCC	GTCAGATCGG	100
	TATCCAAAA	ATCGTCGTCT	TCGTGAACAA	GGTTGATGCC	ATCGAGGACA	150
	AAGAGATGTT	GGAGCTTGTT	GAATTGGAGA	TGCGTGAAC T	CCTAACCAGC	200
	TACGGTTTCS	AGGGTGAAGA	AACTCCCATC	ATTTTTGGCT	CTGCTCTCTG	250
5	TGCCCTCSAA	GGAAGACAAC	CCGAGATCGG	TGTTACCAAG	ATTGATGAGC	300
	TCTTGCAGGC	CGTCGACACC	TGGATTCCCA	CTCCTCAGCG	TGAGACTGAC	350
	AAGCCCTTCT	TGATGTCCAT	TGAGGAAGTG	TTCTCTATTT	CCGGACGAGG	400
	AACCGTTGTC	TCCGGCCGTG	TGGAGCGTGG	TATCCTCAAG	AAGGACTCCG	450
	AAGTTGAAAT	TGTCGGCGGT	TCGCCCAGAC	CAATCAAAAC	CAAGGTTACC	500
10	GATATCGAAA	CCTTTAAGAA	GTCTTGCGAC	GAGTCTCGCG	CTGGTGATAA	550
	CTCCGGCTTG	CTCCTACGAG	GCGTTAAGCG	TGAAGATATT	AGCCGTGGCA	600
	TGGTCGTGCG	TGTACCAGGA	AGTGTCAAGG	CCCATACTGA	ATTCTTAGTT	650
	TCGCTTTACG	TCCTCACCAG	AGCTGAGGGT	GGGCGCAAAT	CTGGATTGAG	700
	CAGCAAGTAC	CGCCACAGAG	TGTTCAATCG	CACTGCCGGT	ATGTAATACT	750
15	GTGATAATTT	CGTTGACATG	GTAATGATTG	AATTCTATAG	ACGAAGCGGC	800
	TCAGCTCAGC	TGGCCCGGAG	AAGATCAAGA	CAAGATGGCT	ATGCCAGGAG	850
	ACAATATCGA	AATGATTGTC	ACCACCTTGC	ACCCAGTTGC	CGCCGA	896

20

2) INFORMATION FOR SEQ ID NO: 1880

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 798 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Erwinia amylovora*
 (B) STRAIN: ATCC 14976

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1880

	CTGGTAGTTG	CTGCGACTGA	CGGCCCAATG	CCTCAGACYC	GTGAGCACAT	50
	CCTGCTGGGT	CGCCAGGTTG	GCGTGCCATA	CATCATCGTG	TTCCTGAACA	100
	AATGTGACAT	GGTTGATGAT	GAAGAGCTGC	TGGAGCTGGT	TGAAATGGAA	150
10	GTMCGTGACC	TGCTGTCACA	GTACGACTTC	CCAGGCGACG	ACACGCCAAT	200
	CGTGCRYGGT	TCTGCGCTGA	AAGCGCTGGA	RGGCGAAGCA	GAGTGGGAAG	250
	CGAAGATCAT	CGAACTGGCT	GGCCATCTGG	ATAACTACAT	CCCGGAACCA	300
	GAGCGTGCGA	TTGACAAACC	GTTCTGCTG	CCAATTGAAG	ACGTGTTCTC	350
	CATCTCTGGC	CGTGGTACCG	TTGTTACCGG	TCGTGTAGAG	CGCGGTRTSG	400
15	TTAAAGTGGG	TGAAGAAGTT	GAAATCGTTG	GTATCAAAGA	TACCGTGAAA	450
	TCAACCTGTA	CCGGCGTTGA	GATGTTCCGT	AAGCTGCTGG	ACGAAGGCCG	500
	TGCGGGTGAG	AACTGTGGTA	TCCTGCTGCG	CGGTATCAAG	CGCGAAGATA	550
	TCCAGCGTGG	TCAGGTTCTG	GCGAAGCCAG	GCACCATCAA	GCCACACACC	600
	AAGTTCGAGT	CAGAAAGTTA	TATTCTGTCT	AAAGACGAAG	GCGGCCGTCA	650
30	TACTCCGTTT	TTCAAAGGCT	ACCGTCCACA	GTTCTACTTC	CGTACTACTG	700
	ACGTGACCGG	GACTATCGAA	CTGCCAGAAG	GCGTTGAGAT	GGTGATGCCA	750
	GGCGACAACA	TTCAGATGGT	TGTGACCCTG	ATCCACCCGA	TCGCCATG	798

2) INFORMATION FOR SEQ ID NO: 1881

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 810 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Salmonella choleraesuis* subsp. *choleraesuis*
 serotype Typhimurium
 (B) STRAIN: ATCC 14028
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1881

	ATCCTGGTTG	TTGCTGCGAC	TGACGGYCCG	ATGCCGCAGA	CCCGTGAGCA	50
	CATCCTGCTG	GGTCGTCAGG	TAGGCGTTCC	GTACATCATC	GTGTTCCCTGA	100
20	ACAAATGCGA	CATGGTTGAT	GACGAAGAGC	TGCTGGAAC	GGTTGAAATG	150
	GAAGTTCGYG	AACTGCTGTC	TCAGTACGAC	TTCCCGGGCG	ACGACACTCC	200
	GATCGTTTCG	GGTTCCTGCT	TGAAAGCGCT	GGAAGGCGAC	GCAGAGTGGG	250
	AAGCGAAAAT	CATCGAACTG	GCTGGCTTCC	TGGATTCTTA	CATYCCGGAA	300
	CCAGAGCGTG	CGATTGACAA	GCCGTTCTTG	CTGCCGATCG	AAGACGTATT	350
25	CTCCATCTCC	GGTCGTGGTA	CCGTTGTTAC	CGGTCGTGTA	GARCGCGGTA	400
	TCATCAAAGT	GGGCGAAGAA	GTTGAAATCG	TTGGTATCAA	AGAGACTCAG	450
	AAGTCTACCT	GTAAGGCGCT	TGAAATGTTC	CGCAAAGTGC	TGGACGAAGG	500
	CCGTGCCGGT	GAGAACGTAG	GTGTTCTGCT	GCGTGGTATC	AAACGTGAAG	550
	AAATCGAACG	TGGTCAGGTA	CTGGCTAAGC	CGGGCACCAC	CAAGCCGCAC	600
30	ACCAAGTTTC	AATCTGAAGT	GTACATTCTG	TCCAAAGATG	AAGGCGGCCG	650
	TCATACTCCG	TTCTTCAAAG	GCTACCGTCC	GCAGTTCTAC	TTCCGTACTA	700
	CTGACGTGAC	TGGCACCATC	GAAGTCCCGG	AAGGCGTAGA	GATGGTAATG	750
	CCGGGCGACA	ACATCAAAAT	GGTTGTTACC	CTGATCCACC	CGATCGCGAT	800
	GGACGACGGT					810

2) INFORMATION FOR SEQ ID NO: 1882

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 888 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Staphylococcus cohnii*
 (B) STRAIN: BM10711
 (C) ACCESSION NUMBER : AF015628
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1882

```

      ATGAATTTT  ATTTAGAGGA  GTTTAACTTG  TCTATTCCCG  ATTCAGGTCC      50
      ATACGGTATA  ACTTCATCAG  AAGACGGAAA  GGTATGGTTC  ACACAACATA      100
      AGGCAAACAA  AATCAGCAGT  CTAGATCAGA  GTGGTAGGAT  AAAAGAATTC      150
5     GAAGTTCCTA  CCCCTGATGC  TAAAGTGATG  TGTTTAATTG  TATCTTCACT      200
      TGGAGACATA  TGGTTTACAG  AGAATGGTGC  AAATAAAATC  GGAAAGCTCT      250
      CAAAAAAGG  TGGCTTTACA  GAATATCCAT  TGCCACAGCC  GGATTCTGGT      300
      CCTTACGGAA  TAACGGAAGG  TCTAAATGGC  GATATATGGT  TTACCCAATT      350
      GAATGGAGAT  CGTATAGGAA  AGTTGACAGC  TGATGGGACT  ATTTATGAAT      400
10    ATGATTTGCC  AAATAAGGGA  TCTTATCCTG  CTTTTATTAC  TTTAGGTTTCG      450
      GATAACGCAC  TTTGGTTCAC  GGAGAACCAA  AATAATTCTA  TTGGAAGGAT      500
      TACAAATACA  GGGAAATTAG  AAGAATATCC  TCTACCAACA  AATGCAGCGG      550
      CTCCAGTGGG  TATCACTAGT  GGTAACGATG  GTGCACTCTG  GTTTGTCGAA      600
      ATTATGGGCA  ACAAATAGG  TCGAATCACT  ACAACTGGTG  AGATTAGCGA      650
15    ATATGATATT  CCAACTCCAA  ACGCACGTCC  ACACGCTATA  ACCGCGGGGA      700
      AAAATAGCGA  AATATGGTTT  ACTGAATGGG  GGGCAAATCA  AATCGGCAGA      750
      ATTACAAACG  ACAAACAAT  TCAAGAATAT  CAACTTCAA  CAGAAAATGC      800
      GGAACCTCAT  GGTATTACCT  TTGGAAAAGA  TGGATCCGTA  TGGTTTGCAT      850
      TAAAATGTAA  AATTGGGAAG  CTGAATTTGA  ACGAATGA      888
20

```

2) INFORMATION FOR SEQ ID NO: 1883

25 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

30

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1883

35 AGCCGCTTGA GCAAATTAAA CTA

23

2) INFORMATION FOR SEQ ID NO: 1884

40

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

45

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1884

50

GTATCCCGCA GATAAATCAC CAC

23

2) INFORMATION FOR SEQ ID NO: 1885

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 21 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1885

AGCGAAAAAC ACCTTGCCGA C

21

15

2) INFORMATION FOR SEQ ID NO: 1886

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 18 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

25 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1886

GACGCCCCGCG CCACCACT

18

30

2) INFORMATION FOR SEQ ID NO: 1887

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 19 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

40

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1887

45 GACGCCCCGCG ACACCACTA

19

2) INFORMATION FOR SEQ ID NO: 1888

50

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 bases
(B) TYPE: Nucleic acid

- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1888

GACGCCCCGCA ACACCACTA

19

10

2) INFORMATION FOR SEQ ID NO: 1889

(i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1889

GTTTCGCAACT GCAGCTGCTG

20

25

2) INFORMATION FOR SEQ ID NO: 1890

(i) SEQUENCE CHARACTERISTICS:

30

- (A) LENGTH: 19 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1890

TTCGCAACGG CAGCTGCTG

19

40

2) INFORMATION FOR SEQ ID NO: 1891

(i) SEQUENCE CHARACTERISTICS:

45

- (A) LENGTH: 18 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1891

CCGGAGCTGC CGAICGGG

18

5

2) INFORMATION FOR SEQ ID NO: 1892

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 18 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

15 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1892

CGGAGCTGCC AARCGGGG

18

20

2) INFORMATION FOR SEQ ID NO: 1893

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 18 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

30

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1893

35 GGAGCTGGCG ARCGGGGT

18

2) INFORMATION FOR SEQ ID NO: 1894

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 18 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
45 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1894

50

GACCGGAGCT AGCGARCG

18

2) INFORMATION FOR SEQ ID NO: 1895

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 19 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

10 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1895

CGGAGCTAGC AARCGGGGT 19
15

2) INFORMATION FOR SEQ ID NO: 1896

20 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

25 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1896

GAAACGGAAC TGAATGAGGC G 21
30

2) INFORMATION FOR SEQ ID NO: 1897

35 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

40 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1897

CATTACCATG GGCGATAACA G 21
45

50 2) INFORMATION FOR SEQ ID NO: 1898

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases

- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

5 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1898

CCATTACCAT GAGCGATAAC AG

22

2) INFORMATION FOR SEQ ID NO: 1899

15 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 861 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Klebsiella pneumoniae*
- (B) STRAIN: 15571
- (C) ACCESSION NUMBER: AF124984

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1899

30	ATGCGTTATA TTCGCCTGTG TATTATCTCC CTGTTAGCCA CCCTGCCGCT	50
	GGCGGTACAC GCCAGCCCGC AGCCGCTTGA GCAAATTAAA CTAAGCGAAA	100
	GCCAGCTGTC GGGCCGCGTA GGCATGATAG AAATGGATCT GGCCAGCGGC	150
	CGCACGCTGA CCGCCTGGCG CGCCGATGAA CGCTTTCCCA TGATGAGCAC	200
	CTTTAAAGTA GTGCTCTGCG GCGCAGTGCT GGCGCGGGTG GATGCCGGTG	250
35	ACGAACAGCT GGAGCGAAAG ATCCACTATC GCCAGCAGGA TCTGGTGGAC	300
	TACTCGCCCG TCAGCGAAAA ACACCTTGCC GACGGCATGA CGGTCGGCGA	350
	ACTCTGCGCC GCCGCCATTA CCATGAGCGA TAACAGCGCC GCCAATCTGC	400
	TACTGGCCAC CGTCGGCGGC CCCGCAAGAT TGA CTGCCTT TTTGCGCCAG	450
	ATCGGCGACA ACGTCACCCG CCTTGACCGC TGGGAAACGG AACTGAATGA	500
40	GGCGCTTCCC GGCAGCGCCC GCGACACCAC TACCCCGGCC AGCATGGCCG	550
	CGACCCTGCG CAAGCTGCTG ACCAGCCAGC GTCTGAGCGC CCGTTCGCAA	600
	CGGCAGCTGC TGCAGTGGAT GGTGGACGAT CGGGTCGCCG GACCGTTGAT	650
	CCGCTCCGTG CTGCCGGCGG GCTGGTTTAT CGCCGATAAG ACCGGAGCTG	700
	GCGAGCGGGG TGC GCGCGGG ATTGTCGCC TGCTTGGCC GAATAACAAA	750
45	GCAGAGCGCA TTGTGGTGAT TTATCTGCGG GATACCCCGG CGAGCATGGC	800
	CGAGCGAAAT CAGCAAATCG CCGGGATCGG CGCGGCGCTG ATCGAGCACT	850
	GGCAACGCTA A	861

50

2) INFORMATION FOR SEQ ID NO: 1900

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 780 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

5

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Klebsiella pneumoniae*
- (B) STRAIN: SLK-47
- (C) ACCESSION NUMBER: Y11069

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1900

```

15 CTGTTAGCCA CCCTGCCGCT GCGGTACAC GCCAGCCCGC AGCCGCTTGA      50
   GCAAATTAAA CTAAGCGAAA GCCAGCTGTC GGGCCGCGTA GGCATGATAG      100
   AAATGGATCT GGCCAGCGGC CGCACGCTGA CCGCCTGGCG CGCCGATGAA      150
   CGCTTTCCCA TGATGAGCAC CTTTAAAGTA GTGCTCTGCG GCGCAGTGCT      200
   GCGCGGGTG GATGCCGGTG ACGAACAGCT GGAGCGAAAG ATCCACTATC      250
20 GCCAGCAGGA TCTGGTGGAC TACTCGCCGG TCAGCGAAAA ACACCTTGCC      300
   GACGGCATGA CGGTCGGCGA ACTCTGCGCC GCCGCCATTA CCATGAGCGA      350
   TAACAGCGCC GCCAATCTGC TACTGGCCAC CGTCGGCGGC CCCGCAGGAT      400
   TGA CTGCTT TTTGCGCCAG ATCGGCGACA ACGTCACCCG CCTTGACCGC      450
   TGGGAAACGG AACTGAATGA GCGGCTTCCC GCGACGCCC GCGCCACCAC      500
25 TACCCCGGCC AGCATGGCCG CGACCCTGCG CAAGCTGCTG ACCAGCCAGC      550
   GTCTGAGCGC CCGTTCGCAA CGGCAGCTGC TGCAGTGGAT GGTGGACGAT      600
   CGGGTCGCCG GACCGTTGAT CCGCTCCGTG CTGCCGGCGG GCTGGTTTAT      650
   CGCCGATAAG ACCGGAGCTG GCGAGCGGGG TCGCGCGGGG ATTGTCGCCC      700
   TGCTTGCCCC GAATAACAAA GCAGAGCGCA TTGTGGTGAT TTATCTGCGG      750
30 GATACCCCGG CGAGCATGGC CGAGCGAAAT      780

```

2) INFORMATION FOR SEQ ID NO: 1901

35

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 861 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

40

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Escherichia coli*
- (C) ACCESSION NUMBER: U92041

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1901

```

50 ATGCGTTATA TTCGCCTGTG TATTATCTCC CTGTTAGCCA CCCTGCCGCT      50
   GCGGTACAC GCCAGCCCGC AGCCGCTTGA GCAAATTAAA CTAAGCGAAA      100
   GCCAGCTGTC GGGCCGCGTA GGCATGATAG AAATGGATCT GGCCAGCGGC      150
   CGCACGCTGA CCGCCTGGCG CGCCGATGAA CGCTTTCCCA TGATGAGCAC      200

```

CTTTAAAGTA GTGCTCTGCG GCGCAGTGCT GGCGCGGGTG GATGCCGGTG 250
 ACGAACAGCT GGAGCGAAAG ATCCACTATC GCCAGCAGGA TCTGGTGGAC 300
 TACTCGCCGG TCAGCGAAAA ACACCTTGCC GACGGCATGA CGGTCGGCGA 350
 ACTCTGCGCC GCCGCCATTA CCATGAGCGA TAACAGCGCC GCCAATCTGC 400
 5 TACTGGCCAC CGTCGGCGGC CCCGCAGGAT TGA CTGCCTT TTTGCGCCAG 450
 ATCGGCGACA ACGTCACCCG CCTTGACCGC TGGGAAACGG AACTGAATGA 500
 GGCCTTCCC GGCACGCCC GCAACACCAC TACCCCGGCC AGCATGGCCG 550
 CGACCCTGCG CAAGCTGCTG ACCAGCCAGC GTCTGAGCGC CCGTTCGCAA 600
 CGGCAGCTGC TGCAGTGGAT GGTGGACGAT CGGGTCGCCG GACCGTTGAT 650
 10 CCGCTCCGTG CTGCCGGCGG GCTGGTTTAT CGCCGATAAG ACCGGAGCTG - 700
 GCGAGCGGGG TGCGCGCGGG ATTGTGCCCC TGCTTGGCCC GAATAACAAA 750
 GCAGAGCGCA TTGTGGTGAT TTATCTGCGG GATACCCCGG CGAGCATGGC 800
 CGAGCGAAAT CAGCAAATCG CCGGGATCGG CGCGGCGCTG ATCGAGCACT 850
 GGCAACGCTA A 861
 15

2) INFORMATION FOR SEQ ID NO: 1902

20 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 861 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

25

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Klebsiella pneumoniae*
 30 (B) STRAIN: 803
 (C) ACCESSION NUMBER: AF164577

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1902

35 ATGCGTTATA TTCGCCTGTG TATTATCTCC CTGTTAGCCA CCCTGCCGCT 50
 GGCGGTACAC GCCAGCCCGC AGCCGCTTGA GCAAATTAAA CAAAGCGAAA 100
 GCCAGCTGTC GGGCCGCGTA GGCATGATAG AAATGGATCT GGCCAGCGGC 150
 CGCACGCTGA CCGCCTGGCG CGCCGATGAA CGCTTTCCCA TGATGAGCAC 200
 CTTTAAAGTA GTGCTCTGCG GCGCAGTGCT GGCGCGGGTG GATGCCGGTG 250
 40 ACGAACAGCT GGAGCGAAAG ATCCACTATC GCCAGCAGGA TCTGGTGGAC 300
 TACTCGCCGG TCAGCGAAAA ACACCTTGCC GACGGCATGA CGGTCGGCGA 350
 ACTCTGCGCC GCCGCCATTA CCATGAGCGA TAACAGCGCC GCCAATCTGC 400
 TGCTGGCCAC CGTCGGCGGC CCCGCAGGAT TGA CTGCCTT TTTGCGCCAG 450
 ATCGGCGACA ACGTCACCCG CCTTGACCGC TGGGAAACGG AACTGAATGA 500
 45 GGCCTTCCC GGCACGCCC GCGACACCAC TACCCCGGCC AGCATGGCCG 550
 CGACCCTGCG CAAGCTGCTG ACCAGCCAGC GTCTGAGCGC CCGTTCGCAA 600
 CGGCAGCTGC TGCAGTGGAT GGTGGACGAT CGGGTCGCCG GACCGTTGAT 650
 CCGCTCCGTG CTGCCGGCGG GCTGGTTTAT CGCCGATAAG ACCGGAGCTG 700
 CCGAGCGGGG TGCGCGCGGG ATTGTGCCCC TGCTTGGCCC GAATAACAAA 750
 50 GCAGAGCGCA TTGTGGTGAT TTATCTGCGG GATACGCCGG CGAGCATGGC 800
 CGAGCGAAAT CAGCAAATCG CCGGGATCGG CGCGGCGCTG ATCGAGCACT 850
 GGCAACGCTA A 861

2) INFORMATION FOR SEQ ID NO: 1903

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 896 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

10

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Klebsiella pneumoniae*
 (B) STRAIN: ATCC 700603
 (C) ACCESSION NUMBER: AF132290

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1903

ATGCGTTATT TTCGCCTGTG TATTATCTCC CTGTTAGCCA CCCTGCCGCT 50
 GGCGGTACAC GCCAGCCCGC AGCCGCTTGA GCAAATTAAA CTAAGCGAAA 100
 20 GCCAGCTGTC GGGCAGCGTA GGCATGATAG AAATGGATCT GGCCAGCGGC 150
 CGCACGCTGA CCGCCTGGCG CGCCGATGAA CGCTTTCCCA TGATGAGCAC 200
 CTTTAAAGTA GTGCTCTGCG GCGCAGTGCT GGCGCGGGTG GATGCCGGTG 250
 ACGAACAGCT GGAGCGAAAG ATCCACTATC GCCAGCAGGA TCTGGTGGAC 300
 TACTCGCCGG TCAGCGAAAA ACACCTTGCC GACGGCATGA CGGTCGGCGA 350
 25 ACTCTGTGCC GCCGCCATTA CCATGAGCGA TAACAGCGCC GCCAATCTGC 400
 TGCTGGCCAC CGTCGGCGGC CCCGCAGGAT TGA CTGCCTT TTTGCGCCAG 450
 ATCGGCGACA ACGTCACCCG CCTTGACCGC TGGGAAACGG AACTGAATGA 500
 GGCGCTTCCC GGCGACGCC GCGACACCAC TACCCCGGCC AGCATGGCCG 550
 CGACCCGTGC CAAGCTGCTG ACCAGCCAGC GTCTGAGCGC CCGTTCGCAA 600
 30 CGGCAGCTGC TGCAGTGGAT GGTGGACGAT CGGGTCGCCG GACCGTTGAT 650
 CCGCTCCGTG CTGCCGGCGG GCTGGTTTAT CGCCGATAAG ACCGGAGCTG 700
 CCAAACGGGG TGCGCGCGGG ATTGTCGCCC TGCTTGGCCC GAATAACAAA 750
 GCAGAGCGGA TTGTGGTGAT TTATCTGCGG GATACGCCGG CGAGCATGGC 800
 CGAGCGAAAT CAGCAAATCG CCGGGATCGG CGCGGCGCTG ATCGAGCACT 850
 35 GGCAACGCTA ACCCGGCGGT GGCCGCGCGC GTTATCCGGC TCGTAG 896

2) INFORMATION FOR SEQ ID NO: 1904

40

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 861 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 45 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 50 (A) ORGANISM: *Escherichia coli*
 (B) STRAIN: JC2926
 (C) ACCESSION NUMBER: AF148851

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1904

	ATGCGTTATA	TTCGCCTGTG	TATTATCTCC	CTGTTAGCCA	CCCTGCCGCT	50
	GGCGGTACAC	GCCAGCCCGC	AGCCGCTTGA	GCAAATTAAA	CTAAGCGAAA	100
5	GCCAGCTGTC	GGGCCGCGTA	GGCATGATAG	AAATGGATCT	GGCCAGCGGC	150
	CGCACGCTGA	CCGCCTGGCG	CGCCGATGAA	CGCTTTCCCA	TGATGAGCAC	200
	CTTTAAAGTA	GTGCTCTGCG	GCGCAGTGCT	GGCGCGGGTG	GATGCCGGTG	250
	ACGAACAGCT	GGAGCGAAAG	ATCCACTATC	GCCAGCAGGA	TCTGGTGGAC	300
	TACTCGCCGG	TCAGCGAAAA	ACACCTTGCC	GACGGCATGA	CGGTCGGCGA	350
10	ACTCTGCGCC	GCCGCCATTA	CCATGAGCGA	TAACAGCGCC	GCCAATCTGC	400
	TACTGGCCAC	CGTCGGCGGC	CCCGCAGGAT	TGACTGCCTT	TTTGCGCCAG	450
	ATCGGCGACA	ACGTCACCCG	CCTTGACCGC	TGGGAAACGG	AACTGAATGA	500
	GGCGCTTCCC	GGCGACGCCC	GCGACACCAC	TACCCCGGCC	AGCATGGCCG	550
	CGACCCTGCG	CAAGCTGCTG	ACCAGCCAGC	GTCTGAGCGC	CCGTTGCGAA	600
15	CGGCAGCTGC	TGCAGTGGAT	GGTGGACGAT	CGGGTCGCCG	GACCGTTGAT	650
	CCGCTCCGTG	CTGCCGGCGG	GCTGGTTTAT	CGCCGATAAG	ACCGGAGCTA	700
	GCGAGCGGGG	TGCGCGCGGG	ATTGTGCCCC	TGCTTGCCCC	GAATAACAAA	750
	GCAGAGCGCA	TTGTGGTGAT	TTATCTGCGG	GATACCCCGG	CGAGCATGGC	800
	CGAGCGAAAT	CAGCAAATCG	CCGGGATCGG	CGCGGCGCTG	ATCGAGCACT	850
20	GGCAACGCTA	A				861

2) INFORMATION FOR SEQ ID NO: 1905

25

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 861 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

30

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

35

- (A) ORGANISM: *Pseudomonas aeruginosa*
- (C) ACCESSION NUMBER: AF096930

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1905

40	ATGCGTTATA	TTCGCCTGTG	TATTATCTCC	CTGTTAGCCA	CCCTGCCGCT	50
	GGCGGTACAC	GCCAGCCCGC	AGCCGCTTGA	GCAAATTAAA	CTAAGCGAAA	100
	GCCAGCTGTC	GGGCCGCGTA	GGCATGATAG	AAATGGATCT	GGCCAGCGGC	150
	CGCACGCTGA	CCGCCTGGCG	CGCCGATGAA	CGCTTTCCCA	TGATGAGCAC	200
	CTTTAAAGTA	GTGCTCTGCG	GCGCAGTGCT	GGCGCGGGTG	GATGCCGGTG	250
45	ACGAACAGCT	GGAGCGAAAG	ATCCACTATC	GCCAGCAGGA	TCTGGTGGAC	300
	TACTCGCCGG	TCAGCGAAAA	ACACCTTGCC	GACGGCATGA	CGGTCGGCGA	350
	ACTCTGCGCC	GCCGCCATTA	CCATGAGCGA	TAACAGCGCC	GCCAATCTAC	400
	TACTGGCCAC	CGTCGGCGGC	CCCGCAGGAT	TGACTGCCTT	TTTGCGCCAG	450
	ATCGGCGACA	ACGTCACCCG	CCTTGACCGC	TGGGAAACGG	AACTGAATGA	500
50	GGCGCTTCCC	GGCGACGCCC	GCGACACCAC	TACCCCGGCC	AGCATGGCCG	550
	CGACCCTGCG	CAAGCTGCTG	ACCAGCCAGC	GTCTGAGCGC	CCGTTGCGAA	600
	CGGCAGCTGC	TGCAGTGGAT	GGTGGACGAT	CGGGTCGCCG	GACCGTTGAT	650
	CCGCTCCGTG	CTGCCGGCGG	GCTGGTTTAT	CGCCGATAAG	ACCGGAGCTA	700

GCAAACGGGG	TGCGCGCGGG	ATTGTCGCCC	TGCTTGGCCC	GAATAACAAA	750
GCAGAGCGCA	TTGTGGTGAT	TTATCTGCGG	GATACGCCGG	CGAGCATGGC	800
CGAGCGAAAT	CAGCAAATCG	CCGGGATCGG	CGCGGCGCTG	ATCGAGCACT	850
GGCAACGCTA	A				861

5

2) INFORMATION FOR SEQ ID NO: 1906

- 10 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 20 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

15

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1906

20 CCTTATTCCC TTTTTTGCGG

20

2) INFORMATION FOR SEQ ID NO: 1907

25

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 22 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

30

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1907

35

CACCTATCTC AGCGATCTGT CT

22

40 2) INFORMATION FOR SEQ ID NO: 1908

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 23 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

45

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1908

50

AACAGCGGTA AGATCCTTGA GAG

23

2) INFORMATION FOR SEQ ID NO: 1909

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 22 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1909

ATGACTTGGT TAAGTACTCA CC

22

15

2) INFORMATION FOR SEQ ID NO: 1910

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 22 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

25 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1910

ATGACTTGGT TGAGTACTCA CC

22

30

2) INFORMATION FOR SEQ ID NO: 1911

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 22 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

40

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1911

45 CCATAACCAT GGGTGATAAC AC

22

50

2) INFORMATION FOR SEQ ID NO: 1912

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
(B) TYPE: Nucleic acid

1000

- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1912

CCATAACCAT GAGTGATAAC AC

22

10

2) INFORMATION FOR SEQ ID NO: 1913

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

15

20

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1913

CGCCTTGATC ATTGGAACC

20

25

2) INFORMATION FOR SEQ ID NO: 1914

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

30

35

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1914

40 CGCCTTGATC GTTGAACC

20

45

2) INFORMATION FOR SEQ ID NO: 1915

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1915

CGCCTTGATA GTTGGGAACC

20

5

2) INFORMATION FOR SEQ ID NO: 1916

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

15 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1916

CGTGGGTCTT GCGGTATCAT

20

20

2) INFORMATION FOR SEQ ID NO: 1917

25 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

30

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1917

35 CGTGGGTCTG GCGGTATCAT

20

2) INFORMATION FOR SEQ ID NO: 1918

40 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

45

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1918

50

GTGGGTCTCA CGGTATCATT G

21

2) INFORMATION FOR SEQ ID NO: 1919

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 21 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1919

CGTGGGTCTC TCGGTATCAT T

21

15

2) INFORMATION FOR SEQ ID NO: 1920

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

25 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1920

CGTGGNTCTC GCGGTATCAT

20

30

2) INFORMATION FOR SEQ ID NO: 1921

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 21 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

40

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1921

45 CGTGGGTCTA GCGGTATCAT T

21

2) INFORMATION FOR SEQ ID NO: 1922

50

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases
(B) TYPE: Nucleic acid

- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1922

GTTTTCCAAT GATTAGCACT TTTA

24

10

2) INFORMATION FOR SEQ ID NO: 1923

(i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 24 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1923

GTTTTCCAAT GATAAGCACT TTTA

24

25

2) INFORMATION FOR SEQ ID NO: 1924

(i) SEQUENCE CHARACTERISTICS:

30

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1924

GTTTTCCAAT GCTGAGCACT TTT

23

40

2) INFORMATION FOR SEQ ID NO: 1925

45

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1925

CGTTTTCCAA TGATGAGCAC TTT

23

5

2) INFORMATION FOR SEQ ID NO: 1926

(i) SEQUENCE CHARACTERISTICS:

10 (A) LENGTH: 23 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

15 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1926

GTTTTCCAAT GGTGAGCACT TTT

23

20

2) INFORMATION FOR SEQ ID NO: 1927

25 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 861 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

30

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

35 (A) ORGANISM: *Neisseria meningitidis*
(B) STRAIN: MC9690-129
(C) ACCESSION NUMBER: AF126482

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1927

40 ATGAGTATTC AACATTTTCG TGTCGCCCTT ATTCCCTTTT TTGCGGCATT 50
TTGCCTTCCT GTTTTTGCTC ACCCAGAAAC GCTGGTGAAA GTAAAAGATG 100
CTGAAGATCA GTTGGGTGCA CGAGTGCGGT ACATCGAACT GGATCTCAAC 150
AGCGGTAAGA TCCTTGAGAG TTTTCGCCCC GAAGAACGTT TTCCAATGAT 200
GAGCACTTTT AAAGTTCTGC TATGTGGTGC GGTATTATCC CGTGTTGACG 250
45 CCGGGCAAGA GCAACTCGGT CGCCGCATAC ACTATTCTCA GAATGACTTG 300
GTTGAGTACT CACCAGTCAC AGAAAAGCAT CTTACGGATG GCATGACAGT 350
AAGAGAATTA TGCAGTGCTG CCATAACCAT GAGTGATAAC ACTGCTGCCA 400
ACTTACTTCT GACAACGATC GGAGGACCGA AGGAGCTAAC CGCTTTTTTG 450
CACAAATGTT GGGATCATGT AACTCGCCTT GATCGTTGGG AACCGGAGCT 500
50 GAATGAAGCC ATACCAAACG ACGAGCGTGA CACCACGATG CCTGCAGCAA 550
TGGCAACAAC GTTGCGCAAA CTATTAAGTG GCGAACTACT TACTCTAGCT 600
TCCCGGCAAC AATTAATAGA CTGGATGGAG GCGGATAAAG TTGCAGGACC 650
ACTTCTGCGC TCGGCCCTTC CGGCTGGCTG GTTTATTGCT GATAAATCTG 700

GAGCCGGTGA	GCGTGGGTCT	CGCGGTATCA	TTGCAGCACT	GGGGCCAGAT	750
GGTAAGCCCT	CCCGTATCGT	AGTTATCTAC	ACGACGGGGA	GTCAGGCAAC	800
TATGGATGAA	CGAAATAGAC	AGATCGCTGA	GATAGGTGCC	TCACTGATTA	850
AGCATTGGTA	A				861

5

2) INFORMATION FOR SEQ ID NO: 1928

10 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 861 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

15

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Escherichia coli*
- (B) STRAIN: HB251
- (C) ACCESSION NUMBER: X57972

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1928

25	ATGAGTATTC	AACATTTCCG	TGTCGCCCTT	ATTCCCTTTT	TTGCGGCATT	50
	TTGCCTTCCT	GTTTTTGCTC	ACCCAGAAAC	GCTGGTGAAA	GTAAAAGATG	100
	CTGAAGATCA	GTTGGGTGCA	CGAGTGGGTT	ACATCGAACT	GGATCTCAAC	150
	AGCGGTAAGA	TCCTTGAGAG	TTTTCGCCCC	GAAGAACGTT	TTCCAATGAT	200
	GAGCACTTTT	AAAGTTCTGC	TATGTGGCGC	GGTATTATCC	CGTGTTGACG	250
30	CCGGGCAAGA	GCAACTCGGT	CGCCGCATAC	ACTATTCTCA	GAATGACTTG	300
	GTTAAGTACT	CACCAGTCAC	AGAAAAGCAT	CTTACGGATG	GCATGACAGT	350
	AAGAGAATTA	TGCAGTGCTG	CCATAACCAT	GAGTGATAAC	ACTGCGGCCA	400
	ACTTACTTCT	GACAACGATC	GGAGGACCGA	AGGAGCTAAC	CGCTTTTTTG	450
	CACAACATGG	GGGATCATGT	AACTCGCCTT	GATCATTGGG	AACCGGAGCT	500
35	GAATGAAGCC	ATACCAAACG	ACGAGCGTGA	CACCACGATG	CCTGCAGCAA	550
	TGGCAACAAC	GTTGCGCAAA	CTATTAAGTG	GCGAACTACT	TACTCTAGCT	600
	TCCCGGCAAC	AATTAATAGA	CTGGATGGAG	GCGGATAAAG	TTGCAGGACC	650
	ACTTCTGCGC	TCGGCCCTTC	CGGCTGGCTG	GTTTATTGCT	GATAAATCTG	700
	GAGCCGGTGA	GCGTGGGTCT	CGCGGTATCA	TTGCAGCACT	GGGGCCAGAT	750
40	GGTAAGCCCT	CCCGTATCGT	AGTTATCTAC	ACGACGGGGA	GTCAGGCAAC	800
	TATGGATGAA	CGAAATAGAC	AGATCGCTGA	GATAGGTGCC	TCACTGATTA	850
	AGCATTGGTA	A				861

45

2) INFORMATION FOR SEQ ID NO: 1929

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 808 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 5 (A) ORGANISM: *Klebsiella oxytoca*
 (B) STRAIN: 26W
 (C) ACCESSION NUMBER: U09188

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1929

```

10 - ATGAGTATTC AACATTTCCG TGTCGCCCTT ATTCCCTTTT TTGCGGCATT      50
      TTGCCTTCCT GTTTTTGCTC ACCCAGAAAC GCTGGTGAAA GTAAAAGATG      100
      CTGAAGATCA GTTGGGTGCA CGAGTGGGTT ACATCGAGCT GGATCTCAAC      150
      AGCGGTAAGA TCCTTGAGAG TTTTCGCCCC GAAGAACGTT TTCCAATGAT      200
      GAGCACTTTT AAAGTTCTGC TATGTGGTGC GGTATTATCC CGTGTTGACG      250
15  CCGGGCAAGA GCAACTCGGT CGCCGCATAC ACTATTCTCA GAATGACTTG      300
      GTTGAGTACT CACCAGTCAC AGAAAAGCAT CTTACGGATG GCATGACAGT      350
      AAGAGAATTA TGCAGTGCTG CCATAACCAT GAGTGATAAC ACTGCGGCCA      400
      ACTTACTTCT GACAACGATC GGAGGACCGA AGGAGCTAAC CGCTTTTTTG      450
      CACAACATGG GGGATCATGT AACCCGCCTT GATAGTTGGG AACCGGAGCT      500
20  GAATGAAGCC ATACCAAACG ACGAGCGTGA CACCACGATG CCTGCAGCAA      550
      TGGCAACAAC GTTGCGCAAA CTATTAAGTG GCGAACTACT TACTCTAGCT      600
      TCCCGGCAAC AATTAATAGA CTGGATGGAG GCGGATAAAG TTGCAGGACC      650
      ACTTCTGCGC TCGGCCCTTC CGGCTGGCTG GTTTATTGCT GATAAATCTG      700
      GAGCCGGTAA GCGTGGATCT CGCGGTATCA TTGCAGCACT GGGGCCAGAT      750
25  GGTAAGCCCT CCCGTATCGT AGTTATCTAC ACGACGGGGA GTCAGGCAAC      800
      TATGGATG
  
```

30 2) INFORMATION FOR SEQ ID NO: 1930

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 861 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

40 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Escherichia coli*
 (C) ACCESSION NUMBER: AF190692

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1930

```

45  ATGAGTATTC AACATTTTCG TGTCGCCCTT ATTCCCTTTT TTGCGGCATT      50
      TTGCCTTCCT GTTTTTGCTC ACCCAGAAAC GCTGGTGAAA GTAAAAGATG      100
      CTGAAGATCA GTTGGGTGCA CGAGTGGGTT ACATCGAACT GGATCTCAAC      150
      AGCGGTAAGA TCCTTGAGAG TTTTCGCCCC GAAGAACGTT TTCCAATGAT      200
50  GAGCACTTTT AAAGTTCTGC TATGTGGCGC GGTATTATCC CGTGTTGACG      250
      CCGGGCAAGA GCAACTCGGT CGCCGCATAC ACTATTCTCA GAATGACTTG      300
      GTTGAGTACT CACCAGTCAC AGAAAAGCAT CTTACGGATG GCATGACAGT      350
      AAGAGAATTA TGCAGTGCTG CCATAACCAT GAGTGATAAC ACTGCTGCCA      400
  
```

	ACTTACTTCT	GACAACGATC	GGAGGACCGA	AGGAGCTAAC	CGCTTTTTTTG	450
	CACAACATGG	GGGATCATGT	AACTCGCCTT	GATCGTTGGG	AACCGGAGCT	500
	GAATGAAGCC	ATACCAAACG	ACGAGCGTGA	CACCACGATG	CCTGCAGCAA	550
	TGGCAACAAC	GTTGCGCAAA	CTATTAAGT	GCGAACTACT	TACTCTAGCT	600
5	TCCCGGCAAC	AATTAATAGA	CTGGATGGAG	GCGGATAAAG	TTGCAGGACC	650
	ACTTCTGCGC	TCGGCCCTTC	CGGCTGGCTG	GTTTATTGCT	GATAAATCTG	700
	GAGCCGGTGA	GCGTGGGTCT	GGCGGTATCA	TTGCAGCACT	GGGGCCAGAT	750
	GGTAAGCCCT	CCCGTATCGT	AGTTATCTAC	ACGACGGGGA	GTCAGGCAAC	800
	TATGGATGAA	CGAAATAGAC	AGATCGCTGA	GATAGGTGCC	TACTGATTA	850
10	AGCATTGGTA	A				861

2) INFORMATION FOR SEQ ID NO: 1931

15

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 861 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

25

- (A) ORGANISM: *Escherichia coli*
- (B) STRAIN: BM2728
- (C) ACCESSION NUMBER: AF104442

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1931

30

	ATGAGTATTC	AACATTTCCG	TGTCGCCCTT	ATTCCCTTTT	TTGCGGCATT	50
	TTGCCTTCCT	GTTTTTGCTC	ACCCAGAAAC	GCTGGTGAAA	GTAAAAGATG	100
	CTGAAGATCA	GTTGGGTGCA	CGAGTGGGTT	ACATCGAACT	GGATCTCAAC	150
	AGCGGTAAGA	TCCTTGAGAG	TTTTCGCCCC	GAAGAACGTT	TTCCAATGAT	200
35	GAGCACTTTT	AAAGTTCTGC	TATGTGGCGC	GGTATTATCC	CGTGTTGACG	250
	CCGGGCAAGA	GCAACTCGGT	CGCCGCATAC	ACTATTCTCA	GAATGACTTG	300
	GTTGAGTACT	CACCAGTCAC	AGAAAAGCAT	CTTACGGATG	GCATGACAGT	350
	AAGAGAATTA	TGCAGTGCTG	CCATAACCAT	GAGTGATAAC	ACTGCGGCCA	400
	ACTTACTTCT	GACAACGATC	GGAGGACCGA	AGGAGCTAAC	CGCTTTTTTTG	450
40	CACAACATGG	GGGATCATGT	AACTCGCCTT	GATCGTTGGG	AACCGGAGCT	500
	GAATGAAGCC	ATACCAAACG	ACGAGCGTGA	CACCACGATG	CCTGCAGCAA	550
	TGGCAACAAC	GTTGCGCAAA	CTATTAAGT	GCGAACTACT	TACTCTAGCT	600
	TCCCGGCAAC	AATTAATAGA	CTGGATGGAG	GCGGATAAAG	TTGCAGGACC	650
	ACTTCTGCGC	TCGGCCCTTC	CGGCTGGCTG	GTTTATTGCT	GATAAATCTG	700
45	GAGCCGGTGA	GCGTGGGTCT	CTCGGTATCA	TTGCAGCACT	GGGGCCAGAT	750
	GGTAAGCCCT	CCCGTATCGT	AGTTATCTAC	ACGACGGGGA	GTCAGGCAAC	800
	TATGGATGAA	CGAAATAGAC	AGATCGCTGA	GATAGGTGCC	TACTGATTA	850
	AGCATTGGTA	A				861

50

2) INFORMATION FOR SEQ ID NO: 1932

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 861 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
5 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 10 (A) ORGANISM: *Escherichia coli*
(C) ACCESSION NUMBER: AF190695

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1932

15 ATGAGTATTC AACATTTTCG TGTCGCCCTT ATTCCCTTTT TTGCGGCATT 50
TTGCCTTCCT GTTTTGTCTC ACCCAGAAAC GCTGGTGAAA GTAAAAGATG 100
CTGAAGATCA GTTGGGTGCA CGAGTGGGTT ACATCGAACT GGATCTCAAC 150
AGCGGTAAGA TCCTTGAGAG TTTTCGCCCC GAAGAACGTT TTCCAATGCT 200
GAGCACTTTT AAAGTTCTGC TATGTGGTGC GGTATTATCC CGTGTTGACG 250
20 CCGGGCAAGA GCAACTCGGT CGCCGCATAC ACTATTCTCA GAATGACTTG 300
GTTGAGTACT CACCAGTCAC AGAAAAGCAT CTTACGGATG GCATGACAGT 350
AAGAGAATTA TGCAGTGCTG CCATAACCAT GAGTGATAAC ACTGCTGCCA 400
ACTTACTTCT GACAACGATC GGAGGACCGA AGGAGCTAAC CGCTTTTTTG 450
CACAACATGG GGGATCATGT AACTCGCCTT GATCGTTGGG AACCGGAGCT 500
25 GAATGAAGCC ATACCAAACG ACGAGCGTGA CACCACGATG CCTGCAGCAA 550
TGGCAACAAC GTTGCGCAAA CTATTAAGTG GCGAACTACT TACTCTAGCT 600
TCCCGGCAAC AATTAATAGA CTGGATGGAG GCGGATAAAG TTGCAGGACC 650
ACTTCTGCGC TCGGCCCTTC CGGCTGGCTG GTTTATTGCT GATAAATCTG 700
GAGCCGGTGA GCGTGGGTCT AGCGGTATCA TTGCAGCACT GGGGCCAGAT 750
30 GGTAAGCCCT CCCGTATCGT AGTTATCTAC ACGACGGGGA GTCAGGCAAC 800
TATGGATGAA CGAAATAGAC AGATCGCTGA GATAGGTGCC TCACTGATTA 850
AGCATTGGTA A 861

35

2) INFORMATION FOR SEQ ID NO: 1933

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 861 bases
40 (B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

45

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Escherichia coli*
(C) ACCESSION NUMBER: AF190693

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1933

ATGAGTATTC AACATTTCCG TGTCGCCCTT ATTCCCTTTT TTGCGGCATT 50
TTGCCTTCCT GTTTTGTCTC ACCCAGAAAC GCTGGTGAAA GTAAAAGATG 100

CTGAAGATCA GTTGGGTGCA CGAGTGGGTT ACATCGAGCT GGATCTCAAC 150
 AGCGGTAAGA TCCTTGAGAG TTTTCGCCCC GAAGAACGTT TTCCAATGGT 200
 GAGCACTTTT AAAGTTCTGC TATGTGGTGC GGTATTATCC CGTGTTGACG 250
 CCGGGCAAGA GCAACTCGGT CGCCGCATAC ACTATTCTCA GAATGACTTG 300
 5 GTTGAGTACT CACCAGTCAC AGAAAAGCAT CTTACGGATG GCATGACAGT 350
 AAGAGAATTA TGCAGTGCTG CCATAACCAT GAGTGATAAC ACTGCGGCCA 400
 ACTTACTTCT GACAACGATC GGAGGACCGA AGGAGCTAAC CGCTTTTTTG 450
 CACAACATGG GGGATCATGT AACCCGCCCTT GATCGTCGGG AACCGGAGCT 500
 GAATGAAGCC ATACCAAACG ACGAGCGTGA CACCACGATG CCTGCAGCAA 550
 10 TGGCAACAAC GTTGCGCAAA CTATTAAC TGCGAACTACT TACTCTAGCT 600
 TCCCGGCAAC AATTAATAGA CTGGATGGAG GCGGATAAAG TTGCAGGACC 650
 ACTTCTGCGC TCGGCCCTTC CGGCTGGCTG GTTTATTGCT GATAAATCTG 700
 GAGCCGGTGA GCGTGGATCT CGCGGTATCA TTGCAGCACT GGGGCCAGAT 750
 GGTAAGCCCT CCCGTATCGT AGTTATCTAC ACGACGGGGA GTCAGGCAAC 800
 15 TATGGATGAA CGAGATAGAC AGATCGCTGA GATAGGTGCC TCACTGATTA 850
 AGCATTGGTA A 861

20 2) INFORMATION FOR SEQ ID NO: 1934

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 bases
 (B) TYPE: Nucleic acid
 25 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1934

GAACGCCAGC GCGAAATTCA AAAAG

25

35

2) INFORMATION FOR SEQ ID NO: 1935

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 bases
 40 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1935

AGCTCGGCAT ACTTCGACAG G

21

50

2) INFORMATION FOR SEQ ID NO: 1936

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

5

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1936

10

TACCACCCGC ACGGC

15

15 2) INFORMATION FOR SEQ ID NO: 1937

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: DNA

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1937

CGGAGTCGCC GTCGATG

17

30

2) INFORMATION FOR SEQ ID NO: 1938

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 41 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: DNA

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1938

CCGCGCACCA TTGCTTCGTA CACTGAGGAG TCTCCGCGCG G

41

45

2) INFORMATION FOR SEQ ID NO: 1939

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

50

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(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1939

5

CGACCCGGAT GGTAGTATCG ATAATGATCC GCCAGCGGCC GGGTCG

46

10 2) INFORMATION FOR SEQ ID NO: 1940

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 19 bases

(B) TYPE: Nucleic acid

15 (C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1940

GTATCGTTGG TGACGTAAT

19

25

2) INFORMATION FOR SEQ ID NO: 1941

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 18 bases

30 (B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1941

GCAATGGTCC GTTTAAGT

18

40

2) INFORMATION FOR SEQ ID NO: 1942

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 27 bases

45 (B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

50 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1942

GACTGGAACA AAGCCTATAA AAAATCA

27

5 2) INFORMATION FOR SEQ ID NO: 1943

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 bases
- (B) TYPE: Nucleic acid
- 10 (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1943

GCTGGTGGAC GGCCAG

16

20

2) INFORMATION FOR SEQ ID NO: 1944

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 bases
- 25 (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1944

TTTCGCCGCC ATGCGTTAC

19

35

2) INFORMATION FOR SEQ ID NO: 1945

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 17 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

45 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1945

CGGCGACTAC GCGGTAT

17

50

2) INFORMATION FOR SEQ ID NO: 1946

1013

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 17 bases
(B) TYPE: Nucleic acid
5 (C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1946

CGGCGACTTC GCGGTAT

17

15

2) INFORMATION FOR SEQ ID NO: 1947

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 bases
20 (B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

25 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1947

CGGTATACGG CACCATCGT

19

30

2) INFORMATION FOR SEQ ID NO: 1948

- (i) SEQUENCE CHARACTERISTICS:
35 (A) LENGTH: 19 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

40 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1948

GCGGTATACA ACACCATCG

19

45

2) INFORMATION FOR SEQ ID NO: 1949

- 50 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1949

CGGTATACGC CACCATCGT

19

10

2) INFORMATION FOR SEQ ID NO: 1950

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 15 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1950

GGCGACATCG CCTGC

15

25

2) INFORMATION FOR SEQ ID NO: 1951

(i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 17 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

35 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1951

GGCGACAGAG CCTGCTA

17

40

2) INFORMATION FOR SEQ ID NO: 1952

(i) SEQUENCE CHARACTERISTICS:

45 (A) LENGTH: 19 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1952

CCTGCTATGG AGCGATGGT

19

5

2) INFORMATION FOR SEQ ID NO: 1953

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 21 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1953

CGCCTGCTAT AAAGCGATGG T

21

20

2) INFORMATION FOR SEQ ID NO: 1954

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 589 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

30 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Klebsiella pneumoniae* subsp. *pneumoniae*
 (B) STRAIN: ATCC 13883
 35 (C) ACCESSION NUMBER: AF052258

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1954

	ACACCGGTCA ACATTGAGGA AGAGCTTAAG AACTCTTATC TGGATTATGC	50
10	GATGTCGGTC ATTGTTGGCC GTGCGCTGCC GGATGTCCGA GATGGCCTGA	100
	AGCCGGTACA CCGTCGCGTA CTTTACGCCA TGAACGTATT GGGCAATGAC	150
	TGGAACAAAG CCTATAAAAA ATCAGCCCGT GTCGTTGGTG ACGTAATCGG	200
	TAAATACCAC CCGCACGGCG ACTCCGCGGT ATACGACACC ATCGTGCGTA	250
	TGGCGCAGCC GTTCTCGCTG CGTTACATGC TGGTGGACGG CCAGGGTAAC	300
15	TTTGGTTCCA TCGACGGCGA CTCCGCCGCG GCGATGCGTT ATACCGAAAT	350
	TCGTCTGGCG AAAATCGCTC ATGAGCTGAT GGCCGATCTT GAAAAAGAGA	400
	CGGTTCGATT CGTCGACAAC TATGACGGTA CGGAGCGTAT TCCGGACGTC	450
	ATGCCGACCA AAATTCCTAA CCTGCTGGTG AACGGCGCCT CCGGGATCGC	500
	CGTAGGGATG GCCACCAACA TACCGCCACA TAACCTGACG GAAGTGATTA	550
50	ACGGCTGTCT GGCATATGTT GACGATGAAG ACATCAGCA	589

2) INFORMATION FOR SEQ ID NO: 1955

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 38 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1955

CGCGCAACCA TTGCTTCGTA CACTGAGGAG, TCTGCGCG

38

15

2) INFORMATION FOR SEQ ID NO: 1956

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 989 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

25 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Candida inconspicua*
(B) STRAIN: ATCC 16783

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1956

CGGTAAACC ACTTTAACTG CTGCAATCAC CAAAGTTTTA TCTGAAGAAG 50
GTGGTGCAGA TTTCTTAGAT TATTCATCTA TTGATAAAGC ACCAGAAGAG 100
35 AGAGCTAGAG GTATTACCAT TTCTACTGCT CATGTTGAAT ATGAAACTCC 150
AAACAGACAT TATTCACATG TTGATTGTCC AGGTCATCAA GATTATATTA 200
AGAACATGAT TACTGGTGCA GCTCAAATGG ATGGTGCTAT TATTGTTGTT 250
GCAGCTACTG ATGGTCAAAT GCCACAAACT AAGGAACATT TATTATTAGC 300
TAGACAAGTT GGTGTTCAAC ATTTAGTTGT TTTTGTTAAC AAGTGTGATA 350
40 CCGTTGATGA TCCAGAAATG TTRGAATTAG TTGAAATGGA AATGAGAGAA 400
TTATTGACCG AATATGGATT YGATGGTGAT AACACACCAG TTATTATGGG 450
TTCTGCATTA ATGGCATTAG AAGGTAAGAG ACCAGAAAGT GGTAAAGAAT 500
CTATTGTTAA GTTAATGGAA GCTGTTGATA CTTGGATTCC AACTCCACAA 550
AGAGACTTAG AAAAACCATT CTTATTACCA ATTGATGAAG TTTTCTCTAT 600
45 TTCTGGTAGA GGTACTGTTG TTTCTGGTAC TGTTGATAGA GGTACATTAA 650
AGAAGGGTGA AGAAGTTGAA ATTGTTGGTG GTAAAGAAGG TGTTATTAAG 700
ACTACTGTTA CCGGTATTGA AATGTATCAC AAGGAATTAG ATCAAGCACA 750
AGCTGGTGAT ACTCCAGGTA TTTTGTTAAG AGGTGTTAAG AGAGATCAAA 800
TTGCAAGAGG TCAAATTCTT GCAAAGCCAG GWTCTGTTAA GGCATACAAG 850
50 AAGTTCTTAT CATCATTATA CATTTTAACA AAGGAAGAAG GTGGTAGACA 900
TACTCCATTT TCTGAAAATT ACAGACCTCA AATGTACATT AGAACTTCCA 950
ATGTTAATGT TACTTTGAAG TTCCAGAAA CTGAAGAAG 989

2) INFORMATION FOR SEQ ID NO: 1957

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 991 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

- (ii) MOLECULE TYPE: Genomic DNA

10

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Candida utilis*
 (B) STRAIN: ATCC 22023

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1957

	GGTAAGACCA	CCCTTACTGC	CGCCATCACC	AAGTGCCTTG	CTGAGAAGGG	50
	AGGTGCCTCG	TTCTTGGA	ACAGTGCCAT	CGACAAGGCG	CCAGAGGAGA	100
	GAGCAAGAGG	TATCACCATC	TCCACTGCGC	ACGTTGAGTA	TGAAACTGCC	150
20	AACAGACACT	ACTCGCACGT	TGACTGTCCA	GGTCACGCTG	ATTACATCAA	200
	GAACATGATT	ACCGGTGCTG	CGCAGATGGA	CGGTGCTATC	ATTGTCGTTG	250
	CAGCCACTGA	CGGTCAGATG	CCACAGACCA	GAGAACACTT	GTTGCTTGCC	300
	AGACAAGTTG	GTGTCCAGCA	CATTGTTGTC	TTCGTCAACA	AGGTTGACAC	350
	CATCGACGAC	CCTGAGATGC	TTGAGCTTGT	TGAAATGGAG	ATGAGAGAGT	400
25	TGCTTACTTC	GTATGGATTT	GACGGTGATA	ACACCCCAGT	TATCATGGGT	450
	TCTGCTTTGT	GTGCTTTGGA	AGGCCGTGAG	CCAGAGATTG	GTGCTAAGGC	500
	CATTGACAAG	TTGATGGAGG	CCATTGATGA	GTACATCCCA	ACTCCTCAGA	550
	GAGACCTGGA	AAAGCCATTC	YTGATGGGTG	TTGAAGACGT	GTTCTCGATC	600
	TCTGGTAGAG	GTACCGTTGT	CACRGGCCGT	GTTGAGCGTG	GTAACCTGAA	650
30	GAAAGGTGAT	GAAATTGAAC	TTGTTGGCTA	CAACAAGAAC	CCAATCAAGA	700
	CCACCGTCAC	CGGTATCGAA	ATGTTCAAGA	AGGAGTTGGA	ATCTGCCATG	750
	GCTGGTGACA	ACTGTGGTAT	CTTGTTGCGT	GGTATCAAGA	GAGATGACGT	800
	CAAGAGAGGT	ATGGTTGCTG	CTAAGCCAGG	CTCCGTCTCT	GCACACACCA	850
	AGTTCCTCGC	TTCCTTGATC	ATCCTGACRA	AGGAGGAAGG	TGGTCGTCAC	900
35	AGTGCCTTTG	CTGAGAACTA	CAGACCACAG	ATGTTTCATCA	GAACCGGAGA	950
	TGTCACCACC	ATCTTGACAT	GGCCAGAGGA	GCACGCTGAC	C	991

40 2) INFORMATION FOR SEQ ID NO: 1958

(i) SEQUENCE CHARACTERISTICS:

- 45 (A) LENGTH: 985 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

50 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Candida zeylanoides*
 (B) STRAIN: ATCC 7351

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1958

	CGGTAAGACC	ACTTTGACCG	CCGCCATCAC	CAAGGTGTTG	AGCGCCAAAG	50
	GTGGTGCTTC	CTTCTTGAC	TACGGGTCCA	TCGACAGAGC	CCCTGAGGAG	100
5	AGAGCCAGAG	GTATTACTAT	CTCGACTGCC	CACGTTGAGT	ACGAGACCGA	150
	TAAGAGACAC	TACGCCCACG	TTGATTGCCC	TGGTCACGCT	GATTACATCA	200
	AGAACATGAT	CACTGGTGCC	GCCCCAAATG	ACGGTGCCAT	TATTGTCGTT	250
	GCTGCTTCTG	ATGGCCAAAT	GCCGCAGACC	AGAGAGCACT	TGTTGCTTGC	300
	CAGACAGGTT	GGTGTGCAGA	ACTTGGTGTG	GTTTGTTAAC	AAGGTGGACA	350
10	CCATCGACGA	CCCCGAAATG	TTGGAGTTGG	TGGAGATGGA	AATGAGAGAA	400
	TTGTTGACCC	ACTACGGCTT	TGACGGTGAC	AACACCCCTG	TCATCATGGG	450
	TTCGGCGTTG	TGTGCCTTGG	AAGACAGGCA	GCCTGAGATT	GGCGAGCAAG	500
	CCATCATGAA	GTTGTTGGAC	GCTGTCGACG	AGTACATTCC	CACTCCTCAG	550
	AGAGACTTGG	AGCAACCATT	TTTGATGCCC	GTTGAGGATG	TTTTCTCCAT	600
15	CTCTGGCAGA	GGTACTGTTG	TCACCGGTCG	TGTTGAGAGA	GGCTCATTGA	650
	AGAAGGGTGA	GGAGATTGAG	ATTGTTGGCG	ACTTCCCCAA	GCCCTTCAAG	700
	ACTACCGTCA	CCGGCATTGA	GATGTTCAAG	AAGGAGTTGG	ATGCCGCGAT	750
	GGCGGGCGAC	AACGCCGGGA	TCTTGTTGAG	AGGTGTCAAG	AGAGACGAGG	800
	TCTCGAGAGG	TATGGTTTTG	GCCAAGCCCG	GTA CTGTAC	TTCGCACACC	850
20	AAGGTGTTGG	CGTCGCTTTA	CATCTTGACC	AAAGAGGAAG	GTGGCCGCCA	900
	CTCGCCCTTT	GGTGAGAACT	ACAAGCCACA	GTTATTCATC	AGAACCTCCG	950
	ATGTCACTGG	TACTTTGAGG	TTCCCCGCCG	GTGAG		985

25

2) INFORMATION FOR SEQ ID NO: 1959

(i) SEQUENCE CHARACTERISTICS:

- | | |
|----|--------------------------|
| | (A) LENGTH: 973 bases |
| 30 | (B) TYPE: Nucleic acid |
| | (C) STRANDEDNESS: Double |
| | (D) TOPOLOGY: Linear |

(ii) MOLECULE TYPE: Genomic DNA

35

(vi) ORIGINAL SOURCE:

- | | |
|--|---|
| | (A) ORGANISM: <i>Candida catenulata</i> |
| | (B) STRAIN: ATCC 10565 |
| | (C) ACCESSION NUMBER: |

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1959

	CGGTAAGACC	ACCTTGACTG	CCGCCATCAC	CAAGGTTCTC	TCCGAGAAGG	50
	GTGGTGCCGA	CTTCTTGAC	TACGGTGCCA	TTGACAGAGC	CCCCGAGGAG	100
15	CGTGCCCGTG	GTATCACCAT	CTCCACTGCC	CACGTTGAGT	ACGAGACTGA	150
	CAACCGTCAC	TACGCCCACA	TTGACTGTCC	CGGTCACGCT	GATTACATCA	200
	AGAACATGAT	TACCGGTGCC	GCCCAGATGG	ACGGTGCCAT	TATTGTCCTT	250
	GCTGCTACTG	ACGGTGCCAT	GCCCCAGACC	CGCGAGCACT	TGCTTCTCGC	300
	CCGTCAGGTT	GGTATCCAGG	AATTGGTTGT	GTTTGTGAAC	AAGGTTGACA	350
50	CCATCGACGA	CCCCGAGATG	TTGGAGCTCG	TTGAGATGGA	GATCCGCGAG	400
	TTGTTGTCTG	AGTTCGGTTT	TGACGGTGAC	AACACCCCGG	TCATCATGGG	450
	TTCCGCTTTG	TGCGCTTTGG	AGGGCAAGCA	GCCCCGAGATT	GGTGAGCAGG	500
	CTATCACCAA	GTTGATGGCC	GCCGTTGACG	AGCACATCCC	CACCCCCCAG	550

CGTGA CTTGG AGCAGCCTTT CTTGATGCCT GTTGAGGGTG TTTTCTCTAT 600
 CTCTGGCCGT GGTACCGTGG TGA CTTGGTAA GGTGCCCCGT GGTGTCCTCA 650
 AGAAGGGTGA GGAGATTGAG ATTGTTGGCA ACTTTGACAA GCCCTACAAG 700
 GTGACTGTTA CTGGTATTGA GATGTTCAAG AAGGAGTTGG ACCAGGCCAT 750
 5 GGCTGGTGAC AACGCCGGTA TCTTGTTCG TGGTGTCAAG CGTGACGAGG 800
 TGTCTCGTGG TATGGTTTTG GCCAAGCCCC GCACTGTTGT CTCGCACAAG 850
 AAGGTTTTGG CTTCGCTTTA CATCTTGACC CAGGAGGAGG GTGGCCGTAA 900
 GACCGGCTTC GGCTCCAAC ACAAGCCCCA GTTGTTCCTG CGCACTACCG 950
 ACGTCACTGG TACCCTCACC TTC 973
 10

2) INFORMATION FOR SEQ ID NO: 1960

15 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 985 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Candida krusei*
 25 (B) STRAIN: ATCC 28870

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1960

AAGACTACCT TGA CTTGCTGC AATCACCAAG GTCTTAGCTG ATCAAGGTGG 50
 30 TGCTGATTTT TTAGATTATG CATCTATTGA CAAGGCTCCT GAAGAAAGAG 100
 CAAGAGGTAT TACTATCTCT ACTGCTCACG TTGAGTATGA AACCCCAAAC 150
 AGACATTATT CTCATGTCGA TTGTCCTGGC CATCAAGATT ATATTAAGAA 200
 TATGATTACT GGTGCTGCAC AAATGGATGG TGCTATTATT GTTGTGCTG 250
 CTACTGATGG TCAAATGCCA CAACTAAGG AACATTTATT ATTAGCAAGA 300
 35 CAAGTTGGTG TTCAACATTT AGTTGTCTTT GTTAATAAAT GTGACACCAT 350
 TGATGACCCA GAAATGTTGG AATTAGTTGA AATGGAAATG AGAGAACTAT 400
 TGTCTGAATA TGGTTTTGAT GGTGATAACA CTCCAGTTAT TATGGGTTCT 450
 GCATTGATGG CTTTAGAAGA CAAGAGACCT GAAGTTGGTA AGGAATCTAT 500
 TTTAAAGTTA ATGGAAGCYG TTGACACATG GATTCCAACC CCAGAGAGAG 550
 10 ATTTAGAAAA ACCATTTTTG TTACCTATTG ATGAAGTTTT CTCAATCTCT 600
 GGTAGAGGTA CTGTCGTTTC TGGTACTGTC GAAAGAGGTA CTTTGAAGAA 650
 GGGTGAAGAA GTTGAAATTG TTGGTGGTAA GGATGGTTCT ATTAAACTA 700
 CTGTCACAGG TATTGAAATG TATCACAAGG AATTAGACCA AGCGCAAGCA 750
 GGTGATACTC CAGGTATTTT ATTAAGAGGT GTCAAGAGAG ACCAAATCAA 800
 15 GAGAGGTCAA ATTTTAGCAA AGCCAGATTC CGTTAAGGCA TACAAGAAGT 850
 TCTTGGCTTC CCTTTATATC TTAACCAAGG AAGAAGGTGG TAGACATACA 900
 CCATTCTCTG AAAACTACAG ACCACAAATG TACATCAGAA CTACCAATGT 950
 TAACGTTACT TTGAAGTTCC CAGACACTGA AGAAG 985

30

2) INFORMATION FOR SEQ ID NO: 1961

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1961

GCTCAAGGCA GATGGCATTG CC

22

2) INFORMATION FOR SEQ ID NO: 1962

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1962

GGACAAGGCG GTTGCGTTTG AT

22

2) INFORMATION FOR SEQ ID NO: 1963

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1963

CATTCCTGTC TCGCTCGACA GT

22

2) INFORMATION FOR SEQ ID NO: 1964

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1964

5

ATCTGCCTGC CCGTCTTGC

19

10 2) INFORMATION FOR SEQ ID NO: 1965

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 816 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

20 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Plasmid pGS05
(C) ACCESSION NUMBER: M36657

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1965

25

ATGAATAAAT CGCTCATCAT TTTCGGCATC GTCAACATAA CCTCGGACAG 50
TTTCTCCGAT GGAGGCCGGT ATCTGGCGCC AGACGCAGCC ATTGCGCAGG 100
CGCGTAAGCT GATGGCCGAG GGGGCAGATG TGATCGACCT CCGTCCGGCA 150
TCCAGCAATC CCGACGCCGC GCCTGTTTCG TCCGACACAG AAATCGCGCG 200
30 TATCGCGCCG GTGCTGGACG CGCTCAAGGC AGATGGCATT CCCGTCTCGC 250
TCGACAGTTA TCAACCCGCG ACGCAAGCCT ATGCCTTGTC GCGTGGTGTG 300
GCCTATCTCA ATGATATTCG CGGTTTTCCA GACGCTGCGT TCTATCCGCA 350
ATTGGCGAAA TCATCTGCCA AACTCGTCGT TATGCATTCG GTGCAAGACG 400
GGCAGGCAGA TCGGCGCGAG GCACCCGCTG GCGACATCAT GGATCACATT 450
35 GCGGCGTTCT TTGACGCGCG CATCGCGGCG CTGACGGGTG CCGGTATCAA 500
ACGCAACCGC CTTGTCCTTG ATCCCGGCAT GGGGTTTTTT CTGGGGGGCTG 550
CTCCCGAAAC CTCGCTCTCG GTGCTGGCGC GGTTCGATGA ATTGCGGCTG 600
CGCTTCGATT TGCCGGTGCT TCTGTCTGTT TCGCGCAAAT CCTTTCTGCG 650
CGCGCTCACA GGCCGTGGTC CGGGGGATGT CGGGGCCGCG ACACTCGCTG 700
10 CAGAGCTTGC CGCCGCCGCA GGTGGAGCTG ACTTCATCCG CACACACGAG 750
CCGCGCCCCT TGC GCGACGG GCTGGCGGTA TTGGCGGCGC TGAAAGAAAC 800
CGCAAGAATT CGTTAA 816

15

2) INFORMATION FOR SEQ ID NO: 1966

(i) SEQUENCE CHARACTERISTICS:

- 50 (A) LENGTH: 19 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1966

5 CATGCCAGTC TTGCCAACG

19

2) INFORMATION FOR SEQ ID NO: 1967

10

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

15 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1967

20

CAGCAATAAG TAATCCAGCG ATG

23

25 2) INFORMATION FOR SEQ ID NO: 1968

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 bases

(B) TYPE: Nucleic acid

30 (C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1968

GGAGAGATTT CACCGCATAG

20

40

2) INFORMATION FOR SEQ ID NO: 1969

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 bases

45 (B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1969

AGCCAACCAT CATGCTATTC CA

22

2) INFORMATION FOR SEQ ID NO: 1970

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 1206 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Transposon Tn10
 (C) ACCESSION NUMBER: J01830

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1970

	ATGAATAGTT	CGACAAAGAT	CGCATTGGTA	ATTACGTTAC	TCGATGCCAT	50
	GGGGATTGGC	CTTATCATGC	CAGTCTTGCC	AACGTTATTA	CGTGAATTTA	100
	TTGCTTCGGA	AGATATCGCT	AACCACTTTG	GCGTATTGCT	TGCACTTTAT	150
20	GCGTTAATGC	AGGTTATCTT	TGCTCCTTGG	CTTGGAAAAA	TGTCTGACCG	200
	ATTTGGTCGG	CGCCCAGTGC	TGTTGTTGTC	ATTAATAGGC	GCATCGCTGG	250
	ATTACTTATT	GCTGGCTTTT	TCAAGTGCGC	TTTGGATGCT	GTATTTAGGC	300
	CGTTTGCTTT	CAGGGATCAC	AGGAGCTACT	GGGGCTGTCG	CGGCATCGGT	350
	CATTGCCGAT	ACCACCTCAG	CTTCTCAACG	CGTGAAGTGG	TTCGGTTGGT	400
25	TAGGGGCAAG	TTTTGGGCTT	GGTTTAATAG	CGGGGCCTAT	TATTGGTGGT	450
	TTTGCAGGAG	AGATTTCACC	GCATAGTCCC	TTTTTTATCG	CTGCGTTGCT	500
	AAATATTGTC	ACTTTCCTTG	TGGTTATGTT	TTGGTTCCGT	GAAACCAAAA	550
	ATACACGTGA	TAATACAGAT	ACCGAAGTAG	GGGTTGAGAC	GCAATCGAAT	600
	TCGGTATACA	TCACTTTATT	TAAAACGATG	CCCATTTTGT	TGATTATTTA	650
30	TTTTTCAGCG	CAATTGATAG	GCCAAATTCC	CGCAACGGTG	TGGGTGCTAT	700
	TTACCGAAAA	TCGTTTTGGA	TGGAATAGCA	TGATGGTTGG	CTTTTCATTA	750
	GCGGGTCTTG	GTCTTTTACA	CTCAGTATTC	CAAGCCTTTG	TGGCAGGAAG	800
	AATAGCCACT	AAATGGGGCG	AAAAACGGC	AGTACTGCTC	GAATTTATTG	850
	CAGATAGTAG	TGCATTTGCC	TTTTTAGCGT	TTATATCTGA	AGGTTGGTTA	900
35	GATTTCCCTG	TTTTAATTTT	ATTGGCTGGT	GGTGGGATCG	CTTTACCTGC	950
	ATTACAGGGA	GTGATGTCTA	TCCAAACAAA	GAGTCATGAG	CAAGGTGCTT	1000
	TACAGGGATT	ATTGGTGAGC	CTTACCAATG	CAACCGGTGT	TATTGGCCCA	1050
	TTACTGTTTA	CTGTTATTTA	TAATCATTCA	CTACCAATTT	GGGATGGCTG	1100
	GATTTGGATT	ATTGGTTTAG	CGTTTTACTG	TATTATTATC	CTGCTATCGA	1150
40	TGACCTTCAT	GTTAACCCCT	CAAGCTCAGG	GGAGTAAACA	GGAGACAAGT	1200
	GCTTAG					1206

15 2) INFORMATION FOR SEQ ID NO: 1971

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 21 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1971

CYGACTGYGC CATCCTYATC A

21

5

2) INFORMATION FOR SEQ ID NO: 1972

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 21 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

15 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1972

MGICAGCTCA TYITTGCWKS C

21

20

2) INFORMATION FOR SEQ ID NO: 1973

25 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

30

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1973

35 RACACCRGIY TTGGWITCCT T

21

2) INFORMATION FOR SEQ ID NO: 1974

40

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

45

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1974

50

ACAAGGGITG GRMSAAGGAG AC

22

2) INFORMATION FOR SEQ ID NO: 1975

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 21 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1975

TGRCCRGGGT GGTTRAGGAC G

21

15

2) INFORMATION FOR SEQ ID NO: 1976

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 21 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

25 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1976

GATGGAYTCY GTYAAITGGG A

21

30

2) INFORMATION FOR SEQ ID NO: 1977

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 21 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

40

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1977

15 GATGGAYTCY GTYAARTGGG A

21

2) INFORMATION FOR SEQ ID NO: 1978

50

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
(B) TYPE: Nucleic acid

- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1978

CATCITGYAA TGGYAATCTY AAT

23

10

2) INFORMATION FOR SEQ ID NO: 1979

(i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1979

CATCYTGYAA TGGYAASCTY AAT

23

25

2) INFORMATION FOR SEQ ID NO: 1980

(i) SEQUENCE CHARACTERISTICS:

30

- (A) LENGTH: 22 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1980

40

TCRATGGCIT CIAIRAGRGT YT

22

2) INFORMATION FOR SEQ ID NO: 1981

45

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1981

TGGACACCIS CAAGIGGKCY G

21

5

2) INFORMATION FOR SEQ ID NO: 1982

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 21 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

15 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1982

TGGACACYIS CAAGIGGKCY G

21

20

2) INFORMATION FOR SEQ ID NO: 1983

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 21 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

30

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1983

35 CYGAYTGCGC YATICTCATC A

21

2) INFORMATION FOR SEQ ID NO: 1984

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 21 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
45 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1984

50

CYGAYTGYGC YATYCTSATC A

21

2) INFORMATION FOR SEQ ID NO: 1985

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 1383 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

10

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Cryptococcus neoformans*
 (B) STRAIN: M1-106
 (C) ACCESSION NUMBER: U81804

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1985

	ATGGGTAAGG	ACAAGCTGCA	CGTCAACGTC	GTTGTTATCG	GTCACGTCGA	50
	CTCCGGTAAG	TCGACCACCA	CCGGTCACTT	GATCTACAAG	TGCGGTGGTA	100
20	TCGACAAGCG	AACCATTGAG	AAGTTCGAGA	AGGAGGCTCA	AGAGCTCGGA	150
	AAGTCTTCTT	TCAAGTACGC	TTGGGTCTT	GACAAGCTTA	AGGCCGAGCG	200
	AGAGCGAGGT	ATCACCATCG	ACATTGCTCT	TTGGAAGTTC	GAGACCCCTA	250
	AGTACCAGGT	TACCGTCATT	GACGCCCCCG	GTCACCGAGA	CTTCATCAAG	300
	AACATGATCA	CCGGTACCTC	CCAGGCTGAC	TGTGCCATCC	TCATCATTGC	350
25	CACCGGTATC	GGTGAGTTCG	AGGCTGGTAT	CTCCAAGGAC	GGTCAGACCC	400
	GAGAGCACGC	CCTCCTCGCC	TTCACCCTCG	GTGTCAGGCA	GCTCATTGTT	450
	GCTTGCAACA	AGATGGACAC	CTGCAAGTGG	TCTGAGGACC	GATTCAACGA	500
	AATCGTCAAG	GAGACCAACG	GTTTCATCAA	GAAGGTTGGT	TACAACCCCA	550
	AGGCTGTCCC	CTTCGTCCCC	ATCTCTGGTT	GGCACGGTGA	CAACATGTTG	600
30	GAGGAGACCA	CCAACATGCC	CTGGTACAAG	GGATGGACCA	AGGAGACCAA	650
	GTCCGGTGTT	TCCAAGGGTA	AGACCCTTCT	CGAGGCCATC	GACGCCAGTA	700
	GGCCCCCTAC	CCGACCCACC	GACAAGCCCC	TCCGTCTCCC	TCTCCAGGAC	750
	GTCTACAAGA	TCGGTGGTAT	CGGCACAGTC	CCTGTCGGCC	GAGTCGAGAC	800
	CGGTGTCATC	AAGGCCGGTA	TGGTCGTCAA	GTTGCCCCCC	ACCAACGTCA	850
35	CCACTGAAGT	CAAGTCCGTT	GAGATGCACC	ACGAGCAGAT	CCCCGAGGGT	900
	CTCCCCGGAG	ACAACGTTGG	TTTCAACGTC	AAGAACGTTT	CCATCAAGGA	950
	CATCCGACGA	GGTAACGTCT	GTGGTGACTC	CAAGAACGAC	CCCCCTATGG	1000
	AGGCTGCTTC	TTTCAACGCC	CAGGTTATCG	TCCTTAACCA	CCCTGGTCAG	1050
	ATCGGTGCCG	GTTACACCCC	CGTTCTCGAC	TGTCACACTG	CCCACATTGC	1100
40	TTGCAAGTTC	TCTGAGTTGA	TCGAGAAGAT	TGACCGACGA	ACCGGTAAGG	1150
	TCATGGAGGC	CGCCCCCAAG	TTCGTCAAGT	CTGGTGACGC	CGCCATTGTC	1200
	AAGCTTGTTT	CCCAGAAGCC	TCTCTGTGTT	GAGACCTACG	CCGACTACCC	1250
	CCCTCTTGGT	CGATTGCGCG	TCCGAGACAT	GCGACAGACC	GTTGCCGTTG	1300
	GTGTTATTAA	GAGTGTGGAG	AAGTCCGATG	GGAAGAGCGG	CAAGGTTACC	1350
15	AAGGCCGCCG	AGAAGGCTGC	TAAGAAGAAG	TAA		1383

2) INFORMATION FOR SEQ ID NO: 1986

30

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1380 bases
 (B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

5

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Cryptococcus neoformans*

(B) STRAIN: B3501

(C) ACCESSION NUMBER: U81803

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1986

	ATGGGTAAGG	ACAAGCTGCA	CGTCAACGTC	GTTGTTATCG	GTCACGTCGA	50
	CTCCGGTAAG	TCGACCACCA	CCGGTCACTT	GATCTACAAG	TGCGGTGGTA	100
15	TCGACAAGCG	AACCATTGAG	AAGTTCGAGA	AGGAGGCTCA	AGAGCTCGGA	150
	AAGTCTTCTT	TCAAGTACGC	TTGGGTTCTT	GACAAGCTTA	AGGCCGAGCG	200
	AGAGCGAGGT	ATCACCATCG	ACATTGCTCT	TTGGAAGTTC	GAGACCCCCA	250
	GGTACCAGGT	CACCGTCATT	GACGCCCCCG	GTCACCGAGA	CTTCATCAAG	300
	AACATGATCA	CCGGTACCTC	CCAGGCTGAC	TGTGCCATCC	TCATCATTGC	350
20	CACCGGTATC	GGTGAGTTCG	AGGCCGGTAT	CTCCAAGGAC	GGTCAGACCC	400
	GAGAGCACGC	CCTCCTCGCC	TTCACCCTCG	GTGTCAGGCA	GCTCATTGTT	450
	GCTTGCAACA	AGATGGACAC	CTGCAAGTGG	TCCGAGGACC	GATTCAACGA	500
	AATCGTCAAG	GAGACCAACG	GTTTCATCAA	GAAGGTTGGC	TACAACCCCA	550
	AGGCTGTCCC	CTTCGTCCCC	ATCTCTGGTT	GGCACGGTGA	CAACATGTTG	600
25	GAGGAGACCA	CCAACATGCC	CTGGTACAAG	GGATGGACCA	AGGAGACCAA	650
	GTCTGGTGTT	TCCAGGGGTA	AGACCCTTCT	CGAGGCCATC	AGCGCCAGTA	700
	GGCCCCATAC	CCGACCCACC	GACAAGCCCC	TCCGTCTCCC	TCTCCAGGAC	750
	GTCTACAAGA	TCGGTGGTAT	CGGCACAGTC	CCTGTCGGCC	GAGTCGAGAC	800
	CGGTGTCATC	AAGGCCGGTA	TGGTCGTCAA	GTTTCGCCCC	ACCAACGTCA	850
30	CCACTGAAGT	CAAGTCCGTT	GAGATGCACC	ACGAGCAGAT	CCCCGAGGGT	900
	CTTCCCGGAG	ACAACGTTGG	TTTCAACGTC	AAGAACGTTT	CCATCAAGGA	950
	CATCCGACGA	GGTAACGTCT	GTGGTGACTC	CAAGAACGAC	CCCCCTATGG	1000
	AGGCTGCTTC	TTTCAACGCC	CAGGTTATCG	TCCTTAACCA	CCCTGGTCAG	1050
	ATCGGTGCCG	GTTACACCCC	CGTTCTCGAC	TGTCACACTG	CCCACATTGC	1100
35	CTGCAAGTTT	GCTGAGTTGA	TCGAGAAGAT	TGACCGACGA	ACCGGTAAGG	1150
	TCATGGAGGC	CGCCCCCAAG	TTCGTCAAGT	CTGGTGACGC	CGCCATTGTC	1200
	AAGCTTGTTG	CCCAGAAGCC	CCTCTGTGTT	GAGACCTACG	CCGACTACCC	1250
	CCCTCTTGGT	CGATTGCGCG	TCCGAGACAT	GCGACAGACC	GTTGCCGTTG	1300
	GTGTTATCAA	GAGCGTGGAC	AAGACCGAGA	AGGGTGGA	GGTCACCAAG	1350
40	GCTGCTGAGA	AGGCTGCCAA	GAAGAAGTAA			1380

2) INFORMATION FOR SEQ ID NO: 1987

15

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1377 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

50

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Saccharomyces cerevisiae*
 (C) ACCESSION NUMBER: X01638

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1987

```

      ATGGGTAAAG AGAAGTCTCA CATTACGTT GTCGTTATCG GTCATGTCGA      50
      TTCTGGTAAG TCTACCACTA CCGGTCATTT GATTTACAAG TGTGGTGGTA      100
      TTGACAAGAG AACCATCGAA AAGTTCGAAA AGGAAGCCGC TGAATTAGGT      150
10    AAGGGTTCTT TCAAGTACGC TTGGGTTTTG GACAAGTTAA AGGCTGAAAG      200
      AGAAAGAGGT ATCACTATCG ATATTGCTTT GTGGAAGTTC GAAACTCCAA      250
      AGTACCAAGT TACCGTTATT GATGCTCCAG GTCACAGAGA TTTCATCAAG      300
      AACATGATTA CTGGTACTTC TCAAGCTGAC TGTGCTATCT TGATTATTGC      350
      TGGTGGTGTC GGTGAATTCT AAGCCGGTAT CTCTAAGGAT GGTCAAACCA      400
15    GAGAACACGC TTTGTTGGCT TTCACCTTGG GTGTTAGACA ATTGATTGTT      450
      GCTGTCAACA AGATGGACTC CGTCAAATGG GACGAATCCA GATTCCAAGA      500
      AATTGTCAAG GAAACCTCCA ACTTTATCAA GAAGGTTGGT TACAACCCAA      550
      AGACTGTTCC ATTCGTCCCA ATCTCTGGTT GGAACGGTGA CAACATGATT      600
      GAAGCTACCA CCAACGCTCC ATGGTACAAG GGTGCGGAAA AGGAAACCAA      650
20    GGCCGGTGTC GTCAAGGGTA AGACTTTGTT GGAAGCCATT GACGCCATTG      700
      AACCAACCATC TAGACCAACT GACAAGCCAT TGAGATTGCC ATTGCAAGAT      750
      GTTTACAAGA TCGGTGGTAT TGGTACTGTG CCAGTCGGTA GAGTTGAAAC      800
      CGGTGTCATC AAGCCAGGTA TGGTTGTTAC TTTGCCCCCA GCTGGTGTTA      850
      CCACTGAAGT CAAGTCCGTT GAAATGCATC ACGAACAATT GGAACAAGGT      900
25    GTTCCAGGTG ACAACGTTGG TTTCAACGTC AAGAACGTTT CCGTTAAGGA      950
      AATCAGAAGA GGTAACGTCT GTGGTGACGC TAAGAACGAT CCACCAAAGG      1000
      GTTGCGCTTC TTTCAACGCT ACCGTCATTG TTTTGAACCA TCCAGGTCAA      1050
      ATCTCTGCTG GTTACTCTCC AGTTTTGGAT TGTACACTG CTCACATTGC      1100
      TTGTAGATTC GACGAATTGT TGGAAAAGAA CGACAGAAGA TCTGGTAAGA      1150
30    AGTTGGAAGA CCATCCAAAG TTCTTGAAGT CCGGTGACGC TGCTTTGGTC      1200
      AAGTTCGTTT CATCTAAGCC AATGTGTGTT GAAGCTTTCA GTGAATACCC      1250
      ACCATTAGGT AGATTGCTG TCAGAGACAT GAGACAAACT GTCGCTGTCG      1300
      GTGTTATCAA GTCTGTTGAC AAGACTGAAA AGGCCGCTAA GGTACCAAG      1350
      GCTGCTCAAA AGGCTGCTAA GAAATAA      1377
35

```

2) INFORMATION FOR SEQ ID NO: 1988

40 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1377 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

45

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Saccharomyces cerevisiae*
 50 (C) ACCESSION NUMBER: M10992

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1988

	ATGGGTAAG	AGAAGTCTCA	CATTAACGTT	GTCGTTATCG	GTCATGTCGA	50
	TTCTGGTAAG	TCTACCACTA	CCGGTCATTT	GATTTACAAG	TGTGGTGGTA	100
	TTGACAAGAG	AACCATCGAA	AAGTTCGAAA	AGGAAGCCGC	TGAATTAGGT	150
	AAGGGTTCTT	TCAAGTACGC	TTGGGTTTTG	GACAAGTTAA	AGGCTGAAAG	200
5	AGAAAGAGGT	ATCACTATCG	ATATTGCTTT	GTGGAAGTTC	GAAACTCCAA	250
	AGTACCAAGT	TACCGTTATT	GATGCTCCAG	GTCACAGAGA	TTTCATCAAG	300
	AACATGATTA	CTGGTACTTC	TCAAGCTGAC	TGTGCTATCT	TGATTATTGC	350
	TGGTGGTGTC	GGTGAATTCG	AAGCCGGTAT	CTCTAAGGAT	GGTCAAACCA	400
	GAGAACACGC	TTTGTGGCT	TTCACCTTGG	GTGTTAGACA	ATTGATTGTT	450
10	GCTGTCAACA	AGATGGACTC	CGTCAAATGG	GACGAATCCA	GATTCCAAGA	500
	AATTGTCAAG	GAAACCTCCA	ACTTTATCAA	GAAGGTGGT	TACAACCCAA	550
	AGACTGTTCC	ATTCTGTTCC	ATCTCTGGTT	GGAACGGTGA	CAACATGATT	600
	GAAGCTACCA	CCAACGCTCC	ATGGTACAAG	GGTTGGGAAA	AGGAAACCAA	650
	GGCCGGTGTC	GTCAAGGGTA	AGACTTTGTT	GGAAGCCATT	GACGCCATTG	700
15	AACAACCATC	TAGACCAACT	GACAAGCCAT	TGAGATTGCC	ATTGCAAGAT	750
	GTTTACAAGA	TTGGTGGTAT	TGGTACTGTG	CCAGTCGGTA	GAGTTGAAAC	800
	CGGTGTCATC	AAGCCAGGTA	TGGTTGTTAC	TTTTGCCCCA	GCTGGTGTTA	850
	CCACTGAAGT	CAAGTCCGTT	GAAATGCATC	ACGAACAATT	GGAACAAGGT	900
	GTTCCAGGTG	ACAACGTTGG	TTTCAACGTC	AAGAACGTTT	CCGTTAAGGA	950
20	AATCAGAAGA	GGTAACGTCT	GTGGTGACGC	TAAGAACGAT	CCACCAAAGG	1000
	GTTGCGCTTC	TTTCAACGCT	ACCGTCATTG	TTTTGAACCA	TCCAGGTCAA	1050
	ATCTCTGCTG	GTTACTCTCC	AGTTTTGGAT	TGTCACACTG	CTCACATTGC	1100
	TTGTAGATTC	GACGAATTGT	TGGAAAAGAA	CGACAGAAGA	TCTGCTAAGA	1150
	AGTTGGAAGA	CCATCCAAAG	TTCTTGAAGT	CCGGTGACGC	TGCTTTGGTC	1200
25	AAGTTCGTTC	CATCTAAGCC	AATGTGTGTT	GAAGCTTTCA	GTGAATACCC	1250
	ACCATTAGGT	AGATTGCTG	TCAGAGACAT	GAGACAAACT	GTCGCTGTCG	1300
	GTGTTATCAA	GTCTGTTGAC	AAGACTGAAA	AGGCCGCTAA	GGTTACCAAG	1350
	GCTGCTCAAA	AGGCTGCTAA	GAAATAA			1377

30

2) INFORMATION FOR SEQ ID NO: 1989

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 1377 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

40 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Eremothecium gossypii*
 (B) STRAIN: ATCC 10895
 45 (C) ACCESSION NUMBER: X73978

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1989

	ATGGGTAAGG	AAAAGACTCA	CGTTAACGTT	GTCGTCATCG	GTCACGTCGA	50
50	CTCTGGTAAG	TCTACTACCA	CCGGTCACTT	GATCTACAAG	TGTGGTGGTA	100
	TTGACAAGAG	AACCATCGAG	AAGTTCGAGA	AGGAGGCTGC	CGAGTTGGGT	150
	AAGGGTTCTT	TCAAGTACGC	CTGGGTTTTG	GACAAATTGA	AGGCTGAGAG	200
	AGAGAGAGGT	ATCACCATCG	ACATTGCGTT	GTGGAAGTTC	GAGACTCCAA	250

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AGTACCACGT CACTGTCATT GACGCCCCAG GCCACAGAGA CTTTCATCAAG      300
AACATGATTA CCGGTACTTC TCAAGCTGAC TGTGCCATCT TGATCATTTGC      350
TGGTGGTGTC GGTGAGTTCG AGGCTGGTAT CTCCAAGGAC GGTGAGACCA      400
GAGAGCACGC TTTGTTGGCT TACACCTTGG GTGTCAAGCA GTTGATCGTT      450
5  GCCATCAACA AGATGGACTC CGTCAAGTGG GACGAGTCCA GATACCAGGA      500
   GATTGTCAAG GAGACCTCCA ACTTCATCAA GAAGGTCGGT TACAACCCTA      550
   AGACTGTTCC ATTCGTTCCA ATCTCCGGCT GGAACGGTGA CAACATGATT      600
   GAGGCCACCA CCAACGCCCC ATGGTACAAG GGCTGGGAGA AGGAGACCAA      650
   GGCTGGTGCC GTCAAGGGTA AGACCTTGTT GGAGGCCATT GACGCCATTG      700
10 AGCCACCTGT CAGACCAACT GACAAGGCAT TGAGATTGCC ATTGCAGGAT      750
   GTCTACAAGA TCGGTGGTAT TGGTACGGTT CCAGTCGGCA GAGTCGAGAC      800
   CGGTGTCATC AAGCCAGGTA TGGTTGTTAC CTTGCCCCCA TCCGGTGTCA      850
   CCACTGAAGT CAAGTCCGTC GAGATGCACC ACGAGCAATT GGAGGAGGGT      900
   GTCCAGGTG ACAACGTTGG TTTCAACGTC AAGAACGTCT CCGTCAAGGA      950
15 GATCAGAAGA GGTAACGTTT GCGGTGACTC CAAGAACGAC CCACCAAAGG     1000
   CTGCTGAGTC CTTCAACGCT ACCGTCATTG TCTTGAACCA CCCAGGTCAA     1050
   ATCTCTGCCG GTTACTCTCC AGTCTTGAC TGTCACTG CCCACATTGC     1100
   TTGTAAGTTC GACGAGTTGT TGGAGAAGAA CGACAGAAGA ACCGGTAAGA     1150
   AGTTGGAAGA CTCTCCAAAG TTCCTAAAGG CCGGTGACGC TGCCATGGTC     1200
20 AAGTTTGTCC CATCCAAGCC AATGTGTGTT GAGGCTTTCA CCGACTACCC     1250
   ACCATTGGGT AGATTGCTG TCAGAGACAT GAGACAGACC GTTGCTGTGCG     1300
   GTGTCATCAA GTCTGTTGTC AAGTCCGACA AGGCTGGTAA GGTACCAAG      1350
   GCCGCCAAA AGGCTGGTAA GAAATAG      1377

```

25

2) INFORMATION FOR SEQ ID NO: 1990

- (i) SEQUENCE CHARACTERISTICS:
- 30 (A) LENGTH: 1377 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
- 35 (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Eremothecium gossypii*
 (C) ACCESSION NUMBER: A29820
- 40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1990

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ATGGGTAAGG AAAAGACTCA CGTTAACGTT GTCGTCATCG GTCACGTCGA      50
CTCTGGTAAG TCTACTACCA CCGGTCACTT GATCTACAAG TGTGGTGGTA     100
15 TTGACAAGAG AACCATCGAG AAGTTCGAGA AGGAGGCTGC CGAGTTGGGT     150
   AAGGGTTCTT TCAAGTACGC CTGGGTTTTG GACAAATTGA AGGCTGAGAG     200
   AGAGAGAGGT ATCACCATCG ACATTGCGTT GTGGAAGTTC GAGACTCCAA     250
   AGTACCACGT CACTGTCATT GACCCCCCAG GCCACAGAGA CTTTCATCAAG     300
   AACATGATTA CCGGTACTTC TCAAGCTGAC TGTGCCATCT TGATCATTTGC     350
30 TGGTGGTGTC GGTGAGTTCG AGGCTGGTAT CTCCAAGGAC GGTGAGACCA     400
   GAGAGCACGC TTTGTTGGCT TACACCTTGG GTGTCAAGCA GTTGATCGTT     450
   GCCATCAACA AGATGGACTC CGTCAAGTGG GACGAGTCCA GATACCAGGA     500
   GATTGTCAAG GAGACCTCCA ACTTCATCAA GAAGGTCGGT TACAACCCTA     550

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	AGACTGTTCC	ATTCTGTTCCA	ATCTCCGGCT	GGAACGGTGA	CAACATGATT	600
	GAGGCCACCA	CCAACGCCCC	ATGGTACAAG	GGCTGGGAGA	AGGAGACCAA	650
	GGCTGGTGCC	GTCAAGGGTA	AGACCTTGTT	GGAGGCCATT	GACGCCATTG	700
	AGCCACCTGT	CAGACCAACT	GACAAGGCAT	TGAGATTGCC	ATTGCAGGAT	750
5	GTCTACAAGA	TCGGTGGTAT	TGGTACGGTT	CCAGTCGGCA	GAGTCGAGAC	800
	CGGTGTCATC	AAGCCAGGTA	TGGTTGTTAC	CTTCGCCCCA	TCCGGTGTCA	850
	CCACTGAAGT	CAAGTCCGTC	GAGATGCACC	ACGAGCAATT	GGAGGAGGGT	900
	GTCCCAGGTG	ACAACGTTGG	TTTCAACGTC	AAGAACGTCT	CCGTCAAGGA	950
	GATCAGAAGA	GGTAACGTTT	GCGGTGACTC	CAAGAACGAC	CCACCAAAGG	1000
10	CTGCTGAGTC	CTTCAACGCT	ACCGTCATTG	TCTTGAACCA	CCCAGGTCAA	1050
	ATCTCTGCCG	GTTACTCTCC	AGTCTTGAC	TGTCACACTG	CCCACATTGC	1100
	TTGTAAGTTC	GACGAGTTGT	TGGAGAAGAA	CGACAGAAGA	ACCGGTAAGA	1150
	AGTTGGAAGA	CTCTCCAAAG	TTCCTAAAGG	CCGGTGACGC	TGCCATGGTC	1200
	AAGTTTGTCC	CATCCAAGCC	AATGTGTGTT	GAGGCTTTCA	CCGACTACCC	1250
15	ACCATTGGGT	AGATTGCTG	TCAGAGACAT	GAGACAGACC	GTTGCTGTGC	1300
	GTGTCATCAA	GTCTGTTGTC	AAGTCCGACA	AGGCTGGTAA	GGTCACCAAG	1350
	GCCGCCAAA	AGGCTGGTAA	GAAATAG			1377

20

2) INFORMATION FOR SEQ ID NO: 1991

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1646 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Aspergillus oryzae*
- (B) STRAIN: KBN616
- (C) ACCESSION NUMBER: AB007770
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1991

	TGGGGTAAGT	TTATCAACCC	GTCGAGTTGT	GTTGCATCTC	AGATCATGGC	50
	TGACAAGTAC	TTTCCTCCTT	ACAGTAAGGA	AGACAAGCAG	CACATCAACA	100
40	TCGTGCTTAT	CGGCCACGTC	GATTCCGGCA	AGTCCACCAC	CACTGGTCAC	150
	TTGATCTACA	AGTGTGGTGG	TATCGACCAG	CGTACCATCG	AGAAGTTCGA	200
	GAAGGAAGCC	GCTGAGCTCG	GTAAGGGTTC	CTTCAAGTAC	GCCTGGGTTC	250
	TTGACAAGCT	CAAGTCCGAG	CGTGAGCGTG	GTATCACCAT	CGATATCGCC	300
	CTCTGGAAGT	TCCAGACCTC	CAAGTATGAG	GTCACCGTCA	TTGGTAAGCA	350
45	TTTGAGTTCC	AACCTACGTT	GCCCAACATT	TACAGTCATC	TAACAAAGTT	400
	CAATAGATGC	CCCCGGTCAC	CGTGACTTCA	TCAAGAACAT	GATCACTGGT	450
	ACTTCCCAGG	CTGACTGCGC	TATCCTCATC	ATTGCCTCCG	GTAAGTGGTGA	500
	ATTCGAGGCT	GGTATCTCCA	AGGATGGTCA	GACCCGTGAG	CACGCTCTGC	550
	TCGCTTTCAC	CCTCGGTGTC	CGTCAGCTCA	TCGTTGCCCT	CAACAAGATG	600
50	GACACCTGCA	AGTGGTCTCA	GGATCGTTAC	AACGAAATCG	TTAAGGAGAC	650
	TTCCAACCTT	ATCAAGAAGG	TCGGATACAA	CCCCAAGAGC	GTTCCCTTTCG	700
	TCCCCATCTC	CGGTTTCAAC	GGTGACAACA	TGATTGAGGC	CTCCACCAAC	750
	TGCCCCCTGGT	ACAAGGGCTG	GGAGAAGGAG	ACCAAGGCTG	GCAAGTCCAC	800

	CGGTAAGACC	CTTCTCGAGG	CCATCGATGC	CATCGAGCCC	CCCGTCCGTC	850
	CCACCGACAA	GCCTCTCCGT	CTTCCCCTCC	AGGATGTCTA	CAAGATCTCT	900
	GGTATCGGTA	CTGTGCCCCG	CGGTCGTGTC	GAGACTGGTG	TCATCAAGCC	950
	TGGTATGGTC	GTTACTTTCG	CTCCTGCCAA	CGTGACCACT	GAAGTCAAGT	1000
5	CCGTTGAAAT	GCACCACCAG	CAGCTCCAGG	CCGGTAACCC	CGGTGACAAC	1050
	GTTGGTTTCA	ACGTCAAGAA	CGTCTCCGTC	AAGGAAGTCC	GCCGTGGTAA	1100
	CGTTGCCGGT	GACTCCAAGA	ACGACCCCCC	TGCTGGCTGC	GATTCCTTCA	1150
	ACGCCCAGGT	CATCGTCCTT	AACCACCCCG	GTCAGGTCGG	CAACGGTTAC	1200
	GCTCCCGTCC	TGGACTGCCA	CACCGCTCAC	ATTGCTTGCA	AGTTCGCTGA	1250
10	GCTCCTTGAG	AAGATTGACC	GCCGTACCGG	TAAATCTGTT	GAGGACAAGC	1300
	CCAAGTTCAT	CAAGTCTGGT	GATGCTGCCA	TCGTCAAGAT	GATTCCTTCC	1350
	AAGCCCATGT	GTGTGGAGTC	TTTCACTGAC	TTCCCCCCTC	TTGGTCGTTT	1400
	CGCTGTCCGT	GACGTAAGTT	TTTCCCTCTT	GACTATCTTC	ACAATTTTTTC	1450
	ACATATTTTC	ACGCCTCGTC	CCACTCTTTT	TCCTCCCTTC	CTCTTTGGTT	1500
15	CCCCTTTTTG	CCTGCAAGTT	CTCTATAGCT	AACATGATGT	CTAGATGCGT	1550
	CAAACGTGTT	CCGTCGGAGT	TATCAAGTCG	GTTGAGAAGA	ACACTGGCGG	1600
	TTCTGGCAAG	GTCACCAAGG	CCGCCCAGAA	GGCTGGCAAG	AAATAA	1646

20

2) INFORMATION FOR SEQ ID NO: 1992

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1380 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

30

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Aureobasidium pullulans*
- (B) STRAIN: R106
- (C) ACCESSION NUMBER: U19723

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1992

	ATGGGTAAGG	AAAAGTCCCA	CATCAACGTC	GTCGTTATCG	GCCACGTCGA	50
	CTCCGGTAAG	TCGACCACCA	CCGGTCACTT	GATCTACAAG	TGCGGTGGTA	100
40	TCGACAAGCG	TACCATCGAG	AAGTTCGAGA	AGGAAGCCGC	CGAACTCGGC	150
	AAGGGTTCCT	TCAAGTACGC	CTGGGTCCTC	GACAAGCTGA	AGTCTGAGCG	200
	TGAGCGTGGT	ATCACTATCG	ATATCGCTCT	GTGGAAGTTC	GAGACCCCCA	250
	AGTACATGGT	CACCGTCATC	GATGCCCCCG	GTCACCGTGA	TTTCATCAAG	300
	AACATGATCA	CTGGTACCTC	CCAGGCTGAC	TGCGCCATTG	TCATCATTGC	350
45	CGCCGGTACT	GGTGAGTTCG	AGGCTGGTAT	CTCCAAGGAT	GGCCAGACTC	400
	GTGAGCACGC	CCTTCTCGCC	TACACCCTTG	GTGTCAAGCA	GCTCATCGTC	450
	GCTATCAACA	AGATGGACAC	CACCAAGTGG	TCTGAGGCCC	GTTACCAGGA	500
	GATCATCAAG	GAGACCTCCG	GTTTCATCAA	GAAGGTCGGC	TACAACCCCA	550
	AGCACGTTCC	CTTTGTCCCC	ATCTCGGGTT	TCAACGGTGA	CAACATGATT	600
50	GAGGTTTCTT	CCAAC TGCCC	CTGGTACAAG	GGTTGGGAGA	AGGAGACCAA	650
	GGCCAAGGCC	ACTGGTAAGA	CTCTCCTCGA	GGCCATTGAC	GCCATCGACC	700
	CTCCTTCGCG	CCCCACCGAC	AAGCCCCTCC	GTCTTCCCCT	CCAGGATGTC	750
	TACAAGATCG	GTGGTATTGG	CACGGTGCCC	GTCGGCCGTG	TCGAGACCGG	800

	TACCATCAAG	GGTGGTATGG	TCGTACACCTT	CGCCCCCGCT	GGTGTCACCA	850
	CTGAGGTCAA	GTCCGTCGAG	ATGCACCACG	AGCAGCTCTC	CGAGGGTCTC	900
	CCCGGTGACA	ACGTCGGCTT	CAACGTCAAG	AACGTCTCCG	TCAAGGAGAT	950
	CCGTCTGGT	AACGTTGCCG	GTGACTCCAA	GAACGACCCC	CCCAAGGGTT	1000
5	GCGACTCCTT	CAACGCCCAG	GTCATCGTCC	TCAACCACCC	CGGTCAGGTC	1050
	GGTGCTGGTT	ACGCACCCGT	CCTCGATTGC	CACACTGCCC	ACATCGCCTG	1100
	CAAGTTCTCC	GAGCTTGTTG	AGAAGATTGA	CCGCCGTACC	GGCAAGTCCG	1150
	TTGAGGCCGC	CCCCAAGTTC	ATCAAGTCTG	GTGACGCCGC	CATCGTCAAG	1200
	ATGGTTCCCT	CCAAGCCTAT	GTGTGTTGAG	GCCTTCACTG	ACTACCCTCC	1250
10	TCTCGGTCGT	TTCGCCGTCC	GTGACATGAG	ACAGACCGTC	GCTGTCCGGT	1300
	TCATCAAGTC	CGTCGCCAAG	TCCGACAAGC	AGGGTGCCGG	TAAGGTTACC	1350
	AAGGCCGCTG	TCAAGGCTGG	CAAGAAGTAA			1380

15

2) INFORMATION FOR SEQ ID NO: 1993

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1383 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Histoplasma capsulatum*
- (B) STRAIN: 186AS
- (C) ACCESSION NUMBER: U14100

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1993

	ATGGGTAAGG	AAGACAAGAC	TCACATTAAC	CTCGTCGTCA	TCGGCCACGT	50
	CGATTCCGGC	AAATCTACCA	CCACTGGTCA	TTTGATCTAC	AAATGCCGGT	100
35	GTATTGACAG	CCGTACCATT	GAGAAGTTCG	AAAAGGAAGC	CGAAGAGTTG	150
	GGCAAGAAAT	CCTTCAAATA	TGCGTGGGTC	CTTGACAAAC	TGAAGTCTGA	200
	GCGTGAGCGT	GGTATCACCA	TCGATATTGC	CCTCTGGAAA	TTCGAGACTC	250
	CGAAGTACAG	TGTCACTGTC	ATTGATGCTC	CCGGCCATCG	TGACTTCATC	300
	AAGAACATGA	TCACTGGTAC	CTCCAGGCT	GACTGCGCTA	TCCTCATCAT	350
40	TGCTGCCGGT	ACTGGTGAGT	TCGAGGCTGG	TATCTCCAAG	GATGGCCAGA	400
	CTCGTGAGCA	CGCTCTGCTT	GCTTTCACCC	TTGGTGTGAG	GCAACTCATC	450
	GTTGCCATCA	ACAAGATGGA	CACCACCAAG	TGGTCCGAGT	CCCGTTTCAA	500
	CGAAATCATC	AAGGAGGTTT	CCAACCTTCAT	CAAGAAGGTC	GGATATAACC	550
	CCAAGGCTGT	TCCCTTCGTG	CCAATCTCTG	GTTTCGAGGG	TGACAACATG	600
45	ATTGAACCCT	CCCCCAACTG	CACATGGTAC	AAGGGCTGGA	ACAAGGAGAC	650
	TGCCTCTGGC	AAGTCTTCTG	GTAAACCCT	TCTCGATGCC	ATTGACGCCA	700
	TTGAACCCCC	AACCCGTCCT	ACCGATAAGC	CCCTCCGTCT	TCCCCCTCCAG	750
	GATGTGTACA	AAATCTCTGG	TATTGGCACT	GTTCCCGTCG	GACGTGTTGA	800
	GACTGGTGTC	ATCAAGCCCCG	GTATGGTCGT	GACTTTCGCT	CCCTCCAACG	850
50	TCACCACTGA	AGTCAAGTCC	GTCGAAATGC	ACCACCAACA	ACTCCAGGCT	900
	GGTTACCCTG	GCGACAACGT	CGGCTTCAAC	GTCAAGAACG	TTTCAGTCAA	950
	GGAAGTCCGC	CGTGGAACG	TTGCTGGCGA	CTCCAAAAAT	GATCCCCCTA	1000
	AGGGCTGCGA	ATCCTTCAAT	GCCCAGGTCA	TCGTCTTAA	CCACCCCGGC	1050

CAGGTTGGCG CTGGTTATGC CCCAGTCCTC GACTGCCACA CTGCCCACAT 1100
 TGCTTGCAAG TTCTCTGAGC TTATTGAGAA GATCGACCGC CGTACCGGAA 1150
 AGTCTGTTGA GAACAACCCC AAGTTCATCA AGTCTGGTGA TGCTGCTATC 1200
 GTCAAGATGG TTCCCTCCAA GCCCATGTGC GTGGAGCCCT TCACTGACTA 1250
 5 TCCCCCTCTT GGACGTTTCG CTGTCCGTGA CATGAGACAA ACCGTCGCTG 1300
 TCGGTGTCAT CAAGTCCGTC ATCAAGTCTG ACAAGACTGC TGGCAAGGTC 1350
 ACCAAGGCCG CGCAGAAGGC CACCAAGAAA TAA 1383

10

2) INFORMATION FOR SEQ ID NO: 1994

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1383 bases
 - 15 (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Double
 - (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- 20 (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Neurospora crassa*
 - (C) ACCESSION NUMBER: D45837

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1994

ATGGGCAAGG AGGACAAGAC TCACATCAAC GTCGTCGTTA TCGGCCACGT 50
 CGATTCCGGC AAGTCTACCA CTACCGGTCA CTTGATCTAC AAGTGCGGTG 100
 GTATCGACAA GCGTACCATC GAGAAGTTCG AGAAGGAAGC CGCTGAGCTC 150
 30 GGTAAGGGTT CCTTCAAGTA TGCCTGGGTT CTTGACAAGC TCAAGGCCGA 200
 GCGTGAGCGT GGTATCACCA TCGATATCGC CCTCTGGAAG TTCGAGACTC 250
 CCAAGTACTA CGTCACCGTC ATCGATGCCC CCGGTCATCG TGATTTTCATC 300
 AAGAACATGA TCACTGGTAC CTCCCAGGCT GATTGCGCTA TCCTCATCAT 350
 TGCCGCCGGT ACTGGTGAGT TCGAGGCTGG TATCTCCAAG GATGGCCAGA 400
 35 CCCGTGAGCA CGCCCTGCTC GCCTACACCC TCGGTGTCAA GCAGCTCATT 450
 GTTGCCATCA ACAAGATGGA CACCACCCAG TGGTCCCAGA CTCGTTTCGA 500
 GGAGATCATC AAGGAGACCA AGAACTTCAT CAAGAAGGTT GGCTACAACC 550
 CCGCTGGTGT CGCTTTCGTC CCCATCTCCG GCTTCAACGG CGACAACATG 600
 CTTGAGCCCT CCACCAACTG CCCCTGGTAC AAGGGTTGGG AGAAGGAGAC 650
 40 CAAGGCCGGC AAGGCCACTG GCAAGACCCT CCTCGAGGCC ATCGACGCCA 700
 TTGAGCCCCC CAAGCGTCCT ACCGACAAGC CCCTCCGTCT TCCCCTCCAG 750
 GATGTCTACA AGATCGGTGG TATCGGCACA GTGCCCCGTCG GCCGTATCGA 800
 GACTGGTGTC CTCAAGCCCG GTATGGTCGT TACCTTCGCT CCTTCCAACG 850
 TCACCACTGA AGTCAAGTCC GTCGAGATGC ACCACGAGCA GCTTGCTCAG 900
 45 GGTGTCCCCG GTGACAACGT CGGCTTCAAC GTGAAGAAGC TTTCCGTCAA 950
 GGATATCCGC CGTGGTAACG TTGCCGGTGA CTCCAAGAAC GACCCCCCTG 1000
 CTGGCGCCGC CTCTTTCACC GCCCAGGTCA TCGTTCTCAA CCACCCCGGT 1050
 CAGGTCGGTG CCCGCTACGC CCCCCTCCTC GACTGCCACA CTGCCCACAT 1100
 TGCCTGCAAG TTCGCCGAGC TCCTCGAGAA GATCGACCGC CGTACTGGTA 1150
 50 AGGCTGTTGA GGCCTCCCCC AAGTTCATCA AGTCTGGTGA TGCTGCCATC 1200
 GTCAAGATGA TTCCCTCCAA GCCCATGTGC GTTGAGGCTT TCACCGACTA 1250
 CCCTCCCCTC GGCCGTTTCG CCGTCCGTGA CATGCGTCAG ACCGTCGCCG 1300
 TCGGTGTCAT CAAGGCCGTC GACAAGTCCA CCGTGCCGC TGGCAAGGTC 1350

ACCAAGTCCG CTGCCAAGGC CGCCAAGAAG TAA

1383

5 2) INFORMATION FOR SEQ ID NO: 1995

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1383 bases
(B) TYPE: Nucleic acid
10 (C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

15 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Podospira anserina*
(C) ACCESSION NUMBER: X74799

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1995

20 ATGGGCAAGG AGGACAAGAC TCACATCAAC GTCGTCGTTA TCGGCCACGT 50
CGATTCCGGC AAGTCGACCA CCACTGGTCA CTTGATCTAC AAGTGCGGTG 100
GTATTGACAA GCGTACCATC GAGAAGTTCG AGAAGGAAGC TGCTGAGCTC 150
GGCAAGGGCT CTTTCAAGTA TGCCTGGGTT CTTGACAAGT TGAAGGCCGA 200
25 GCGTGAGCGT GGTATCACCA TCGATATTGC CCTCTGGAAG TTCGAGACCC 250
CCAAGTACTA TGTCACCGTC ATTGATGCCC CCGGCCATCG TGATTTTCATC 300
AAGAACATGA TTAAGGTGAC TTCCAGGCC GATTGCGCCA TTCTCATCAT 350
TGCCGCCGGT ACTGGTGAGT TCGAGGCTGG TATCTCCAAG GATGGCCAGA 400
CCCGTGAGCA CGCTCTCCTC GCCTACACCC TCGGTGTGAA GCAGCTCATC 450
30 GTCGCCATCA ACAAGATGGA CACCACCAAG TGGTCCGAGG CCCGCTTCAA 500
CGAGATCATC AAGGAGACCT CCAACTTCAT CAAGAAGGTC GGCTACAACC 550
CCAAGACTGT TGCCTTCGTC CCCATCTCCG GTTTCAACGG CGACAACATG 600
CTTGAGGCTT CCACCAACTG CCCCTGGTAC AAGGGCTGGG AGAAGGAGGT 650
CAAGGGTGGC AAGGCCACCG GCAAGACCCT CCTTGAGGCC ATCGACTCCA 700
35 TCGAGCCCCC CAAGCGTCCC ACCGACAAGC CCCTCCGTCT TCCCCTCCAG 750
GATGTCTACA AGATCGGCGG TATCGGCACA GTCCCTGTCG GCCGTATCGA 800
GACTGGTATC CTCAAGCCCG GTATGGTCGT TACCTTCGCT CCTTCCAACG 850
TCACCACTGA AGTCAAGTCC GTCGAGATGC ACCACGAGCA GCTCGCTGAG 900
GGTGTTCCTG GTGACAACGT TGGTTTCAAC GTGAAGAAGC TCTCCGTCAA 950
40 GGAAATCCGC CGTGGCAACG TTGCCGGTGA CTCCAAGAAG GACCCCCCCA 1000
TGGGCGCCGC CTCTTTTCGAT GCCCAGGTCA TCGTCCCTCAA CCACCCCGGC 1050
CAGGTCGGTG CTGGTTACGC CCCCCTCCTC GATTGCCACA CTGCCCACAT 1100
CGCCTGCAAG TTCTCTGAGC TCCTGCAGAA GATCGACCGC CGTACTGGTA 1150
AGGCCGTTGA GGAGAGCCCC AAGTTCATCA AGTCTGGTGA TGCTGCCATC 1200
45 GTCAAGATGG TTCCCTCCAA GCCCATGTGC GTTGAGGCTT TCACTGAGTA 1250
CCCTCCCCTC GGTCGTTTCG CCGTCCGTGA CATGCGTCAG ACCGTCGCTG 1300
TCGGTGTTCAT CAAGAAGGTC GAGAAGGCCG CTGCTGGTTC CGGCAAGGTT 1350
ACCAAGTCCG CTGCCAAGGC TGGCAAGAAA TAA 1383

50

2) INFORMATION FOR SEQ ID NO: 1996

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1386 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Podospora curvicolla*
 (B) STRAIN: VLV
 (C) ACCESSION NUMBER: X96614

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1996

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15  ATGGGCAAGG AGGACAAGAC TCACATCAAC GTCGTCGTTA TCGGCCACGT      50
    CGATTCCGGC AAGTCGACCA CCACTGGTCA CTTGATCTAC AAGTGCGGTG      100
    GTATTGACAA GCGTACCATC GAGAAGTTCG AGAAGGAAGC TGCTGAGCTC      150
    GGCAAGGGCT CTTTCAAGTA TGCCTGGGTT CTTGACAAGT TGAAGGCCGA      200
20  GCGTGAGCGT GGTATCACCA TTGATATCGC CCTCTGGAAG TTCGAGACCC      250
    CCAAGTACTA TGTCACCGTC ATCGATGCCC CCGGCCATCG TGATTTTCATC      300
    AAGAACATGA TTA CTGGTAC TTCCAGGCC GATTGCGCCA TTCTCATCAT      350
    TGCCGCCGGT ACTGGTGAGT TCGAGGCTGG TATCTCCAAG GATGGCCAGA      400
    CCCGTGAGCA CGCTCTCCTC GCCTACACCC TCGGTGTGAA GCAGCTCATC      450
25  GTCGCCATCA ACAAGATGGA CACCACCAA TGGTCCGAGG CCCGCTTCAA      500
    CGAGATCATC AAGGAGACCT CCAACTTCAT CAAGAAGGTC GGCTACAACC      550
    CCAAGACTGT TGCCTTCGTC CCCATCTCCG GTTTCAACGG CGACAACATG      600
    CTTGAGGCTT CCACCAACTG CCCCTGGTAC AAGGGTTGGG AGAAGGAGGT      650
    CAAGGGTGGC AAGGCTACTG GCAAGACCCT CCTCGAGGCC ATCGACTCCA      700
30  TCGAGCCCCC CAAGCGTCCC ACCGACAAGC CCCTCCGTCT TCCCCTTCAG      750
    GACGTTTACA AGATCGGCGG TATCGGCACA GTCCCTGTCT GCCGTATCGA      800
    GACTGGTATC CTAAGCCCG GTATGGTCGT TACCTTCGCC CCTTCCAACG      850
    TCACCACTGA AGTCAAGTCC GTCGAGATGC ACCACGAGCA GCTCTCTGAG      900
    GGTGTCCCCG GTGACAACGT TGGTTTCAAC GTGAAGAACG TCTCCGTCAA      950
35  GGAAATCCGC CGTGGCAACG TTGCCGGTGA CTCCAAGAAC GACCCCCCTC     1000
    TTGGCGCCGC TTCTTTTCGAT GCCCAGGTCA TCGTCCCTCAA CCACCCCGGC     1050
    CAGGTCGGTG CTGGTTACGC CCCCGTCTC GATTGCCACA CTGCCCACAT     1100
    CGCCTGCAAG TTCGCTGAGC TCCTGCAGAA GATCGATCGC CGTACTGGTA     1150
    AGGCTGTTGA GGAGAGCCCT AAGTTCATCA AGTCTGGTGA TGCTGCCATC     1200
40  GTCAAGATGA TTCCCTCCAA GCCCATGTGC GTTGAGGCTT TCACTGAGTA     1250
    CCCTCCCCTC GGTGCTTTTCG CTGTCCGTGA CATGCGTCAG ACCGTCGCTG     1300
    TCGGTGTCAT CAAGAAGGTC GAGAAGGCCG CTGCTGGTTC CGGCAAGGTC     1350
    ACCAAGTCCG CTGCCAAGGC TGGTGGCAAG AAATAA                        1386

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45

2) INFORMATION FOR SEQ ID NO: 1997

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1383 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 5 (A) ORGANISM: *Sordaria macrospora*
 (B) STRAIN: 000
 (C) ACCESSION NUMBER: X96615

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1997

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10 ATGGGTAAGG AAGACAAGGC TCACATCAAC GTCGTCGTTA TCGGCCACGT      50
   CGATTCCGGC AAGTCCACCA CTACCGGTCA CCTGATCTAC AAGTGCGGTG      100
   GTATCGACAA GCGTACCATC GAGAAGTTCG AGAAGGAAGC CGCTGAGCTC      150
   GGCAAGGGTT CCTTCAAGTA TGCCTGGGTT CTTGACAAGC TCAAGGCCGA      200
15 GCGTGAGCGT GGTATCACCA TCGATATCGC CCTCTGGAAG TTCGAGACTC      250
   CCAAGTACTA CGTCACCGTC ATCGATGCCC CCGGCCATCG TGATTTTCATC      300
   AAGAACATGA TCACTGGTAC CTCCCAGGCT GATTGCGCTA TTCTCATCAT      350
   TGCCGCTGGT ACTGGTGAGT TCGAGGCTGG TATCTCCAAG GATGGCCAGA      400
   CTCGTGAGCA CGCTCTTCTC GCCTACACCC TCGGTGTCAA GCAGCTCATC      450
20 GTTGCCATCA ACAAGATGGA CACCACCCAG TGGTCCCAGG CTCGTTTCGA      500
   GGAGATCATC AAGGAGACCA AGAACTTCAT CAAGAAGGTC GGCTACAACC      550
   CCGCCACCGT CGCTTTCGTC CCCATCTCCG GCTTCAACGG CGACAACATG      600
   CTTGAGGCCT CCACCAACTG CCCCTGGTAC AAGGGTTGGG AGAAGGAGAC      650
   CAAGGCCGGC AAGTCCACTG GCAAGACCCT CCTCGAGGCC ATCGACGCCA      700
25 TTGAGCAGCC CAAGCGCCCG ACCGACAAGC CCCTCCGTCT TCCCCTCCAG      750
   GATGTCTACA AGATCGGCGG TATCGGCACA GTGCCCCTCG GCCGTATCGA      800
   GACTGGTGTC CTCAAGCCCG GTATGGTCGT TACCTTCGCT CTTTCCAACG      850
   TCACCACTGA AGTCAAGTCC GTCGAGATGC ACCACGAGCA GCTTGCTCAG      900
   GGTGTTCCCG GTGACAACGT CGGCTTCAAC GTGAAGAACG TTTCCGTCAA      950
30 GGATATCCGT CGTGGAACG TTGCCGGTGA CTCCAAGAAC GACCCCCCTG      1000
   TCGGCGCTGC CTCTTTCACC GCCCAGGTCA TCGTCCTTAA CCACCCCGGT      1050
   CAGGTCGGTG CCGGCTACGC TCCCGTCCTC GATTGCCACA CTGCCACAT      1100
   TGCCTGCAAG TTCGCCGAGC TCCTCGAGAA GATCGATCGC CGTACTGGTA      1150
   AGGCTGTTGA GACTTCTCCC AAGTTCATCA AGTCTGGTGA TGCTGCCATC      1200
35 GTCAAGATGA TTCCCTCCAA GCCCATGTGC GTCGAGGCTT TCACCGACTA      1250
   CCCTCCCCTC GGTGTTTTCG CCGTCCGTGA CATGCGTCAG ACCGTCGCTG      1300
   TCGGTGTCAT CAAGGCCGTC GACAAGACCC AGGCTGTCGC TGGCAAGGTC      1350
   ACCAAGTCTG CTGCCAAGGC TGCCAAGAAG TAA                          1383

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10

2) INFORMATION FOR SEQ ID NO: 1998

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 1383 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

50 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Trichoderma reesei*

(B) STRAIN: QM9414

(C) ACCESSION NUMBER: Z23012

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1998

5
 ATGGGTAAGG AGGACAAGAC TCACATCAAC GTGGTCGTCA TCGGCCACGT 50
 CGACTCCGGC AAGTCTACCA CCACTGGTCA CTTGATCTAC CAGTGCGGTG 100
 GTATCGACAA GCGTACCATT GAGAAGTTCG AGAAGGAAGC CGCCGAAGTC 150
 GGCAAGGGTT CCTTCAAGTA CGCGTGGGTT CTTGACAAGC TCAAGGCCGA 200
 10 GCGTGAGCGT GGTATCACCA TCGACATTGC CCTCTGGAAG TTCGAGACTC 250
 CCAAGTACTA TGTACCGTC ATTGACGCTC CCGGCCACCG TGACTTCATC 300
 AAGAACATGA TCACTGGTAC TTCCCAGGCC GACTGCGCTA TCCTCATCAT 350
 CGCTGCCGGT ACTGGTGAGT TCGAGGCTGG TATCTCCAAG GATGGCCAGA 400
 CCCGTGAGCA CGCTCTGCTC GCCTACACCC TGGGTGTCAA GCAGCTCATC 450
 15 GTCGCCATCA ACAAGATGGA CACTGCCAAC TGGGCCGAGG CTCGTTACCA 500
 GGAAATCATC AAGGAGACTT CCAACTTCAT CAAGAAGGTC GGCTTCAACC 550
 CCAAGGCCGT TGCTTTCGTC CCCATCTCCG GCTTCAACGG TGACAACATG 600
 CTCACCCCTT CCACCAACTG CCCCTGGTAC AAGGGCTGGG AGAAGGAGAC 650
 CAAGGCTGGC AAGTTCACCG GCAAGACCCT CCTTGAGGCC ATCGACTCCA 700
 20 TCGAGCCCCC CAAGCGTCCC ACGGACAAGC CCCTGCGTCT TCCCCTCCAG 750
 GACGTCTACA AGATCGGTGG TATCGGAACA GTTCCCGTCG GCCGTATCGA 800
 GACTGGTGTC CTCAAGCCCG GTATGGTCGT TACCTTCGCT CCCTCCAACG 850
 TCACCACTGA AGTCAAGTCC GTCGAGATGC ACCACGAGCA GCTCGCTGAG 900
 GGCCAGCCTG GTGACAACGT TGGTTTCAAC GTGAAGAACG TTTCCGTCAA 950
 25 GGAAATCCGC CGTGGCAACG TTGCCGGTGA CTCCAAGAAC GACCCCCCCA 1000
 TGGGCGCCGC TTCTTTCACC GCCCAGGTCA TCGTCATGAA CCACCCCGGC 1050
 CAGGTCGGTG CCGGCTACGC CCCCCTCCTC GACTGCCACA CTGCCACAT 1100
 TGCCTGCAAG TTCGCCGAGC TCCTCGAGAA GATCGACCGC CGTACCGGTA 1150
 AGGCTACCGA GTCTGCCCCC AAGTTCATCA AGTCTGGTGA CTCCGCCATC 1200
 30 GTCAAGATGA TCCCCTCCAA GCCCATGTGC GTTGAGGCTT TCACCGACTA 1250
 CCCTCCCCTG GGTCGTTTCG CCGTCCGTGA CATGCGCCAG ACCGTCGCTG 1300
 TCGGTGTCAT CAAGGCCGTC GAGAAGTCCT CTGCCGCCGC CGCCAAGGTC 1350
 ACCAAGTCCG CTGCCAAGGC CGCCAAGAAA TAA 1383

35

2) INFORMATION FOR SEQ ID NO: 1999

(i) SEQUENCE CHARACTERISTICS:

40 (A) LENGTH: 29 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

45 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1999

CATGTCAAYA TTGGTACTAT TGGTCATGT

29

50

2) INFORMATION FOR SEQ ID NO: 2000

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 bases
(B) TYPE: Nucleic acid
5 (C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: DNA
- 10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2000
- CCACCYTCIC TCAMGTTGAA RCGTT 25
- 15 2) INFORMATION FOR SEQ ID NO: 2001
- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 bases
20 (B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: DNA
- 25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2001
- ACYACITTRA CIGCYGCIAT YAC 23
- 30 2) INFORMATION FOR SEQ ID NO: 2002
- (i) SEQUENCE CHARACTERISTICS:
35 (A) LENGTH: 21 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: DNA
- 40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2002
- CCIGARGARA GAGCIMGWGG T 21
- 45 2) INFORMATION FOR SEQ ID NO: 2003
- 50 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2003

CATYTCRAIR TTGTCACCTG G

21

2) INFORMATION FOR SEQ ID NO: 2004

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1360 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Candida albicans*
- (B) STRAIN: SC5314
- (C) ACCESSION NUMBER: Genome project

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2004

GCTGCCTTCG	ACCGTTCTAA	ACCTCATGTC	AACATTGGTA	CTATTGGTCA	50
TGTTGATCAT	GGTAAACTA	CATTGACTGC	TGCTATCACC	AAAGTTTTAG	100
CCGAACAAGG	TGGTGCCAAC	TTCTTGGATT	ATGGTTCTAT	TGATAGAGCT	150
CCAGAAGAAA	GAGCTAGAGG	TATCACTATT	TCCACTGCCC	ACGTTGAATA	200
CGAAACCAAG	AACAGACACT	ATGCCCACGT	TGATTGTCCA	GGACACGCTG	250
ATTATATCAA	AAATATGATT	ACTGGTGCCG	CTCAAATGGA	TGGTGCTATC	300
ATTGTTGTTG	CTGCCACTGA	TGGTCAAATG	CCTCAAACCA	GAGAACATTT	350
GTTATTGGCC	AGACAAGTTG	GTGTTCAAGA	CTTGGTTGTG	TTTGTCAACA	400
AAGTCGATAC	TATTGATGAC	CCTGAAATGT	TGGAATTAGT	CGAAATGGAA	450
ATGAGAGAAT	TGTTATCCAC	CTACGGTTTT	GATGGTGACA	ACACTCCAGT	500
TATTATGGGA	TCTGCTTTAA	TGGCTTTGGA	AGACAAGAAA	CCAGAAATTG	550
GTAAGGAAGC	TATCTTGAAA	TTGTTAGATG	CTGTCGATGA	ACACATTCCA	600
ACTCCATCAA	GAGACTTGGA	ACAACCATTT	TTGTTACCAG	TTGAAGACGT	650
GTTCTCCATC	TCCGGTAGAG	GAACGTGTGT	CACTGGTAGA	GTTGAAAGAG	700
GTGTTTTGAA	GAAGGGTGAA	GAAATCGAAA	TTGTTGGTGG	TTTTGACAAA	750
CCTTACAAGA	CTACTGTTAC	CGGTATTGAA	ATGTTCAAAA	AAGAATTAGA	800
CTCTGCTATG	GCTGGTGACA	ACTGTGGTGT	TTTGTTAAGA	GGTGTTAAAA	850
GAGATGAAAT	CAAGAGAGGT	ATGGTTTTGG	CCAAACCAGG	TACTGCTACT	900
TCTCACAAGA	AGTTCTTGGC	TTCCTTGAT	ATTTTGACTT	CCGAAGAAGG	950
TGGTCGTTCC	ACTCCATTG	GTGAAGGTTA	CAAGCCTCAA	TGCTTCTTCA	1000
GAACTAACGA	TGTCCTACC	ACATTTTCAT	TCCCAGAAGG	AGAAGGTGTT	1050
GATCATTCTC	AAATGATCAT	GCCAGGTGAC	AACATTGAAA	TGGTTGGTGA	1100
ATTGATCAAA	TCTTGTCCT	TAGAAGTCAA	CCAACGTTTC	AACTTGAGAG	1150
AAGGTGGTAA	AACTGTTGGT	ACTGGTTTGA	TTACCAGAAT	CATCGAATAA	1200
ACAGAATGTG	CACTGTGAAT	AATAAAAAGA	AAAGAGGTAT	ATATAGGTGA	1250
CTTTGTATTT	TGTATTGAAC	AATAAAATTC	TGTAAATAGT	AAGGGCCTCA	1300
GAAGTTTTGA	TTTGATTAT	GCCATGTGGA	CTTGTAAGAG	TATCCTTCTC	1350
AAACTTCTTG					1360

2) INFORMATION FOR SEQ ID NO: 2005

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1342 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Schizosaccharomyces pombe*

(C) ACCESSION NUMBER: Genome project

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2005

```

AAGCCGCATG TCAATATTGG TACTATTGGT CATGTTGACC ACGGTAAAC 50
GACGTTGACG GCTGCTATTA CTAAATGCCT TTCTGATCTT GGTCAAGCTA 100
GTTTTATGGA TTATAGTCAA ATTGACAAGG CCCCCGAGGA AAAGGCACGT 150
GGTATTACCA TTTTCATCTGC CCATGTTGAA TACGAAACTG CTAATCGTCA 200
CTATGCCCAT GTGGATTGTC CTGGTCACGC CGATTACATT AAGAATATGA 250
TTACTGGTGC TGCTACAATG GATGGCGCTA TCATTGTTGT TTCTGCTACC 300
GATGGTCAAA TGCCTCAAAC TCGTGAACAT TTGCTTCTGG CTCGTCAAGT 350
CGGTGTAAAG CAAATTGTTG TATACATCAA TAAAGTCGAT ATGGTCGAGC 400
CTGATATGAT CGAGCTTGTC GAAATGGAAA TCGGTGAGCT ACTCTCCGAA 450
TACGGATTTG ATGGTGACAA TACTCCAATT GTTAGCGGCA GTGCTTTATG 500
TGCCTTAGAG GGTCTGAGC CTGAGATTGG TCTCAATAGT ATTACTAAAT 550
TGATGGAAGC TGTTGATAGT TATATTACTC TTCCTGAAAG AAAAACGGAT 600
GTCCTTTCT TGATGGCCAT CGAGGACGTT TTTTCAATTT CAGGTCGCGG 650
AACTGTAGTC ACTGGCCGTG TCGAGCGCGG TACTTTAAAG AAGGGTGCTG 700
AAATCGAAAT CGTCGGTTAT GGTAGCCATT TAAAGACTAC CGTTACTGGA 750
ATTGAAATGT TCAAAAAGCA GCTTGATGCC GCCGTTGCCG GTGACAATTG 800
TGGCCTTTTA CTTTCGTTCTA TCAAGCGAGA GCAATTAAAA CGTGGAATGA 850
TTGTCGCTCA ACCAGGAACC GTTGCTCCTC ATCAGAAATT CAAGGCATCA 900
TTCTATATTT TGACAAAAGA GGAAGGAGGT CGTCGTACCG GTTTCGTTGA 950
CAAGTATCGT CCCCACCTGT ACAGTCGTAC TTCCGACGTT ACTGTCGAAC 1000
TTACCCACCC TGATCCTAAC GACTCAGACA AAATGGTTAT GCCTGGAGAC 1050
AATGTCGAGA TGATCTGTAC GCTTATTCAC CCCATTGTCA TCGAAAAAGG 1100
ACAACGCTTC ACAGTTCGTG AGGGTGGAAG CACTGTAGGC ACAGCTTTGG 1150
TTACTGAACT TTTGGATTAG TGCATTTATG AACTTATTGG CTTTAAAAAT 1200
TTTGCATGCT GAATACCAAT ATTATGTCCC TTCTCAGAAT TCTATAACTA 1250
CAGTGTCATT ATTGTAATAA GACTTTTGCA TCCATTGACA ATGGTATTTG 1300
ATACTTTTAT AGTTTCTACT ATTGTTAGCC AAAGTTATAA AA 1342

```

2) INFORMATION FOR SEQ ID NO: 2006

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 18 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2006

TGGAGCCGGT GAGCGTGG

18

2) INFORMATION FOR SEQ ID NO: 2007

1045

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2007

TGGAGCCAGT GAGCGTGG

18

2) INFORMATION FOR SEQ ID NO: 2008

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2008

TCTGGAGCCG ATGAGCGTG

19

2) INFORMATION FOR SEQ ID NO: 2009

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2009

CTGGAGCCAG TAAGCGTGG

19

2) INFORMATION FOR SEQ ID NO: 2010

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 861 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Double
 - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Klebsiella pneumoniae*
 (B) STRAIN: KMK107
 (C) ACCESSION NUMBER: AF027199

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2010

```

ATGAGTATTC AACATTTTTCG TGTCGCCCTT ATTCCCTTTT TTGCGGCATT      50
TTGCCTTCCT GTTTTTTGCTC ACCCAGAAAC GCTGGTGAAA GTAAAAGATG      100
CTGAAGATCA GTTGGGTGCA CGAGTGGGTT ACATCGAACT GGATCTCAAC      150
AGCGGTAAGA TCCTTGAGAG TTTTCGCCCC GAAGAACGTT TTCCAATGAT      200
GAGCACTTTT AAAGTTCTGC TATGTGGTGC GGTATTATCC CGTGTTGACG      250
CCGGGCAAGA GCAACTCGGT CGCCGCATAC ACTATTCTCA GAATGACTTG      300
GTTAAGTACT CACCAGTCAC AGAAAAGCAT CTTACGGATG GCATGACAGT      350
AAGAGAATTA TGCAGTGCTG CCATAACCAT GAGTGATAAC ACTGCTGCCA      400
ACTTACTTCT GACAACGATC GGAGGACCGA AGGAGCTAAC CGCTTTTTTG      450
CACAAATGCG GGGATCATGT AACTCGCCTT GATCGTTGGG AACCGGAGCT      500
GAATGAAGCC ATACCAAACG ACGAGCGTGA CACCACGACG CCTGCAGCAA      550
TGGCAACAAC GTTGCGCAAA CTATTAAGT GCGAACTACT TACTCTAGCT      600
TCCCGGCAAC AATTAATAGA CTGGATGGAG GCGGATAAAG TTGCAGGACC      650
ACTTCTGCGC TCGGCCCTTC CGGCTGGCTG GTTTATTGCT GATAAATCTG      700
GAGCCAGTGA GCGTGGGTCT CGCGGTATCA TTGCAGCACT GGGGCCAGAT      750
GGTAAGCCCT CCCGTATCGT AGTTATCTAC ACGACGGGGA GTCAGGCAAC      800
TATGGATGAA CGAAATAGAC AGATCGCTGA GATAGGTGCC TCACTGATTA      850
AGCATTGCTA A                                     861
  
```

2) INFORMATION FOR SEQ ID NO: 2011

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 861 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Klebsiella pneumoniae*
 (B) STRAIN: CLSis L-491
 (C) ACCESSION NUMBER:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2011

```

ATGAGTATTC AACATTTCCG TGTCGCCCTT ATTCCCTTTT TTGCGGCATT      50
TTGCTTTCCT GTTTTTTGCTC ACCCAGAAAC GCTGGTGAAA GTAAAAGATG      100
CTGAAGATCA GTTGGGTGCA CGAGTGGGTT ACATCGAGCT GGATCTCAAC      150
AGCGGTAAGA TCCTTGAGAG TTTTCGCCCC GAAGAACGTT TTCCAATGAT      200
GAGCACTTTT AAAGTTCTGC TATGTGGTGC GGTATTATCC CGTGTTGACG      250
CCGGGCAAGA GCAACTCGGT CGCCGCATAC ACTATTCTCA GAATGACTTG      300
GTTGAGTACT CACCAGTCAC AGAAAAGCAT CTTACGGATG GCATGACAGT      350
AAGAGAATTA TGCAGTGCTG CCATAACCAT GAGTGATAAC ACTGCGGCCA      400
ACTTACTTCT GACAACGATC GGAGGACCGA AGGAGCTAAC CGCTTTTTTG      450
CACAAATGCG GGGATCATGT AACCCGCCTT GATCGTTGGG AACCGGAGCT      500
GAATGAAGCC ATACCAAACG ACGAGCGTGA CACCACGATG CCTGCAGCAA      550
TGGCAACAAC GTTGCGCAAA CTATTAAGT GCGAACTACT TACTCTAGCT      600
  
```

TCCCGGCAAC	AATTAATAGA	CTGGATGGAG	GCGGATAAAG	TTGCAGGACC	650
ACTTCTGCGC	TCGGCCCTTC	CGGCTGGCTG	GTTTATTGCT	GATAAATCTG	700
GAGCCAGTAA	GCGTGGATCT	CGCGGTATCA	TTGCAGCACT	GGGGCCAGAT	750
GGTAAGCCCT	CCCGTATCGT	AGTTATCTAC	ATGACGGGGA	GTCAGGCAAC	800
TATGGATGAA	CGAAATAGAC	AGATCGCTGA	GATAGGTGCC	TCACTGATTA	850
AGCATTGGTA	A				861

2) INFORMATION FOR SEQ ID NO: 2012

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 49 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2012

CCGCGGATTA TTAAACCGCC CTTCCGCGG-MR-HEG-ATGTCAGAGG GATAGATCCA 49

2) INFORMATION FOR SEQ ID NO: 2013

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 353 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Kluyvera ascorbata*
- (B) STRAIN: ATCC 33433

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2013

AGCTTAAGAA	CTCTTATCTG	GATTACGCGA	TGTCGGTCAT	TGTTGGCCGT	50
GCGCTGCCGG	ATGTCCGAGA	TGGCCTGAAG	CCGGTACACC	GTCGCGTACT	100
TTACGCCATG	AACGTATTGG	GCAATGACTG	GAACAAAGCC	TACAAAAAAT	150
CAGCCCGTGT	CGTGGGTGAC	GTGATCGGTA	AATATCACCC	GCATGGTGAT	200
ACTGCCGTCT	ATGACACTAT	CGTCCGTATG	GCACAGCCAT	TCTCACTGCG	250
ATACATGCTG	GATAGTGGTC	AAGGTAACCT	CGGTTCTGTC	GATGGCGACT	300
CCGCCGCAGC	GATGCGTTAT	ACGGAAATCC	GTATGTCGAA	AATCGCCCAT	350
GAG					353

2) INFORMATION FOR SEQ ID NO: 2014

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 355 bases
- (B) TYPE: Nucleic acid

- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Kluyvera georgiana*
- (B) STRAIN: ATCC 51603

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2014

```
AGCTCCTATC TGGATTATGC GATGTCGGTC ATTGTTGGCC GTGCGCTGCC      50
AGATGTCCGA GATGGCCTGA AGCCGGTACA CCGTCGCGTA CTTTACGCCA      100
TGAACGTACT AGGCAATGAC TGAACAAAAG CCTATAAAAA ATCTGCCCGT      150
GTCGTTGGTG ACGTAATCGG TAAATACCAT CCCCATGGTG ACTCGGCGGT      200
CTATGACACG ATCGTCCGCA TGGCGCAGCC ATTCTCGCTG CGTTATATGC      250
TGGTAGACGG TCAGGGTAAC TTCGGTTCTA TCGACGGCGA CTCTGCGGCG      300
GCAATGCGTT ATACGGAAAT CCGTCTGGCG AAAATTGCCC ATGAACTGAT      350
GGCCG
```

2) INFORMATION FOR SEQ ID NO: 2015

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2015

```
CCAAGAAGCT CAAAACATC TG      22
```

2) INFORMATION FOR SEQ ID NO: 2016

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2016

```
TADCCTGTCC AWACAGCCAT      20
```

2) INFORMATION FOR SEQ ID NO: 2017

(i) SEQUENCE CHARACTERISTICS:

1049

- (A) LENGTH: 22 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2017

ACTTTGAATA AGGTCGGTCT AG

22

2) INFORMATION FOR SEQ ID NO: 2018

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2018

ACACTAAACA AGGTTGGTTT AG

22

2) INFORMATION FOR SEQ ID NO: 2019

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2019

ACACTAAACA AGGTCGGTCT AG

22

2) INFORMATION FOR SEQ ID NO: 2020

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2020

GTAGCTCCAG ATGAAATGTT TG

22

2) INFORMATION FOR SEQ ID NO: 2021

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2021

GTAGCTCCAG ACGAAATGTT TG

22

2) INFORMATION FOR SEQ ID NO: 2022

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2022

GTAGCTCCAG ATGAAACGTT TG

22

2) INFORMATION FOR SEQ ID NO: 2023

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2023

GTAAGTCCAG ATGAAATGTT TG

22

2) INFORMATION FOR SEQ ID NO: 2024

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid

1051

- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2024

AGTGAAAAGA TGGCTGCTGC

20

2) INFORMATION FOR SEQ ID NO: 2025

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2025

AGTGAGAAAA TGGCTGCTGC

20

2) INFORMATION FOR SEQ ID NO: 2026

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2026

TCCAAGCATG CATTATGCAA ACG

23

2) INFORMATION FOR SEQ ID NO: 2027

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2027

TCGGTCTAGA TAGAGCTAAA ACG

23

2) INFORMATION FOR SEQ ID NO: 2028

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2028

TATGCTCTTC AACATCACG

20

2) INFORMATION FOR SEQ ID NO: 2029

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2029

AGCCGTTGAG ACTTTGAATA AG

22

2) INFORMATION FOR SEQ ID NO: 2030

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2030

CTTAATGGTC TTGGTATCG

19

2) INFORMATION FOR SEQ ID NO: 2031

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single

1053

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2031

CGTGACTGGG GTTCTGCTAT GA

22

2) INFORMATION FOR SEQ ID NO:2032

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2032

CGTGACTGGG GATCATCAAT GA

22

2) INFORMATION FOR SEQ ID NO: 2033

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2033

CGTGACTGGG GTTCTGCCAT GA

22

2) INFORMATION FOR SEQ ID NO: 2034

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2034

ATCAAGAACA CTGGCTATGT AG

22

2) INFORMATION FOR SEQ ID NO: 2035

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2035

ATCAAGAACA CTGGCTACGT AG

22

2) INFORMATION FOR SEQ ID NO: 2036

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2036

ATCAAGAACA CTGGTTACGT AG

22

2) INFORMATION FOR SEQ ID NO: 2037

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2037

ATCAAAAATA CTGGTTATGT AG

22

2) INFORMATION FOR SEQ ID NO: 2038

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single

1055

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2038

ATCAAGAATA CTGGCTACGT AG

22

2) INFORMATION FOR SEQ ID NO: 2039

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2039

ATCAAAAACA CTGGCTATGT AG

22

2) INFORMATION FOR SEQ ID NO: 2040

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 19 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2040

TGTGACCCCA GACAAACCC

19

2) INFORMATION FOR SEQ ID NO: 2041

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2041

GTTGAGCGGC AGCACTATCT

20

2) INFORMATION FOR SEQ ID NO: 2042

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2042

CACGGGGATT TCTCTATTTA

20

2) INFORMATION FOR SEQ ID NO: 2043

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2043

CACGGGGATT ACTCTATTTA

20

2) INFORMATION FOR SEQ ID NO: 2044

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2044

ACCGTAAGTC GGCCAAGTCA

20

2) INFORMATION FOR SEQ ID NO: 2045

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2045

1057

GTTCTTTCTC CGTATCGTC

19

2) INFORMATION FOR SEQ ID NO: 2046

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2046

ACGGGGATTT TTCTATCTAT

20

2) INFORMATION FOR SEQ ID NO: 2047

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2160 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
- (B) STRAIN: CS109
- (C) ACCESSION NUMBER: Z49094

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2047

ATGAACAAAC	CAACGATTCT	GCGCCTAATC	AAGTATCTGA	GCATTAGCTT	50
CTTAAGCTTG	GTTATCGCAG	CCATTGTCTT	AGGCGGAGGA	GTTTTTTTCT	100
ACTATGTTAG	CAAGGCTCCT	AGCCTATCCG	AGAGTAAACT	AGTTGCAACA	150
ACCTCTAGTA	AAATCTACGA	CAATAAAAAT	CAACTCATTG	CTGACTTGGG	200
TTCTGAACGC	CGCGTCAATG	CCCAAGCTAA	TGATATTCCC	ACAGATTTGG	250
TTAAGGCAAT	CGTTTCTATC	GAAGACCATC	GCTTCTTCGA	CCACAGGGGG	300
ATTGATACCA	TCCGTATCCT	GGGAGCTTTC	TTGCGCAATC	TGCAAAGCAA	350
TTCCCTCCAA	GGTGGATCAA	CTCTCACCCA	ACAGTTGATT	AAATTGACTT	400
ACTTTTCAAC	CTCGACTTCC	GACCAGACTA	TTTCTCGTAA	GGCTCAGGAA	450
GCTTGGTTAG	CGATTTCAGT	AGAACA AAAA	GCAACCAAAC	AGGAAATCTT	500
GACCTACTAT	ATAAATAAGG	TCTACATGTC	TAATGGCAAC	TATGGAATGC	550
AGACAGCAGC	TCAAACTAC	TATGGTAAAG	ACCTCAATAA	TTTAAGTTTA	600
CCTCAGTTAG	CCTTGCTGGC	TGGAATGCCT	CAGGCACCAA	ACCAATATGA	650
CCCCTATTCA	CATCCAGAAG	CAGCCCAAGA	CCGCCGAAAC	TTGGTCTTAT	700
CTGAAATGAA	AAATCAAGGT	TACATCTCTG	CTGAACAGTA	TGAGAAAGCA	750
GTCAATACAC	CAATTACTGA	TGGACTACAA	AGTCTCAAAT	CAGCAAGTAA	800
TTACCCTGCT	TACATGGATA	ATTACCTCAA	GGAAGTCATC	AATCAAGTTG	850
AAGAAGAAAC	TGGCTATAAC	CTTCTAACTA	CTGGGATGGA	TGTTTACACA	900

1058

AATGTAGACC	AAGAAGCTCA	AAAACATCTG	TGGGATATCT	ACAACTCCGA	950
TCAATACGTC	TCTTACCCTG	ACGATGATTT	GCAAAGTCGCA	TCTACGGTCG	1000
TAGATGTTTC	AAATGGTAAA	GTCATCGCAC	AACTTGGTGC	TCGTCATCAA	1050
GCAAGTAATG	TTTCATTCGG	TACCAACCAG	GCCGTAGAAA	CCAATCGTGA	1100
CTGGGGATCA	TCAATGAAAC	CAATCACTGA	CTATGCTCCC	GCTTTAGAAT	1150
ATGGAGTCTA	TGACTCTACT	GCTTCTATTG	TACATGATGT	CCCTTATAAC	1200
TATCCTGGCA	CTGATACTCC	ACTCTACAAC	TGGGATCATG	TCTACTTTGG	1250
AAACATTACA	ATCCAGTATG	CTCTTCAACA	ATCACGAAAT	GTCACAGCCG	1300
TTGAGACTTT	GAATAAGGTC	GGTCTAGATA	GAGCTAAAAC	CTTCCTTAAT	1350
GGTCTTGGA	TCGACTATCC	AAGCATGCAT	TATGCAAACG	CCATTTCAAG	1400
TAACACAAC	GAATCCAACA	AAAAATATGG	TGCAAGTAGT	GAAAAAATGG	1450
CTGCTGCCTA	CGCTGCTTTT	GCTAATGGTG	GTATTTATCA	CAAACCAATG	1500
TATATCAATA	AAATCGTCTT	TAGTGATGGT	AGCGAAAAAG	AATTTTCTGA	1550
TGCTGGTACA	CGAGCTATGA	AAGAGACTAC	TGCCTATATG	ATGACTGAAA	1600
TGATGAAAAC	TGTTTTAACT	TACGGAACAG	GACGTGGAGC	CTACCTACCA	1650
TGGCTTCCAC	AAGCAGGTAA	GACAGGTACT	TCTAACTATA	CTGACGAAGA	1700
AATTGAAAAG	TATATCAAGA	ACACTGGTTA	CGTAGCTCCA	GATGAAATGT	1750
TTGTAGGGTA	TACCCGTAAA	TATGCAATGG	CTGTTTGGAC	AGGATACTCA	1800
AATCGTCTAA	CTCCAATCAT	CGGAGATGGT	TTCCTTGTTG	CTGGTAAAGT	1850
CTATCGTTCA	ATGATAACTT	ACCTTTCTGA	AGATGACCAA	CCTGGAGATT	1900
GGACAATGCC	AGATGGCTTG	TATAGAAATG	GAGAATTCGT	ATTTAAAAAT	1950
GGTGCTCGTT	CTACGTGGAG	CTCACCTGCT	CCACAACAAC	CCCCATCAAC	2000
TGAAAGTTCA	AGCTCATCAT	CAGATAGTTC	AACTTCACAG	TCTAACTCAA	2050
CCACTCCAAG	CACAAATAAT	AGTACGACTA	CCAATCCTAA	CAATAATACG	2100
CAACAATCAA	ATACAACCCC	TGATCAACAA	AATCAGAATC	CTCAACCAGC	2150
ACAACCATAA					2160

2) INFORMATION FOR SEQ ID NO: 2048

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2160 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
- (B) STRAIN: R6
- (C) ACCESSION NUMBER: M90527

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2048

ATGAACAAAC	CAACGATTCT	GCGCCTAATC	AAGTATCTGA	GCATTAGCTT	50
CTTAAGCTTG	GTTATCGCAG	CCATTGTCCT	AGGCGGAGGA	GTTTTTTTCT	100
ACTACGTTAG	CAAGGCTCCT	AGCCTATCCG	AGAGTAAACT	AGTTGCAACA	150
ACTTCTAGTA	AAATCTACGA	CAATAAAAAT	CAACTCATTG	CTGACTTGGG	200
TTCTGAACGC	CGCGTCAATG	CCCAAGCTAA	TGATATTCCC	ACAGATTTGG	250
TTAAGGCAAT	CGTTTCTATC	GAAGACCATC	GCTTCTTCGA	CCACAGGGGG	300
ATTGATACCA	TCCGTATCCT	GGGAGCTTTC	TTGCGCAATC	TGCAAAGCAA	350
TTCCCTCCAA	GGTGGATCAG	CTCTCACTCA	ACAGTTGATT	AAGTTGACTT	400
ACTTTTCAAC	TTCGACTTCC	GACCAGACTA	TTTCTCGTAA	GGCTCAGGAA	450
GCTTGGTTAG	CGATTCAGTT	AGAACAAAAA	GCAACCAAGC	AAGAAATCTT	500
GACCTACTAT	ATAAATAAGG	TCTACATGTC	TAATGGGAAC	TATGGAATGC	550

AGACAGCAGC	TCAAAACTAC	TATGGTAAAG	ACCTCAATAA	TTTAAGTTTA	600
CCTCAGTTAG	CCTTGCTGGC	TGGAATGCCT	CAGGCACCAA	ACCAATATGA	650
CCCCTATTCA	CATCCAGAAG	CAGCCCAAGA	CCGCCGAAAC	TTGGTCTTAT	700
CTGAAATGAA	AAATCAAGGC	TACATCTCTG	CTGAACAGTA	TGAGAAAGCA	750
GTCAATACAC	CAATTACTGA	TGGGCTACAA	AGTCTCAAAT	CAGCAAGTAA	800
TTACCCTGCT	TACATGGATA	ATTACCTCAA	GGAAGTCATC	AATCAAGTTG	850
AAGAAGAAAC	AGGCTATAAC	CTACTCACAA	CTGGGATGGA	TGTCTACACA	900
AATGTAGACC	AAGAAGCTCA	AAAACATCTG	TGGGATATTT	ACAATACAGA	950
CGAATACGTT	GCCTATCCAG	ACGATGAATT	GCAAGTCGCT	TCTACCATTG	1000
TTGATGTTTC	TAACGGTAAA	GTCATTGCCC	AGCTAGGAGC	ACGCCATCAG	1050
TCAAGTAATG	TTTCCTTCGG	AATTAACCAA	GCAGTAGAAA	CAAACCGCGA	1100
CTGGGGATCA	ACTATGAAAC	CGATCACAGA	CTATGCTCCT	GCCTTGGAGT	1150
ACGGTGTCTA	CGAGTCAACT	GCCACTATCG	TTCACGATGA	GCCCTATAAC	1200
TACCCTGGGA	CAAATACCCC	TGTTTATAAC	TGGGATAGGG	GCTACTTTGG	1250
CAACATCACC	TTGCAATACG	CCCTGCAACA	ATCGCGAAAC	GTCCAGCCG	1300
TGGAAACTCT	AAACAAGGTC	GGACTCAACC	GCGCCAAGAC	TTTCCTAAAT	1350
GGTCTCGGAA	TCGACTACCC	AAGTATTCAC	TACTCAAATG	CCATTTCAAG	1400
TAACACAACC	GAATCAGACA	AAAAATATGG	AGCAAGTAGT	GAAAAGATGG	1450
CTGCTGCTTA	CGCTGCCTTT	GCAAATGGTG	GAACCTACTA	TAAACCAATG	1500
TATATCCATA	AAGTCGTCTT	TAGTGATGGG	AGTGAAAAAG	AGTTCTCTAA	1550
TGTCGGAAC	CGTGCCATGA	AAGAAACGAC	AGCCTATATG	ATGACCGACA	1600
TGATGAAAAC	AGTCTTGAGT	TATGGAAC	GACGAAATGC	CTATCTTGCT	1650
TGGCTCCCTC	AGGCTGGTAA	AACAGGAACC	TCTAACTATA	CAGACGAGGA	1700
AATTGAAAAC	CACATCAAGA	CCTCTCAATT	TGTAGCACCT	GATGAACTAT	1750
TTGCTGGCTA	TACGCGTAAA	TATTCAATGG	CTGTATGGAC	AGGCTATTCT	1800
AACCGTCTGA	CACCACTTGT	AGGCAATGGC	CTTACGGTCG	CTGCCAAAGT	1850
TTACCGCTCT	ATGATGACCT	ACCTGTCTGA	AGGAAGCAAT	CCAGAGGATT	1900
GGAATATACC	AGAGGGGCTC	TACAGAAATG	GAGAATTCGT	ATTTAAAAAT	1950
GGTGCTCGTT	CTACGTGGAG	CTCACCTGCT	CCACAACAAC	CCCCATCAAC	2000
TGAAAGTTCA	AGCTCATCAT	CAGATAGTTC	AACCTCACAG	TCTAGCTCAA	2050
CCACTCCAAG	CACAAATAAT	AGTACGACTA	CCAATCCTAA	CAATAATACG	2100
CAACAATCAA	ATACAACCCC	TGATCAACAA	AATCAGAATC	CTCAACCAGC	2150
ACAACCATAA					2160

2) INFORMATION FOR SEQ ID NO: 2049

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2160 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
- (B) STRAIN: URU-E159
- (C) ACCESSION NUMBER: AF139890

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2049

ATGAACAAAC	CAACGATTCT	GCGCCTAATC	AAGTATCTGA	GCATTAGCTT	50
CTTAAGCTTG	GTTATCGCAG	CCATTGTCTT	AGGCGGAGGA	GTTTTTTTCT	100
ACTACGTTAG	CAAGGCTCCT	AGCCTATCCG	AGAGTAAACT	AGTTGCAACA	150
ACTTCTAGTA	AAATCTACGA	CAATAAAAAAT	CAACTCATTG	CTGACTTGGG	200

TTCTGAACGC	CGCGTCAATG	CCCAAGCTAA	TGATATTCCC	ACAGATTTGG	250
TTAAGGCAAT	CGTTTCTATC	GAAGACCATC	GCTTCTTCGA	CCACAGGGGG	300
ATTGATTCCA	TCCGTATCCT	GGGAGCTTTC	TTGCGCAATC	TGCAAAGTAA	350
TTCCCTCCAA	GGTGGATCAA	CTCTCACCCA	ACAGTTGATT	AAGTTGACTT	400
ACTTTTCAAC	CTCGACTTCC	GACCAGACTA	TTTCTCGTAA	GGCTCAGGAA	450
GCTTGGTTAG	CGATTTCAGT	AGAACAAAAA	GCAACCAAAC	AGGAAATCTT	500
GACCTACTAT	ATAAATAAGG	TCTACATGTC	TAATGGCAAC	TATGGAATGC	550
AGACAGCAGC	TCAAAACTAC	TATGGTAAAG	ACCTCAATAA	TTTAAGTTTA	600
CCTCAGTTAG	CCTTGCTGGC	TGGAATGCCT	CAGGCACCAA	ACCAATATGA	650
CCCCTATTCA	CATCCAGAAG	CAGCCCAAGA	CCGCCGAAAC	TTGGTCTTAT	700
CTGAAATGAA	AAATCAAGGT	TACATCTCTG	CTGAACAGTA	TGAGAAAGCA	750
GTCAATACAC	CAATTACTGA	TGGACTACAA	AGTCTCAAAT	CAGCAAGTAA	800
TTACCCTGCT	TACATGGATA	ATTACCTCAA	GGAGGTCATC	AATCAAGTAG	850
AACAAGAAAC	TGGCTATAAC	CTTCTAACTA	CTGGGATGGA	TGTTTACACA	900
AATGTAGACC	AAGAAGCTCA	AAAACATCTG	TGGGATATCT	ACAACTCCGA	950
TCAATACGTC	TCTTACCCTG	ACGATGATTT	GCAAGTCGCA	TCTACGGTCG	1000
TAGATGTTTC	AAATGGTAAA	GTCATCGCCC	AACCTGGAGC	TCGTCACCAA	1050
GCAAGTAACG	TTTCATTTGG	TACCAACCAA	GCTGTGGAAA	CCAATCGTGA	1100
CTGGGGTTCT	GCTATGAAAC	CAATCACCGA	TTATGCACCT	GCCATAGAAT	1150
ACGGTGTTTA	TGATTCCACT	GCAACTATGG	TTAATGATAT	TCCTTATAAC	1200
TATCCGGGAA	CAAGCACACC	TGTCTACAAC	TGGGATAGAG	CATATTTTCGG	1250
TAATATTACT	CTGCAATATG	CTCTTCAACA	ATCACGAAAT	GTCACAGCCG	1300
TTGAGACTTT	GAATAAGGTC	GGTCTAGATA	GAGCTAAAAC	CTTCCTTAAT	1350
GGTCTTGCTA	TCGACTATCC	AAGCATGCAT	TATGCAAACG	CCATTTCAAG	1400
TAATACAACA	GAATCTAATA	AACAATACGG	AGCAAGTAGT	GAAAAAATGG	1450
CTGCTGCTTA	TGCTGCCTTT	GCAAATGGTG	GCACTTACTA	TAAACCAATG	1500
TATATCCATA	AAGTCGTCTT	CAGTGATGGA	AGTAAAAAAG	AGTTCTCTAA	1550
TGTCGGAAC	CGTGCCATGA	AGGAAACGAC	AGCCTATATG	ATGACCGACA	1600
TGATGAAAAC	AGTCTTGACT	TATGGAAC	GGCGTGGAGC	CTATCTTCCT	1650
TGGCTTCCTC	AAGCTGGTAA	AACAGGAACC	TCTAACTATA	CAGATGAGGA	1700
AGTTGAAAAC	CACATCAAGA	ACACTGGCTA	TGTAGCTCCA	GATGAAATGT	1750
TTGTTGGTTA	TACTCGTAAG	TATTCTATGG	CTGTATGGAC	AGGTTATTCTG	1800
AATCGTTTAA	CTCCTATCGT	TGGAGATGGT	TTCCTAGTTG	CAGCTAAAGT	1850
TTATCGCTCA	ATGATAACGT	ATCTATCAGA	AGATACTCAT	CCAGAAGACT	1900
GGACGATGCC	AGACGGACTT	TTCAGAAATG	GAGAATTCGT	ATTTAAAAAT	1950
GGTGCTCGTT	CTACGTGGAA	CTCACCTGCT	CCACAACAAC	CCCCATCAAC	2000
TGAAAGTTCA	AGCTCATCAT	CAGATAGTTC	AACCTCACAG	TCTAGCTCAA	2050
CCACTCCAAG	CACAAATAAT	AGTACGACTA	CCAATCCTAA	CAATAATACG	2100
CAACAATCAA	ATACAACCCC	TGATCAACAA	AATCAGAATC	CTCAACCAGC	2150
ACAACCATAA					2160

2) INFORMATION FOR SEQ ID NO: 2050

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 930 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
- (B) STRAIN: 8303; 35193
- (C) ACCESSION NUMBER: AF046230

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2050

CTGTGGGATA	TCTACAAC	TC	CGATCAATAC	GTCTCTTACC	CTGACGATGA	50
TTTGCAAGTC	GCATCTACGG	TC	CGTAGATGT	TTCAAATGGT	AAAGTCATCG	100
CCCAACTTGG	AGCTCGTCAC	CA	AGCAAGTA	ACGTTTCATT	TGGTACCAAC	150
CAAGCTGTGG	AAACCAATCG	TG	ACTGGGGT	TCTGCTATGA	AACCAATCAC	200
CGATTATGCA	CCTGCCATAG	AA	TACGGTGT	TTATGATTCC	ACTGCAACTA	250
TGGTTAATGA	TATTCCTTAT	AA	CTATCCGG	GAACAAGCAC	ACCTGTCTAC	300
AACTGGGATA	GAGCATATTT	CG	GTAATATT	ACTCTGCAAT	ATGCTCTTCA	350
ACAATCACGA	AATGTCACAG	CC	GTTGAGAC	TTTGAATAAG	GTCGGTCTAG	400
ATAGAGCTAA	AACCTTCCTT	AA	TGGTCTTG	GTATCGACTA	TCCAAGCATG	450
CATTATGCAA	ACGCCATTTT	AA	GTAATACA	ACAGAATCTA	ATAAACAAATA	500
CGGAGCAAGT	AGTGAAAAAA	TG	GCTGCTGC	TTATGCTGCC	TTTGCAAATG	550
GTGGCACTTA	CTATAAACCA	AT	GTATATCC	ATAAAGTCGT	CTTCAGTGAT	600
GGAAGTAAAA	AAGAGTTCTC	TA	ATGTGCGGA	ACTCGTGCCA	TGAAGGAAAC	650
GACAGCCTAT	ATGATGACCG	AC	ATGATGAA	AACAGTCTTG	ACTTATGGAA	700
CTGGGCGTGG	AGCCTATCTT	CC	TGCGCTTC	CTCAAGCTGG	TAAAACAGGA	750
ACCTCTAACT	ATACAGATGA	GG	AAGTTGAA	AACCACATCA	AGAACACTGG	800
CTATGTAGCT	CCAGATGAAA	TG	TTTGTTGG	TTATACTCGT	AAGTATTCTA	850
TGGCTGTATG	GACAGGTTAT	TC	GAAATCGTT	TAACCTCCTAT	CGTTGGAGAT	900
GGTTTCCTAG	TTGCAGCTAA	AG	TTTATCGC			930

2) INFORMATION FOR SEQ ID NO: 2051

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 930 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
- (B) STRAIN: 63509; M11
- (C) ACCESSION NUMBER: AF046238

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2051

CTGTGGGATA	TTTACAATAC	AG	ACGAATAC	GTTGCCTATC	CAGATGATGA	50
CATGCAAGTA	GCTTCGACTA	TT	GTAGATGT	ATCTAATGGT	AACGTTATTG	100
CACAACTTGG	TGCTCGTCAT	CA	AGCAAGTA	ATGTTTCATT	CGGCACCAAC	150
CAGGCTGTGG	AGACCAATCG	TG	ACTGGGGT	TCTTCTATGA	AACCAATCAC	200
TGACTATGCT	CCCGCTTTAG	AA	TATGGAGT	CTATGACTCT	ACTGCTTCTA	250
TTGTACATGA	TGTTCCCTTAT	AA	CTATCCCTG	GCACTGATAC	TCCAGTCTAC	300
AACTGGGATC	ATGTCTACTT	TG	GAAACATT	ACAATCCAGT	ATGCTCTTCA	350
ACAATCACGA	AATGTCACAG	CC	GTTGAGAC	TTTGAATAAG	GTCGGTCTAG	400
ATAGAGCTAA	AACCTTCCTT	AA	TGGTCTTG	GTATCGACTA	TCCAAGCATG	450
CATTATGCAA	ACGCCATTTT	AA	GTAACACA	ACTGAATCCA	ACAAACAGTA	500
CGGTGCAAGT	AGTGAAAAGA	TG	GCTGCTGC	TTATGCCGCC	TTTCTAATG	550
GTGGTATTTA	CCACAAACCA	AT	GTATATCA	ATAAAATCGT	CTTCAGTGAT	600
GGTAGTGAAA	AAGAATTTTC	TG	ATGCTGGT	ACACGAGCTA	TGAAAGAAAC	650
TACTGCCTAT	ATGATGACCG	AA	ATGATGAA	AACGTGTTTA	GCTTACGGAA	700
CCGGACGTGG	TGCTTACCTA	CC	ATGGCTTC	CACAAGCAGG	TAAGACAGGT	750

ACTTCTAACT	ATACTGACGA	CGAAATTGAA	AAGTATATCA	AGAACACTGG	800
CTACGTAGCT	CCAGATGAAA	TGTTTGTGG	TTATACTCGT	AAGTATTCTA	850
TGGCTGTATG	GACTGGTTAC	TCAAATCGTT	TAACTCCAAT	CGTAGGAGAT	900
GGTTTCCTAG	TTGCTGCTAA	GGTTTATCGC			930

2) INFORMATION FOR SEQ ID NO: 2052

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1195 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
- (B) STRAIN: #22/HA5
- (C) ACCESSION NUMBER: AB006877

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2052

GTCTCTTACC	CTGACGATGA	TTTGCAAGTC	GCATCTACGG	TCGTAGATGT	50
TTCCAATGGT	AAAGTCATCG	CCCAACTTGG	AGCTCGTCAC	CAAGCAAGTA	100
ACGTTTCATT	TGGTACCAAC	CAAGCTGTGG	AAACCAATCG	TGACTGGGGT	150
TCAACAATGA	AACCAATCAC	CGATTATGCA	CCTGCCATAG	AATACGGTGT	200
ATATGATTCC	ACTGCAACTA	TGGTTAATGA	TATTCCTTAT	AACTATCCGG	250
GAACAAGCAC	ACCTGTCTAC	AACTGGGATC	GAGCATATTT	TGGTAATATT	300
ACTCTGCAAT	ATGCCCTTCA	ACAATCACGT	AATGTTACAG	CAGTTGAAAC	350
ATTAAACAAG	GTTGGTTTAG	ATCGAGCCAA	AACTTTCCTA	AATGGCTTAG	400
GTATCGATTA	CCCAAGCATA	CACATATGCTA	ACGCCATTTT	AAGTAATACA	450
ACAGAATCTA	ACAAACATTA	CGGTGCAAGT	AGTGAAAAAA	TGGCTGCTGC	500
TTATGCCGCC	TTTGCTAATG	GTGGTATTTA	CCACAAACCA	ATGTATATCA	550
ATAAAATCGT	CTTTAGTGAT	GCTAGTGAGA	AAGAATTTTC	TGATGCTGGT	600
ACACGAGCTA	TGAAAGAAAC	TACTGCCTAT	ATGATGACCG	AAATGATGAA	650
AACTGTTTTA	GCTTACGGAA	CCGGACGTGG	TGCTTACCTA	CCATGGCTTC	700
CACAAGCAGG	TAAGACAGGT	ACTTCTAACT	ATACTGATGA	CGAAATCGAA	750
AAACATATCA	AGAATACTGG	CTACGTAGCT	CCAGATGAAA	TGTTTGTAGG	800
CTATACTCGT	AAGTATTCTA	TGGCTGTATG	GACTGGTTAC	TCAAATCGTT	850
TAACTCCAAT	TGTTGGAGAT	GGTTTCCTAG	TTGCTGCTAA	GGTTTATCGC	900
TCAATGATAT	CGTATCTATC	AGAAGATGAC	CAACCTGGAG	ATTGGACGAT	950
GCCAGACGGC	CTGTTCCGAA	ATGGAGAATT	CGTATTTAAA	AATGGTGCTC	1000
GTTCTACGTG	GAATCACCT	GCTCCACAAC	AACCCCATC	AACTGAAAGT	1050
TCAAGCTCAT	CATCAGATAG	TTCAACTTCA	CAGTCTAGCT	CAACCACTCC	1100
AAGCACAAAT	AATAGTACGA	CTACCAATCC	TAACAATAAT	ACGCAACAAT	1150
CAAATACAAC	CCCTGATCAA	CAAAATCAGA	ATCCTCAACC	AGCAC	1195

2) INFORMATION FOR SEQ ID NO: 2053

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 930 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(B) STRAIN: 17619

(C) ACCESSION NUMBER: AF046237

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2053

CTGTGGGATA	TTTACAATAC	AGACGAATAC	GTTGCCTATC	CAGACGATGA	50
ATTGCAAGTC	GCTTCTACCA	TTGTTGATGT	TTCTAACGGT	AAAGTCATTG	100
CCCAGCTAGG	AGCACGCCAT	CAGTCAAGTA	ATGTTTCCTT	CGGAATTAAC	150
CAAGCAGTAG	AAACAAACCG	CGACTGGGGA	TCAACTATGA	AACCGATCAC	200
AGACTATGCT	CCTGCCTTGG	AGTACGGTGT	CTACGATTCA	ACTGCTACTA	250
TCGTTACGA	TGAGCCCTAT	AACTACCCTG	GGACAAATAC	TCCTGTTTAT	300
AACTGGGATA	GGGGCTACTT	TGGCAACATC	ACCTTGCAAT	ACGCCCTGCA	350
ACAATCGCGA	AACGTCCCAG	CCGTGGAAAC	TCTAAACAAG	GTCGGACTCA	400
ACCGCGCCAA	GACTTTCCTA	AATGGTCTCG	GAATCGACTA	CCCAAGTATT	450
CACTACTCAA	ATGCCATTTC	AAGTAACACA	ACCGAATCAG	ACAAAAAATA	500
TGGAGCAAGT	AGTGAAAAGA	TGGCTGCTGC	TTACGCTGCC	TTTGCAAATG	550
GTGGAACCTA	CTATAAACCA	ATGTATATCC	ATAAAGTCGT	CTTTAGTGAT	600
GGGAGTGAAA	AAGAGTTCTC	TAATGTCGGA	ACTCGTGCCA	TGAAGGAAAC	650
GACAGCCTAT	ATGATGACCG	AAATGATGAA	AACAGTCTTG	AGTTATGGAA	700
CTGGACGAAA	TGCCTATCTT	GCTTGGCTTC	CTCAAGCTGG	TAAAACAGGT	750
ACCTCTAACT	ATACAGATGA	AGAAATTGAA	AAACACATCA	AAAACACTGG	800
CTATGTAGCT	CCAGATGAAA	CGTTTGTTGG	TTATACTCGT	AAGTATTCTA	850
TGGCTGTATG	GACAGGTTAC	ACAAACCGTC	TCACACCAAT	TGTGGGGGAT	900
GGCTTCACAG	TTGCTGCCAA	AGTTTACCGC			930

2) INFORMATION FOR SEQ ID NO: 2054

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 306 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(B) STRAIN: R6

(C) ACCESSION NUMBER: Y07845

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2054

CGTCGCATTC	TCTACGGAAT	GAATGAATTG	GGTGTGACCC	CAGACAAACC	50
CCATAAAAAA	TCTGCTCGTA	TTACAGGGGA	TGTCATGGGT	AAATACCACC	100
CACACGGGGA	TTCCTCTATT	TATGAAGCCA	TGGTCCGTAT	GGCTCAATGG	150
TGGAGCTACC	GTTACATGCT	TGTAGATGGT	CATGGGAATT	TTGGTTCCAT	200
GGATGGAGAT	AGTGCTGCCG	CTCAACGTTA	TACCGAGGCA	CGTATGAGCA	250
AGATTGCTCT	GGAAATGCTT	CGTGATATCA	ACAAAAATAC	AGTTGATTTC	300
GTTGAT					306

2) INFORMATION FOR SEQ ID NO: 2055

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2472 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
- (B) STRAIN: 7785
- (C) ACCESSION NUMBER: Z67739

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2055

ATGTCTAACA	TTCAAAACAT	GTCCCTGGAG	GACATCATGG	GAGAGCGCTT	50
TGGTCGCTAC	TCCAAGTACA	TTATTCAAGA	CCGGGCTTTG	CCAGATATTC	100
GTGATGGGTT	GAAGCCGGTT	CAGCGCCGTA	TTCTTTATTC	TATGAATAAG	150
GATAGCAATA	CTTTTGACAA	GAGCTACCGT	AAGTCGGCCA	AGTCAGTCGG	200
GAACATCATG	GGGAATTTCC	ACCCACACGG	GGATTCTTCT	ATCTATGATG	250
CCATGGTTTCG	TATGTCACAG	AACTGGAAAA	ATCGTGAGAT	TCTAGTTGAA	300
ATGCACGGTA	ATAACGGTTC	TATGGACGGA	GATCCTCCTG	CGGCTATGCG	350
TTATACTGAG	GCACGTTTGT	CTGAAATTGC	AGGCTACCTT	CTTCAGGATA	400
TCGAGAAAAA	GACAGTTCCT	TTTGCATGGA	ACTTTGACGA	TACGGAGAAA	450
GAACCAACGG	TCTTGCCAGC	AGCCTTTCCA	AACCTCTTGG	TCAATGGTTC	500
GACTGGGATT	TCGGCTGGTT	ATGCCACAGA	CATTCTCTCC	CATAATTTAG	550
CTGAGGTCAT	AGATGCTGCA	GTTTACATGA	TTGACCACCC	AACTGCAAAG	600
ATTGATAAAC	TCATGGAATT	CTTACCTGGA	CCAGACTTCC	CTACAGGGGC	650
TATTATTTCAG	GGTCGTGATG	AAATCAAGAA	AGCTTATGAG	ACTGGGAAAG	700
GGCGCGTGGT	TGTTTCGTTCC	AAGACTGAAA	TTGAAAAGCT	AAAAGGTGGT	750
AAGGAACAAA	TCGTTATTAC	TGAGATTTCCT	TATGAAATCA	ATAAGGCCAA	800
TCTAGTCAAG	AAAATCGATG	ATGTTTCGTGT	TAATAACAAG	GTAGCTGGGA	850
TTGCTGAGGT	TCGTGATGAG	TCTGACCGTG	ATGGTCTTCG	TATCGCTATC	900
GAACCTTAAGA	AAGACGCTAA	TACTGAGCTT	GTTCTCAACT	ACTTATTTAA	950
GTACACCGAC	CTACAAATCA	ACTACAACCT	TAATATGGTG	GCGATTGACA	1000
ATTTACACACC	TCGTCAGGTT	GGGATTGTTC	CAATCCTGTC	TAGCTACATC	1050
GCTCACCGTC	GAGAAGTGAT	TTTGGCGCGT	TCACGCTTTG	ACAAAGAAAA	1100
GGCTGAGAAA	CGTCTCCATA	TCGTCGAAGG	TTTGATTTCGT	GTGATTTCGA	1150
TTTTGGATGA	AGTCATTGCT	CTTATCCGTG	CTTCTGAGAA	TAAGGCGGAC	1200
GCCAAGGAAA	ACCTCAAAGT	TAGCTATGAT	TTTACGGAAG	AACAGGCTGA	1250
GGCTATCGTA	ACTTTGCAAC	TGTACCGTTT	GACCAATACC	GATGTGGTTG	1300
TCTTGACAGGA	AGAAGAAGCA	GAGCTTCGTG	AGAAGATTGC	TATGCTGGCG	1350
GCTATTATCG	GTGATGAAAG	GACTATGTAC	AATCTCATGA	AGAAAGAACT	1400
TCGTGAGGTC	AAGAAGAAAT	TTGCAACTCC	TCGTTTGAGT	TCTTTAGAAG	1450
AACTGCGGAA	AGCAATTGAG	ATTGATACAG	CTAGTCTTAT	CGCTGAGGAA	1500
GATACCTACG	TCAGCGTGAC	CAAGGCAGGT	TACATCAAGC	GTACCACTCC	1550
ACGTTCCCTTT	GCGGCTTCCA	CCTTGGAAGA	AATTGGCAAG	CGTGATGATG	1600
ACCGTTTGAT	TTTTGTTCAA	TCTGCCAAGA	CAACCCAGCA	CCTCTTGATG	1650
TTCACAAGTC	TTGGAAATGT	CATCTACAGA	CCAATCCATG	AGTTGGCAGA	1700
TATTCGTTGG	AAGGACATCG	GAGAGCATCT	GAGCCAAACC	ATCACAAACT	1750
TTGAAACGAA	TGAAGAAATC	CTTTATGTGG	AAGTACTGGA	TCAGTTTGAC	1800
GATGCGACAA	CCTACTTTGC	AGTGACTCGC	CTTGGTCAAA	TCAAACGGGT	1850

AGAGCGAAAA	GAATTCACCTC	CATGGCGGAC	CTATAGATCT	AAGTCTGTCA	1900
AGTATGCTAA	GCTCAAAGAC	GATACAGATC	AGATTGTAGC	AGTGGCTCCG	1950
ATTAAACTAG	ATGATGTTGT	CTTGCTTAGT	CAAAATGGTT	ATGCCCTGCG	2000
TTTCAATATC	GAAGAGGTTC	CGGTTGTCCG	TGCTAAGGCA	GCAGGTGTCA	2050
AGGCTATGAA	TTTGAAAGAA	GATGATGTCC	TCCAATCTGG	CTTTATCTGT	2100
AATACTTCGT	CCTTCTACCT	CTTGACCCAG	CGTGGAAGCT	TGAAACGTGT	2150
TTCTATTGAG	GAAATTCTAG	CAACCAGCCG	TGCCAAACGA	GGATTACAAG	2200
TCTTGCGTGA	GTTGAAAAAC	AAACCGCATC	GTGTCTTCTT	GGCAGGAGCA	2250
GTTGCAGAGC	AAGGATTTGT	TGGCGATTTT	TTCAGTACGG	AAGTGGATGT	2300
GAACGACCAA	ACTCTGCTTG	TCCAATCCAA	TAAAGGAACA	ATCTATGAAA	2350
GCCGATTGCA	AGACTTGAAC	TTGTCAGAAC	GCACTAGCAA	TGGAAGCTTC	2400
ATTTCTGACA	CGATTTTCAGA	TGAAGAAGTT	TTTGACGCTT	ATCTTCAGGA	2450
AGTAGTTACT	GAAGATAAAT	AA			2472

2) INFORMATION FOR SEQ ID NO: 2056

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1212 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
- (B) STRAIN: StrR-16

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2056

AAGCTCAAAA	ACATCTGTGG	GATATCTACA	ACTCCGATCA	ATACGTCTCT	50
TACCCTGACG	ATGATTTGCA	AGTCGCATCT	ACGGTCGTAG	ATGTTTCAAA	100
TGGTAAAGTC	ATTGCCCAAC	TTGGAGCTCG	TCACCAAGCA	AGTAACGTTT	150
CATTTGGCAC	CAACCAAGCT	GTGGAAACCA	ATCGTGACTG	GGGTTCAACA	200
ATGAAACCAA	TCACAGACTA	TGCTCCTGCC	TTGGAATACG	GTGTCTACGA	250
TTCAACTGCT	ACTATCGTTC	ACGATGAGCC	CTATAACTAT	CCTGGGACAG	300
ATACCCCTGT	CTATAACTGG	GATAGGGGCT	ACTTTGGCAA	TATCACCTTG	350
CAATACGCCC	TGCAACAATC	GCGAAACGTC	CCAGCCGTGG	AAACACTAAA	400
CAAGGTCGGG	CTCAACCGCG	CCAAGACTTT	TCTAAATGGT	CTCGGAATCG	450
ACTACCCAAG	TATTCACTAC	TCAAATGCCA	TTTCAAGTAA	CACAACCGAG	500
TCAGACAAAA	AATATGGAGC	AAGTAGTGAA	AAGATGGCTG	CTGCTTACGC	550
TGCCTTTGCA	AATGGTGGAA	CTTACTATAA	ACCAATGTAT	ATCCATAAAG	600
TCGTCTTTAG	TGATGGAAGT	GAAAAAGAGT	TCTCTAATGT	CGGAACTCGC	650
GCCATGAAAG	AAACGACTGC	TTACATGATG	ACAGAAATGA	TGAAAAACAGT	700
CTTGACGTAC	GGAATTGGTC	GTGGTGCCTA	CCTGCCTTGG	CTTCCTCAAG	750
CTGGTAAAAC	AGGTACTTCT	AACTATACTG	ACGAAGAAAT	TGAAAAAGTAT	800
ATCAAGAACA	CTGGTTACGT	AACTCCAGAT	GAAATGTTTG	TAGGGTATAC	850
CCGTAAATAT	GCAATGGCTG	TATGGACAGG	CTATTCTAAC	CGTCTGACAC	900
CATTGTAGG	CGATGGCCTT	ACGGTCGCTG	CCAAGGTTTA	CCGCTCTATG	950
ATGACCTACC	TGTCTGAAGG	AAGCAATCCA	GAGGATTGGA	ATATACCAGA	1000
GGGGCTCTAC	AGAAATGGAG	AATTCGTATT	TAAAAATGGT	GCTCGTTCTA	1050
CGTGGAGCTC	ACCTGCTCCA	CAACAACCCC	CATCAACTGA	AAGTTCAAGC	1100
TCATCATCAG	ATAGTTCAAC	TTCACAGTCT	AGCTCAACCA	CTCCAAGCAC	1150
AAATAATAGT	ACGACTACCA	ATCCTAACAA	TAATACGCAA	CAATCAAATA	1200
CAACCCCTGA	TC				1212

2) INFORMATION FOR SEQ ID NO: 2057

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1242 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
- (B) STRAIN: StrR-17

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2057

ATGTAGACCA	AGAAGCTCAA	AAACATCTGT	GGGATATTTA	CAATACAGAC	50
GAATACGTTG	CCTATCCAGA	CGATGAATTG	CAAGTCGCTT	CTACCATTGT	100
TGATGTTTCT	AACGGGAAAG	TTATTGCTCA	GTTAGGTTCT	CGTCACCAAT	150
CAAGCAATGT	TTCCTTCGGA	ATCAACCAAG	CTGTTGAAAC	CAACCGTGAC	200
TGGGGTTCTG	CCATGAAGCC	AATCACAGAC	TATGCTCCTG	CCTTAGAGTA	250
TGACATCTAC	GACTCAACTG	CTTCGATTGT	ACATGATGTT	CCTTATAACT	300
ATCCAGGTAC	TGATACTCCC	CTCTACAACT	GGGATAAAGT	CTACTTTGGA	350
AATATTACAA	TCCAGTATGC	ACTTCAACAG	TCACGTAATG	TCACAGCCGT	400
TGAGACTTTG	AATAAGGTCG	GTCTAGATAG	AGCTAAAACC	TTTCTTAATG	450
GTCTTGGTAT	CGACTATCCA	AGCATGCATT	ATGCAAACGC	CATTTCAAGT	500
AATACGACTG	AGTCAAACAA	AAAGTACGGA	GCAAGTAGTG	AGAAAATGGC	550
TGCTGCTTAC	GCTGCTTTTG	CTAACGGTGG	TATCTACCAT	AAACCAATGT	600
ATATCAACAA	AATCGTCTTT	AGCGATGGTA	GCTCAAAAGA	ATACGCTGAT	650
CCTGGTACTC	GTGCCATGAA	AGAGACGACC	GCCTATATGA	TGACAGAAAT	700
GATGAAGACT	GTCTTGGCAT	ACGGAACGGG	TCGTGGTGCT	TATCTCCCTT	750
GGCTACCTCA	AGCTGGTAAG	ACTGGTACAT	CAAACTATAC	AGATGATGAA	800
ATTGAAAAC	ACATCAAAAA	TACTGGTTAT	GTAGCTCCAG	ACGAAATGTT	850
TGTTGGTTAT	ACTCGCAAAT	ATTCAATGGC	GGTATGGACA	GGTTACTCAA	900
ACCGCCTGAC	TCCTATCGTT	GGTGATGGCT	TCTATGTTGC	AGCTAAGGTT	950
TACCGTTCAA	TGATGACTTA	TCTGTCTGAG	GATAACAACC	CTGGCGACTG	1000
GACTATGCCA	GAAGGTCTCT	ATCGAAGTGG	TGAGTTCGTC	TTTAAAAAAG	1050
GTGCTCGTTC	TGCATGGACT	GCTCCTGCTC	CGCAACAGGC	CCCAACACCA	1100
GAAAGTTCTGA	GCTCGACATC	AGAAAGTTCA	ACTTCACAGT	CAAGCTCAAC	1150
TACTCCAAGC	ACGAATAATA	GTGCAAACAA	TAATACCAAT	AACCAGCAAC	1200
CAAATACAAC	GCCTGGTCAA	CAAAACCAGA	ACCAAAATCA	GA	1242

2) INFORMATION FOR SEQ ID NO: 2058

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1225 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
 (B) STRAIN: StrR-18

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2058

GAAGCTCAAA	AACATCTGTG	GGATATTTAC	AATACAGACG	AATACGTTGC	50
CTATCCAGAC	GATGAATTGC	AAGTCGCTTC	TACCATTGTT	GATGTTTCTA	100
ACGGGAAAGT	TATTGCTCAG	TTAGGTTCTC	GTCACCAATC	AAGCAATGTT	150
TCCTTCGGAA	TCAACCAAGC	TGTTGAAACC	AACCGTGA	GGGGTTCTGC	200
CATGAAGCCA	ATCAGAGACT	ATGCTCCTGC	CTTAGAGTAT	GACATCTACG	250
ACTCAACTGC	TTCGATTGTA	CATGATGTTT	CTTATAACTA	TCCAGGTACT	300
GATACTCCCC	TCTACAACTG	GGATAAAGTC	TACTTTGGAA	ATATTACAAT	350
CCAGTATGCA	CTTCAACAGT	CACGTAATGT	CACAGCCGTT	GAGACTTTGA	400
ATAAGGTCGG	TCTAGATAGA	GCTAAAACCT	TTCTTAATGG	TCTTGGTATC	450
GACTATCCAA	GCATGCATTA	TGCAAAACGCC	ATTTCAAGTA	ATACGACTGA	500
GTCAAACAAA	AAGTACGGAG	CAAGTAGTGA	GAAAAATGGCT	GCTGCTTACG	550
CTGCTTTTGC	TAACGGTGGT	ATCTACCATA	AACCAATGTA	TATCAACAAA	600
ATCGTCTTTA	GCGATGGTAG	CTCAAAAGAA	TACGCTGATC	CTGGTACTCG	650
TGCCATGAAA	GAGACGACCG	CCTATATGAT	GACAGAAATG	ATGAAGACTG	700
TCTTGGCATA	CGGAACGGGT	CGTGGTGCTT	ATCTCCCTTG	GCTACCTCAA	750
GCTGGTAAGA	CTGGTACATC	AAACTATACA	GATGATGAAA	TTGAAAATA	800
CATCAAAAAT	ACTGGTTATG	TAGCTCCAGA	CGAAATGTTT	GTTGGTTATA	850
CTCGCAATA	TTCAATGGCG	GTATGGACAG	GTTACTCAA	CCGCCTGACT	900
CCTATCGTTG	GTGATGGCTT	CTATGTTGCA	GCTAAGGTTT	ACCGTTCAAT	950
GATGACTTAT	CTGTCTGAGG	ATAACAACCC	TGGCGACTGG	ACTATGCCAG	1000
AAGGTCTCTA	TCGAAGTGGT	GAGTTCGTCT	TTAAAAAAGG	TGCTCGTTCT	1050
GCATGGACTG	CTCCTGCTCC	GCAACAGGCC	CCAACACCAG	AAAGTTCGAG	1100
CTCGACATCA	GAAAGTTCAA	CTTACAGTC	AAGCTCAACT	ACTCCAAGCA	1150
CGAATAATAG	TGCAACAAT	AATACCAATA	ACCAGCAACC	AAATACAACG	1200
CCTGGTCAAC	AAAACCAGAA	CCAAA			1225

2) INFORMATION FOR SEQ ID NO: 2059

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 554 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
 (B) STRAIN: StrR-38

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2059

TGGCTACTTT	GGAAACATTA	CAGTCCAGTA	TGCTCTTCAA	CAATCACGAA	50
ATGTCACAGC	CGTTGAGACT	TTGAATAAGG	TCGGTCTAGA	TAGAGCTAAA	100
ACCTTCCTCA	ATGGACTTGG	TATCGATTAT	CCAAGCATGC	TTTATGCAAA	150
CGCCATTTCA	AGTAACACAA	CTGAATCCAA	CAAAAAGTAC	GGAGCAAGTA	200
GTGAAAAAAT	GGCCGCTGCC	TACGCAGCTT	TTGCTAATGG	TGGTACTTAC	250
CACAAACCAA	TGTATATCAA	TAAAATCGTC	TTTAGTGATG	GTAGTGAAAA	300
AGAATTTTCT	GATGCCGCTA	CTCGGGCTAT	GAAAGAAACT	ACTGCCTATA	350

TGATGACCGA	AATGATGAAA	ACTGTCTTAT	TATACGGAAC	CGGACGTGGA	400
GCCTACCTAC	CTTGGCTTCC	ACAAGCAGGT	AAGACAGGTA	CTTCTAACTA	450
TACTGACGAA	GAAATTGAAA	AGTATATCAA	GAATGCTGGT	TACGTAGCTC	500
CAGATGAAAT	GTTTGTGGT	TATACCCGCA	AATATGCAAT	GGCTGTTTGG	550
ACAG					554

2) INFORMATION FOR SEQ ID NO: 2060

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1249 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
- (B) STRAIN: StrR-57

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2060

CAACTGGGAT	GGATGTCTAC	ACAAATGTAG	ACCAAGAAGC	TCAAAAACAT	50
CTGTGGGATA	TTTACAATAC	AGACGAATAC	GTTGCCTATC	CAGACGATGA	100
ATTGCAAGTC	GCTTCTACCA	TTGTTGATGT	TTCTAACGGT	AAAGTCATTG	150
CCCAGCTAGG	AGCACGCCAT	CAGTCAAGTA	ATGTTTCCTT	CGGAATTAAC	200
CAAGCAGTAG	AAACAAACCG	CGACTGGGGA	TCAACTATGA	AACCGATCAC	250
AGACTATGCT	CCTGCCTTGG	AGTACGGTGT	CTACGATTCA	ACTGCTACTA	300
TCGTTACGA	TGAGCCCTAT	AACTACCCTG	GGACAAATAC	TCCTGTTTAT	350
AACTGGGATA	GGGGCTACTT	TGGCAACATC	ACCTTGCAAT	ACGCCCTGCA	400
ACAATCGCGA	AACGTCCCAG	CCGTGGAAAC	TCTAAACAAG	GTCTGGACTCA	450
ACCGCGCCAA	GACTTTCCTA	AATGGTCTAG	GAATCGACTA	CCCAAGTATT	500
CACTACTCAA	ATGCCATTTT	AAGTAACACA	ACCGAATCAG	ACAAAAAATA	550
TGGAGCAAGT	AGTGAAAAGA	TGGCTGCTGC	TTACGCTGCC	TTTGCAAATG	600
GTGGAACCTA	CTATAAACCA	ATGTATATCC	ATAAAGTCGT	CTTTAGTGAT	650
GGGAGTGAAA	AAGAGTTCTC	TAATGTCGGA	ACTCGTGCCA	TGAAGGAAAC	700
GACAGCCTAT	ATGATGACCG	ACATGATGAA	AACAGTCTTG	ACTTATGGAA	750
CTGGACGAAA	TGCCTATCTT	GCTTGGCTCC	CTCAGGCTGG	TAAAAACAGGA	800
ACCTCTAACT	ATACAGACGA	GGAAATTGAA	AACCACATCA	AGACCTCTCA	850
ATTTGTAGCA	CCTGATGAAC	TATTTGCTGG	CTATACGCGT	AAATATTCAA	900
TGGCTGTATG	GACAGGCTAT	TCTAACCGTC	TGACACCACT	TGTAGGCAAT	950
GGCCTTACGG	TCGCTGCCAA	AGTTTACCGC	TCTATGATGA	CCTACCTGTC	1000
TGAAGGAAGC	AATCCAGAAG	ATTGGAATAT	ACCAGAGGGG	CTCTACAGAA	1050
ATGGAGAATT	CGTATTTAAA	AATGGTGCTC	GTTCTACGTG	GAGCTCACCT	1100
GCTCCACAAC	AACCCCCATC	AACTGAAAGT	TCAAGCTCAT	CATCAGATAG	1150
TTCAACTTCA	CAGTCTAGCT	CAACCACTCC	AAGCACAAT	AATAGTACGA	1200
CTACCAATCC	TAACAATAAT	ACGCAACAAT	CAAATACAAC	CCCTGATCA	1249

2) INFORMATION FOR SEQ ID NO: 2061

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 579 bases
- (B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(B) STRAIN: StrR-60

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2061

GAAGTTGAAC	AGACTGGTCA	CCAAGCTCCT	TCATATCCGC	CAACACTGCA	50
ATTTTCTTGC	CACCTTCATT	GGCTGGAATG	GCAGAGAAAG	TCTCTAAAAT	100
CAGTTTCATA	GCAGTTGGAT	TGGCATTATA	AACATCTGAC	AGGATATCTG	150
CTCCATTGGC	TGCTTTCTTC	CACTCGGTAC	GGTTACGCGT	CAATTCAAGA	200
TGTTGGAAGG	CCAAACGAAT	TTGCTCCTCT	GAAACTCCTT	CTTGCAAGGC	250
AACATAGGAT	GCAATCATAG	CATTTGTGCG	ATTGTACTTG	CCAGTTACTG	300
GCAAATCAAG	GGCTTGCTCT	AAGAAATTGA	CCTTGAAGGT	CAGACTATCT	350
TTGCGCTCAA	CCAAGTCGGT	AATTCCCAGC	TCTGCTCCTT	GACCAAAACG	400
AACCACCTTT	TTATCAGTTG	GCAAATAGTC	CTCTACGATA	GGGTCAGCCG	450
GCGCTAAAAG	CAAGGAACCT	GAAGCCATTC	CGTCTGCAAT	TTGCATTTTT	500
CCTTTAGCAA	TCTCAGAACG	GTCTTTGAAA	AAGGCCAAAT	GAGCTTCTCC	550
AACCAAGGTC	ACGATGGCTG	TATGGACAG			579

2) INFORMATION FOR SEQ ID NO: 2062

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1216 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(B) STRAIN: StrR-63

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2062

AAGCTCAAAA	ACATCTGTGG	GATATCTACA	ACTCCGATCA	ATACGTCTCT	50
TACCCTGACG	ATGATTTGCA	AGTCGCATCT	ACGGTCGTAG	ATGTTTCAAA	100
TGGTAAAGTC	ATCGCACAA	TTGGTGCTCG	TCATCAAGCA	AGTAATGTTT	150
CATTCGGTAC	CAACCAGGCC	GTAGAAACCA	ATCGTGACTG	GGGATCATCA	200
ATGAAACCAA	TCACTGACTA	TGCTCCCGCT	TTAGAATATG	GAGTCTATGA	250
CTCTACTGCT	TCTATTGTAC	ATGATGTCCC	TTATAACTAT	CCTGGCACTG	300
ATACTCCACT	CTACAACCTG	GATCATGTCT	ACTTTGGAAA	CATTACAATC	350
CAGTATGCTC	TTCAACAATC	ACGAAATGTC	ACAGCCGTTG	AGACTTTGAA	400
TAAGGTCGGT	CTAGATAGAG	CTAAAACCTT	CCTTAATGGT	CTTGGTATCG	450
ACTATCCAAG	CATGCATTAT	GCAAACGCCA	TTTCAAGTAA	CACAACTGAA	500
TCCAACAAAA	AATATGGTGC	AAGTAGTGAA	AAAATGGCTG	CTGCCTACGC	550
TGCTTTTGCT	AATGGTGGTA	TTTATCACAA	ACCAATGTAT	ATCAATAAAA	600
TCGTCTTTAG	TGATGGTAGC	GAAAAAGAAT	TTTCTGATGC	TGGTACACGA	650
GCTATGAAAG	AGACTACTGC	CTATATGATG	ACTGAAATGA	TGAAAACGTG	700
TTTAACTTAC	GGAACAGGAC	GTGGAGCCTA	CCTACCATGG	CTTCCACAAG	750

CAGGTAAGAC	AGGTACTTCT	AACTATACTG	ACGAAGAAAT	TGAAAAGTAT	800
ATCAAGAACA	CTGGTTACGT	AGCTCCAGAT	GAAATGTTTG	TAGGGTATAC	850
CCGTAAATAT	GCAATGGCTG	TTTGGACAGG	ATACTCAAAT	CGTCTAACTC	900
CAATCATCGG	AGATGGTTTC	CTTGTTGCTG	GTAAAGTCTA	TCGTTCAATG	950
ATAACTTACC	TTTCTGAAGA	TGACCAACCT	GGAGATTGGA	CAATGCCAGA	1000
TGGCTTGAT	AGAAATGGAG	AATTCGTATT	TAAAAATGGT	GCTCGTTCTA	1050
CGTGGAGCTC	ACCTGCTCCA	CAACAACCCC	CATCAACTGA	AAGTTCAAGC	1100
TCATCATCAG	ATAGTTCAAC	TTCACAGTCT	AGCTCAACCA	CTCCAAGCAC	1150
AAATAATAGT	ACGACTACCA	ATCCTAACAA	TAATACGCAA	CAATCAAATA	1200
CAACCCCTGA	TCAACA				1216

2) INFORMATION FOR SEQ ID NO: 2063

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 810 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
- (B) STRAIN: ATCC 700673

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2063

AATACGTCTC	TTACCCCTGAC	GATGATTTGC	AAGTCGCATC	CACGGTCGTA	50
GATGTTTCAA	ATGGTAAAGT	CATCGCCCAA	CTTGGAGCTC	GTCACCAAGC	100
AAGTAACGTT	TCATTTGGTA	CCAACCAAGC	TGTGGAAACC	AATCGTGACT	150
GGGGTTCAAC	AATGAAACCC	ATCACCGATT	ATGCACCTGC	CATAGAATAC	200
GGTGTATATG	ATTCCACTGC	AACTATGGTT	AATGATATTC	CTTATAACTA	250
TCCGGGAACA	AGCACACCTG	TCTACAACCTG	GGATCGAGCA	TATTTTGGTA	300
ATATTACTCT	GCAATATGCC	CTTCAACAAT	CTCGTAACGT	ACCCGCCGTT	350
GAGACACTAA	ACAAGGTTGG	TTTAGATAGA	GCTAAAAGTT	TCCTAAATGG	400
TTTAGGAATC	GACTATCCTG	TAATGCACTA	TTCAAATGCT	ATTTCAAGTA	450
ATACTACCGA	ATCTAGTAAA	CAGTACGGGG	CAAGTAGTGA	AAAAATGGCC	500
ACTGCCTATG	CCGCATTTCG	AAACGGCGGT	ATTTACCACA	AACCAATGTA	550
CATCAATAAG	GTTGTCTTTA	GCGATGGTAG	CGAAAAAGAA	TTTTCTGACC	600
CTGGCACAAG	AGCCATGAAA	GAAACGACTG	CTTACATGAT	GACAGAGATG	650
ATGAAAACAG	TCTGGACTTA	CGGAACTGGT	CGCGGTGCCT	ACCTACCTTG	700
GCTTCCACAA	GCAGGTAAAA	CAGGTACTTC	TAACATACT	GACGAAGAAA	750
TTGAAAAGTA	TATCAAGAAC	ACTGGTTACG	TAGCTCCAGA	TGAAATGTTT	800
GTAGGGTATA					810

2) INFORMATION FOR SEQ ID NO: 2064

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 782 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
 (B) STRAIN: ATCC 700678

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2064

```

TCTTACCCTG ACGATGATTT GCAAGTCGCA TCTACGGTCG TAGATGTTTC      50
AAATGGTAAA GTCATCGCCC AACTTGGAGC TCGTCACCAA GCAAGTAACG      100
TTTCATTTGG TACCAACCAA GCTGTGGAAA CCAATCGTGA CTGGGGATCA      150
ACTATGAAAC CAATCACAGA CTATGCTCCT GCCTTGGAGT ACGGTGTCTA      200
CGATTCAACT GCTACTATCG TTCACGATGA GCCCTATAAC TACCCTGGGA      250
CAGATATCCC TCTCTATAAC TGGGATCGAG CATATTTTCGG TAATATTACT      300
CTGCAATATG CCCTTCAACA ATCTCGTAAC GTACCTGCCG TTGAAACACT      350
AAACAAGGTC GGTCTAGATA AGGCTAAAAC CTTCTTAAT GGTCTTGGA      400
TCGACTATCC AAGCATGCAT TATGCAAACG CCATTTCAAG TAATACAACT      450
GAATCCAACA AAAAATATGG TGCAAGTAGT GAAAAAATAG CTACCGCCTA      500
TGCCGCATTC GCAAATGGTG GTATTTACCA CAAACCAATG TACATCAATA      550
AAGTTGTCTT TAGCGATGGT AGCGAAAAAG AATTTTCTGA CCCTGGCACA      600
AGAGCCATGA AAGAAACGAC TGCTTACATG ATGACAGAAA TGATGAAAAC      650
AGTCTGGACG TACGGAAGTG GTCGTGGTGC CTACCTGCCT TGGCTTCCTC      700
AAGCTGGTAA AACAGGTACC TCTAACTATA CTGACGAAGA AATTGAAAAG      750
TATATCAAGA AACTGGTTA CGTAGCTCCA GA                          782
  
```

2) INFORMATION FOR SEQ ID NO: 2065

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2065

CCAGGACGTG GAGGCGATCA CA 22

2) INFORMATION FOR SEQ ID NO: 2066

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2066

CACCGACAGC GAGCCGATCA GA 22

2) INFORMATION FOR SEQ ID NO: 2067

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2067

AGCTGAGCCA ATTCATGG

18

2) INFORMATION FOR SEQ ID NO: 2068

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1068

ATTCATGGAC CAGAACAAC

19

2) INFORMATION FOR SEQ ID NO: 2069

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2069

CGCTGTCGGG GTTGACCC

18

2) INFORMATION FOR SEQ ID NO: 2070

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single

1073

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2070

GTTGACCCAC AAGCGCCG

18

2) INFORMATION FOR SEQ ID NO: 2071

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2071

CGACTGTCGG CGCTGGGG

18

2) INFORMATION FOR SEQ ID NO: 2072

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3534 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Mycobacterium tuberculosis*
- (B) STRAIN: Rv
- (C) ACCESSION NUMBER: L27989

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2072

GTGCTGGAAG	GATGCATCTT	GGCAGATTCC	CGCCAGAGCA	AAACAGCCGC	50
TAGTCCTAGT	CCGAGTCGCC	CGCAAAGTTC	CTCGAATAAC	TCCGTACCCG	100
GAGCGCCAAA	CCGGGTCTCC	TTCGCTAAGC	TGCGCGAACC	ACTTGAGGTT	150
CCGGGACTCC	TTGACGTCCA	GACCGATTCC	TTCGAGTGCC	TGATCGGTTC	200
GCCGCGCTGG	CGCGAATCCG	CCGCCGAGCG	GGGTGATGTC	AACCCAGTGG	250
GTGGCCTGGA	AGAGGTGCTC	TACGAGCTGT	CTCCGATCGA	GGACTTCTCC	300
GGGTCGATGT	CGTTGTCTGT	CTCTGACCCT	CGTTTCGACG	ATGTCAAGGC	350
ACCCGTCGAC	GAGTGCAAAG	ACAAGGACAT	GACGTACGCG	GCTCCACTGT	400
TCGTCAACGC	CGAGTTCATC	AACAACAACA	CCGGTGAGAT	CAAGAGTCAG	450
ACGGTGTTCA	TGGGTGACTT	CCCGATGATG	ACCGAGAAGG	GCACGTTCAT	500
CATCAACGGG	ACCGAGCGTG	TGGTGGTCAG	CCAGCTGGTG	CGGTCGCCCG	550
GGGTGTACTT	CGACGAGACC	ATTGACAAAGT	CCACCGACAA	GACGCTGCAC	600
AGCGTCAAGG	TGATCCCGAG	CCGCGGCGCG	TGGCTCGAGT	TTGACGTCGA	650
CAAGCGCGAC	ACCGTCGGCG	TGCGCATCGA	CCGCAAACGC	CGGCAACCCG	700

TCACCGTGCT	GCTCAAGGCG	CTGGGCTGGA	CCAGCGAGCA	GATTGTCGAG	750
CGGTTCCGGT	TCTCCGAGAT	CATGCGATCG	ACGCTGGAGA	AGGACAACAC	800
CGTCGGCACC	GACGAGGCGC	TGTTGGACAT	CTACCGCAAG	CTGCGTCCGG	850
GCGAGCCCCC	GACCAAAGAG	TCAGCGCAGA	CGCTGTTGGA	AAACTTGTTT	900
TTCAAGGAGA	AGCGCTACGA	CCTGGCCCCG	GTCGGTCGCT	ATAAGGTCAA	950
CAAGAAGCTC	GGGCTGCATG	TCGGCGAGCC	CATCACGTCG	TCGACGCTGA	1000
CCGAAGAAGA	CGTCGTGGCC	ACCATCGAAT	ATCTGGTCCG	CTTGACGAG	1050
GGTCAGACCA	CGATGACCGT	TCCGGGCGGC	GTCGAGGTGC	CGGTGGAAAC	1100
CGACGACATC	GACCACTTCG	GCAACCGCCG	CCTGCGTACG	GTCGGCGAGC	1150
TGATCCAAAA	CCAGATCCGG	GTCGGCATGT	CGCGGATGGA	GCGGGTGGTC	1200
CGGGAGCGGA	TGACCACCCA	GGACGTGGAG	GCGATCACAC	CGCAGACGTT	1250
GATCAACATC	CGGCCGGTGG	TCGCCGCGAT	CAAGGAGTTC	TTCGGCACCA	1300
GCCAGCTGAG	CCAATTCATG	GACCAGAACA	ACCCGCTGTC	GGGGTTGACC	1350
CACAAGCGCC	GACTGTGCGC	GCTGGGGCCC	GGCGGTCTGT	CACGTGAGCG	1400
TGCCGGGCTG	GAGGTCCGCG	ACGTGCACCC	GTCGCACTAC	GGCCGGATGT	1450
GCCCCGATCGA	AACCCCTGAG	GGGCCCCACA	TCGGTCTGAT	CGGCTCGCTG	1500
TCGGTGTACG	CGCGGGTCAA	CCCGTTCGGG	TTCATCGAAA	CGCCGTACCG	1550
CAAGGTGGTC	GACGGCGTGG	TTAGCGACGA	GATCGTGTAC	CTGACCGCCG	1600
ACGAGGAGGA	CCGCCACGTG	GTGGCACAGG	CCAATTCGCC	GATCGATGCG	1650
GACGGTCGCT	TCGTGAGGCC	GCGCGTGCTG	GTCCGCCGCA	AGGCGGGCGA	1700
GGTGGAGTAC	GTGCCCTCGT	CTGAGGTGGA	CTACATGGAC	GTCTCGCCCC	1750
GCCAGATGGT	GTCGGTGGCC	ACCGCGATGA	TTCCCTTCCT	GGAGCACGAC	1800
GACGCCAACC	GTGCCCTCAT	GGGGGCAAAC	ATGCAGCGCC	AGGCGGTGCC	1850
GCTGGTCCGT	AGCGAGGCCC	CGCTGGTGGG	CACCGGGATG	GAGCTGCGCG	1900
CGGCGATCGA	CGCGGCGACG	TCGTGCTCGC	AAGAAAGCGG	CGTCATCGAG	1950
GAGGTGTCCG	CCGACTACAT	CACTGTGATG	CACGACAACG	GCACCCGGCG	2000
TACCTACCGG	ATGCGCAAGT	TTGCCCGGTC	CAACCACGGC	ACTTGCGCCA	2050
ACCAAGTCCC	CATCGTGGAC	GCGGGCGACC	GAGTCGAGGC	CGGTGAGGTG	2100
ATCGCCGACG	GTCCCTGTAC	TGACGACGGC	GAGATGGCGC	TGGGCAAGAA	2150
CCTGCTGGTG	GCCATCATGC	CGTGGGAGGG	CCACAACACT	GAGGACGCGA	2200
TCATCCTGTC	CAACCGCCTG	GTCGAAGAGG	ACGTGCTCAC	CTCGATCCAC	2250
ATCGAGGAGC	ATGAGATCGA	TGCTCGCGAC	ACCAAGCTGG	GTGCGGAGGA	2300
GATCACCCGC	GACATCCCGA	ACATCTCCGA	CGAGGTGCTC	GCCGACCTGG	2350
ATGAGCGGGG	CATCGTGCGC	ATCGGTGCCG	AGGTTCCGCA	CGGGGACATC	2400
CTGGTCCGCA	AGGTCACCCC	GAAGGGTGAG	ACCGAGCTGA	CGCCGGAGGA	2450
GCGGCTGCTG	CGTGCCATCT	TCGGTGAGAA	GGCCCGCGAG	GTGCGCGACA	2500
CTTCGCTGAA	GGTGCCGCAC	GGCGAATCCG	GCAAGGTGAT	CGGCATTTCG	2550
GTGTTTTCCC	GCGAGGACGA	GGACGAGTTG	CCGGCCGGTG	TCAACGAGCT	2600
GGTGCGTGTG	TATGTGGCTC	AGAAACGCAA	GATCTCCGAC	GGTGACAAGC	2650
TGGCCGGCCG	GCACGGCAAC	AAGGGCGTGA	TCGGCAAGAT	CCTGCCGGTT	2700
GAGGACATGC	CGTTCCTTGC	CGACGGCACC	CCGGTGGACA	TTATTTTGAA	2750
CACCCACGGC	GTGCCGCGAC	GGATGAACAT	CGGCCAGATT	TTGGAGACCC	2800
ACCTGGGTTG	GTGTGCCAC	AGCGGCTGGA	AGGTCGACGC	CGCCAAGGGG	2850
GTTCCGGACT	GGGCCGCCAG	GCTGCCCCGAC	GAAGTGTCTG	AGGCGCATGC	2900
GAACGCCATT	GTGTCGACGC	CGGTGTTTCA	CGGCGCCAG	GAGGCCGAGC	2950
TGCAGGGCCT	GTTGTGCTGC	ACGCTGCCCC	ACCGCGACGG	TGACGTGCTG	3000
GTCGACGCCG	ACGGCAAGGC	CATGCTCTTC	GACGGGCGCA	GCGGCGAGCC	3050
GTTCCCGTAC	CCGGTCACGG	TTGGCTACAT	GTACATCATG	AAGCTGCACC	3100
ACCTGGTGGA	CGACAAGATC	CACGCCCCGCT	CCACCGGGCC	GTAATCGATG	3150
ATCACCCAGC	AGCCGCTGGG	CGGTAAGGCG	CAGTTCGGTG	GCCAGCGGTT	3200
CGGGGAGATG	GAGTGCTGGG	CCATGCAGGC	CTACGGTGCT	GCCTACACCC	3250
TGCAGGAGCT	GTTGACCATC	AAGTCCGATG	ACACCGTCCG	CCGCGTCAAG	3300
GTGTACGAGG	CGATCGTCAA	GGGTGAGAAC	ATCCCGGAGC	CGGGCATCCC	3350
CGAGTCGTTC	AAGGTGCTGC	TCAAAGAACT	GCACTCGCTG	TGCCTCAACG	3400
TCGAGGTGCT	ATCGAGTGAC	GGTGCGGCGA	TCGAACTGCG	CGAAGGTGAG	3450
GACGAGGACC	TGGAGCGGGC	CGCGGCCAAC	CTGGGAATCA	ATCTGTCCCG	3500
CAACGAATCC	GCAAGTTTCG	AGGATCTTGC	GTAA		3534

2) INFORMATION FOR SEQ ID NO: 2073

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2073

CCGAGCAACA TGATTGAACC ATCCACCAAC TGGCTCGG

38

2) INFORMATION FOR SEQ ID NO: 2074

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2074

CCGAGCAACA TGATTGAAGC TTCCACCAAC TGGCTCGG

38

2) INFORMATION FOR SEQ ID NO: 2075

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 41 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2075

CCGAGCCAGG TTCTGAAGTC TCTGCATTAT TAGGTGCTCG G

41

2) INFORMATION FOR SEQ ID NO: 2076

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single

1076

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2076

CCGAGCYGAY AACATTTTCA GATTCACCCA RCGGCTCGG

39

2) INFORMATION FOR SEQ ID NO: 2077

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2077

CCGAGCAACC GATCCAGCTC CAGCTACGCT CGG

33

2) INFORMATION FOR SEQ ID NO: 2078

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2078

CCGAGCCTTG GTCTTCGGCC AAATGAACGC TCGG

34

2) INFORMATION FOR SEQ ID NO: 2079

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2079

CCGAGCGTTC AGTTACTTCA GTCCAAGCCG GCTCGG

36

2) INFORMATION FOR SEQ ID NO: 2080

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2080

CCGAGCCGAA GAGGGCCAAG ATGTCGCTCG G

31

2) INFORMATION FOR SEQ ID NO: 2081

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2081

GRATYRTYAA AGTTGGTGAG GAAG

24

2) INFORMATION FOR SEQ ID NO: 2082

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2082

CMACTTCATC YCGCTTCGTA CC

22

2) INFORMATION FOR SEQ ID NO: 2083

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 44 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single

1078

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2083

CCGCCGATGT TCCGTAAATT ACTTGAIGAA GGTGAGCCG GCGG

44

2) INFORMATION FOR SEQ ID NO: 2084

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 38 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2084

CACGCGTCAA CACCCGTACA AGTCGTCTTT TGC GCGTG

38

2) INFORMATION FOR SEQ ID NO: 2085

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2085

CAAACTAAAG AACATATCTT GCTA

24

2) INFORMATION FOR SEQ ID NO: 2086

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2086

ATATAATTG CATCACCTTC AAG

23

2) INFORMATION FOR SEQ ID NO: 2087

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2087

TCAGCTCGTG GGATTAGGAG AG

22

2) INFORMATION FOR SEQ ID NO: 2088

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2088

AGGCTTCACG CTGTTAGGCT GA

22

2) INFORMATION FOR SEQ ID NO: 2089

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2089

ATGCTGAACT TATTGACCTT

20

2) INFORMATION FOR SEQ ID NO: 2090

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single

1080

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2090

CGTTACTGGA GTCGAAATG

19

2) INFORMATION FOR SEQ ID NO: 2091

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 39 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2091

CGCGACTTGA GATGGAAGTT AGTGAGCTTC TTGGTCGCG

39

2) INFORMATION FOR SEQ ID NO: 2092

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 38 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2092

CGCGACGAAA GAACTTCCTG AAGGTCGTGC AGGTCCAG

38

2) INFORMATION FOR SEQ ID NO: 2093

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2093

TGTTGGCAAT CGAAGACACC

20

2) INFORMATION FOR SEQ ID NO: 2094

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2094

TTCAATTTCT TGACCTACTT TCAA

24

2) INFORMATION FOR SEQ ID NO: 2095

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2095

CGGTCGGGTT GAACGTGG

18

2) INFORMATION FOR SEQ ID NO: 2096

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2096

CGCGACCGGT ACCACGGCCA GTAATCGTGT CGCG

34

2) INFORMATION FOR SEQ ID NO: 2097

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1185 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

1082

(A) ORGANISM: *Mycoplasma pneumoniae*
 (B) STRAIN: ATCC 29342
 (C) ACCESSION NUMBER: AE000019

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2097

ATGGCAAGAG	AGAAATTTGA	CCGATCTAAA	CCCCACGTTA	ATGTAGGTAC	50
TATTGGCCAC	ATTGACCACG	GTAAAACAAC	TTTAACAGCA	GCTATTTGTA	100
CTGTATTAGC	AAAAGAAGGT	AAATCAGCTG	CTACTCGTTA	CGACCAAATC	150
GATAAGGCTC	CGGAAGAAAA	AGCACGGGGA	ATTACGATTA	ACTCCGCTCA	200
CGTGGAGTAC	TCCTCTGACA	AGCGTCACTA	TGCTCACGTT	GACTGTCCAG	250
GACACGCTGA	CTACATTAAG	AACATGATTA	CTGGTGCTGC	ACAAATGGAT	300
GGTGCCATTC	TAGTAGTTTC	AGCAACTGAC	AGTGTTATGC	CCCAAACCCG	350
TGAACACATT	TTGTTGGCCC	GCCAAGTGGG	TGTGCCACGC	ATGGTAGTGT	400
TCCTAAACAA	GTGTGACATT	GCAACTGATG	AAGAAGTGCA	AGAGTTAGTA	450
GCAGAAGAGG	TACGTGACTT	ATTAAC TTCT	TACGGCTTTG	ATGGCAAGAA	500
CACCCCTATT	ATTTATGGTT	CTGCACTTAA	AGCGCTTGAA	GGTGATCCTA	550
AGTGGGAAGC	TAAGATCCAT	GATTTAATGA	ATGCAGTTGA	TGAATGGATT	600
CCAACCTCTG	AACGTGAAGT	GGACAAACCC	TTCTTGTTGG	CAATCGAAGA	650
CACCATGACG	ATTACTGGCC	GTGGTACCGT	GGTTACCGGT	CGGGTTGAAC	700
GTGGTGAATT	GAAAGTAGGT	CAAGAAATTG	AAATCGTTGG	TTTACGTCCA	750
ATCCGTAAAG	CAGTTGTTAC	CGGAATCGAA	ATGTTCAAAA	AGGAACTTGA	800
TTCAGCAATG	GCTGGGGACA	ACGCTGGGGT	ATTACTCCGT	GGTGTGGACC	850
GTAAAGAAGT	GGAACGTGGT	CAAGTGTTAG	CTAAACCAGG	TTCGATTAAA	900
CCGCACAAGA	AATTTAAAGC	GGAAATCTAT	GCTTTAAAGA	AGGAAGAAGG	950
TGGTCGTCAC	ACCGGTTTCT	TAAACGGTTA	CCGTCCCCAA	TTCTACTTCC	1000
GTACTACAGA	CGTTACTGGT	TCGATTTCCT	TACCAGAAAA	CACCGAAATG	1050
GTGCTACCAG	GTGACAATAC	CTCGATTACA	GTTGAATAA	TTGCACCAAT	1100
TGCTTGTGAA	AAAGGTAGTA	AGTTCTCCAT	CCGTGAAGGT	GGTCGAACGG	1150
TTGGTGCTGG	TTCAGTCACG	GAAGTGCTTG	AATAG		1185

2) INFORMATION FOR SEQ ID NO: 2098

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2098

CTGAGTCACA CCGACAAACG TC

22

2) INFORMATION FOR SEQ ID NO: 2099

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2099

CCAGGACTGA ACGGGATACG AA

22

2) INFORMATION FOR SEQ ID NO: 2100

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2100

GCGAGACGAT AGGTTGTC

18

2) INFORMATION FOR SEQ ID NO: 2101

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2609 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Mycobacterium tuberculosis*
- (B) STRAIN: H37Rv
- (C) ACCESSION NUMBER: Z79701

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2101

CAGCCCGCGA	GCGTAACCTG	GCTGCGATTT	CCGGCGCGGA	TTTTCGCAGT	50
GCGGTTACGC	TCGGAAAGCG	CGGGCCTCGC	CCACGCGGCG	GATGATGTCA	100
GCGGGGTGGT	CCTCGGCGAC	GACCCGGACC	ACGATCCACC	CGTAGCGGTG	150
CTGGACTTTC	TCGTGCCGGA	GGATGTCTTT	CCGGTAGTGG	TAGCGACTGG	200
TCAGATGGTG	GTGCGCGTCA	TACTCGGCCG	CGACCTTGAT	GTCTTGCCAG	250
CCCATATCCA	AATGGGCTTC	CGCCCAGCCC	CATTCGTTGC	GCACCGCGAT	300
CTGCGTCTGG	GGGCGCGGAA	AGCCGGCGCG	GATCAACAAC	AAGCGCAGCC	350
AGGTTTCCTT	GGGGGACTGG	GCACCGCCGT	CGACGAGGTC	CAGAGCGGCT	400
CTTGCGGCCT	TCATGCCACG	GCGGCCCCGA	TAGCGCTCGA	TCAGCGGCTC	450
GACGTCGGCC	ACCTTCAAAT	CGGTGGCCTG	TATCAGGGCG	TCGACGGCCG	500
CGACGGCGGG	GTCCAATGGA	AATCGACTGG	TCAGGTCGAG	CGCCGTTTCG	550
TCCGGTGTGG	TCACGCGCAT	GCCCTCGATG	ACGCAGATCT	CGTCGGGCTC	600
GATGCGCTCT	TCCCAGACTT	GCAGCCCCGG	GGCACGGCGG	CGGTTGGTGT	650
CGATGATCGC	GGCGGGAAGA	TCCGCGTCGA	TCCAATTGGC	GCCATGGAAG	700
GCAGAAGCCG	AGTAGCCGGC	CAGCACGCCG	CGGCGGCGCG	AGCGCAGCCA	750
CAGCGCTTTT	GCACGCAATT	GCGCGGTCAG	TTCCACACCC	TGCGGCACGT	800

1084

ACACGTCTTT	ATGTAGCGCG	ACATACCTGC	TGCGCAATTC	GTAGGGCGTC	850
AATACACCCG	CAGCCAGGGC	CTCGCTGCCC	AGAAAGGGAT	CCGTCATGGT	900
CGAAGTGTGC	TGAGTCACAC	CGACAAACGT	CACGAGCGTA	ACCCCAGTGC	950
GAAAGTTCCC	GCCGGAAATC	GCAGCCACGT	TACGCTCGTG	GACATACCGA	1000
TTTCGGCCCC	GCCGCGGCGA	GACGATAGGT	TGTCGGGGTG	ACTGCCACAG	1050
CCACTGAAGG	GGCCAAACCC	CCATTTCGTAT	CCCGTTCAGT	CCTGGTTACC	1100
GGAGGAAACC	GGGGGATCGG	GCTGGCGATC	GCACAGCGGC	TGGCTGCCGA	1150
CGGCCACAAG	GTGGCCGTCA	CCCACCGTGG	ATCCGGAGCG	CCAAAGGGGC	1200
TGTTTGGCGT	CGAATGTGAC	GTCACCGACA	GCGACGCCGT	CGATCGCGCC	1250
TTCACGGCGG	TAGAAGAGCA	CCAGGGTCCG	GTCGAGGTGC	TGGTGTCCTAA	1300
CGCCGGCCTA	TCCGCGGACG	CATTCCCTCAT	GCGGATGACC	GAGGAAAAGT	1350
TCGAGAAGGT	CATCAACGCC	AACCTCACCG	GGGCGTTCGG	GGTGGCTCAA	1400
CGGGCATCGC	GCAGCATGCA	GCGCAACAAA	TTCGGTCGAA	TGATATTCAT	1450
AGGTTTCGGT	TCCGGCAGCT	GGGGCATCGG	CAACCAGGCC	AACTACGCAG	1500
CCTCCAAGGC	CGGAGTGATT	GGCATGGCCC	GCTCGATCGC	CCGCGAGCTG	1550
TCGAAGGCAA	ACGTGACCGC	GAATGTGGTG	GCCCCGGGCT	ACATCGACAC	1600
CGATATGACC	CGCGCGCTGG	ATGAGCGGAT	TCAGCAGGGG	GCGCTGCAAT	1650
TTATCCCAGC	GAAGCGGGTC	GGCACCCCCG	CCGAGGTCGC	CGGGGTGGTC	1700
AGCTTCCTGG	CTTCCGAGGA	TGCGAGCTAT	ATCTCCGGTG	CGGTCATCCC	1750
GGTCGACGGC	GGCATGGGTA	TGGGCCACTG	ACACAACACA	AGGACGCACA	1800
TGACAGGACT	GCTGGACGGC	AAACGGATTC	TGGTTAGCGG	AATCATCACC	1850
GACTCGTCTGA	TCGCGTTTCA	CATCGCACGG	GTAGCCAGG	AGCAGGGCGC	1900
CCAGCTGGTG	CTCACCGGGT	TCGACCGGCT	GCGGCTGATT	CAGCGCATCA	1950
CCGACCGGCT	GCCGGCAAAG	GCCCCGCTGC	TCGAACCTCGA	CGTGCAAAAC	2000
GAGGACACC	TGGCCAGCTT	GGCCGGCCCG	GTGACCGAGG	CGATCGGGGC	2050
GGGCAACAAG	CTCGACGGGG	TGGTGCAATC	GATTGGGTTC	ATGCCGCAGA	2100
CCGGGATGGG	CATCAACCCG	TTCTTCGACG	CGCCCTACGC	GGATGTGTCC	2150
AAGGGCATCC	ACATCTCGGC	GTATTTCGTAT	GCTTCGATGG	CCAAGGCGCT	2200
GCTGCCGATC	ATGAACCCCG	GAGGTTCCAT	CGTCGGCATG	GACTTCGACC	2250
CGAGCCGGGC	GATGCCGGCC	TACAACTGGA	TGACGGTCGC	CAAGAGCGCG	2300
TTGGAGTCGG	TCAACAGGTT	CGTGGCGCGC	GAGGCCGCA	AGTACGGTGT	2350
GCGTTCGAAT	CTCGTTGCCG	CAGGCCCTAT	CCGGACGCTG	GCGATGAGTG	2400
CGATCGTCGG	CGGTGCGCTC	GGCGAGGAGG	CCGGCGCCCA	GATCCAGCTG	2450
CTCGAGGAGG	GCTGGGATCA	GCGCGCTCCG	ATCGGCTGGA	ACATGAAGGA	2500
TGCGACGCCG	GTCGCCAAGA	CGGTGTGCGC	GCTGCTGTCT	GA CTGGCTGC	2550
CGGCGACCAC	GGGTGACATC	ATCTACGCCG	ACGGCGGCGC	GCACACCCAA	2600
TTGCTCTAG					2609

2) INFORMATION FOR SEQ ID NO: 2102

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2102

CACCTTCACC CTGACCGACG

20

2) INFORMATION FOR SEQ ID NO: 2103

1085

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 23 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2103

CGAACCAGCG GAAATAGTTG GAC

23

2) INFORMATION FOR SEQ ID NO: 2104

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 18 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2104

CTGGGCATGG CIGGAGTC

18

2) INFORMATION FOR SEQ ID NO: 2105

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 3297 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Mycobacterium tuberculosis*
 (B) STRAIN: H37rv
 (C) ACCESSION NUMBER: U68480

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2105

ATGACACAGT GCGCGAGCAG ACGCAAAGC ACCCCAAATC GGGCGATTTT	50
GGGGGCTTTT GCGTCTGCTC GCGGGACGCG CTGGGTGGCC ACCATCGCCG	100
GGCTGATTGG CTTTGTGTTG TCGGTGGCGA CGCCGCTGCT GCCCGTCGTG	150
CAGACCACCG CGATGCTCGA CTGGCCACAG CGGGGGCAAC TGGGCAGCGT	200
GACCGCCCCG CTGATCTCGC TGACGCCGGT CGACTTTACC GCCACCGTGC	250
CGTGCGACGT GGTGCGCGCC ATGCCACCCG CGGGCGGGGT GGTGCTGGGC	300
ACCGCACCCA AGCAAGGCAA GGACGCCAAT TTGCAGGCGT GTTTCGTCTG	350
CGTCAGCGCC CAGCGCGTGG ACGTCACCGA CCGCAACGTG GTGATCTTGT	400
CCGTGCCGCG CGAGCAGGTG ACGTCCCCGC AGTGTCAACG CATCGAGGTC	450

ACCTCTACCC	ACGCCGGGCAC	CTTCGCCAAC	TTCGTGCGGC	TCAAGGACCC	500
GTCGGGCGCG	CCGCTGCGCA	GCGGCTTCCC	CGACCCCAAC	CTGCGCCCGC	550
AGATTGTCGG	GGTGTTCACC	GACCTGACCG	GGCCCGCGCC	GCCCGGGCTG	600
GCGGTCTCGG	CGACCATCGA	CACCCGGTTC	TCCACCCGGC	CGACCACGCT	650
GAAACTGCTG	GCGATCATCG	GGGCGATCGT	GGCCACCGTC	GTCGCACTGA	700
TCGCGTTGTG	GCGCCTGGAC	CAGTTGGACG	GGCGGGGCTC	AATTGCCCAG	750
CTCCTCCTCA	GGCCGTTCCG	GCCTGCATCG	TCGCCGGGCG	GCATGCGCCG	800
GCTGATTCCG	GCAAGCTGGC	GCACCTTCAC	CCTGACCGAC	GCCGTGGTGA	850
TATTCGGCTT	CCTGCTCTGG	CATGTCATCG	GCGCGAATTC	GTCGGACGAC	900
GGCTACATCC	TGGGCATGGC	CCGAGTCGCC	GACCACGCCG	GCTACATGTC	950
CAACTATTTC	CGCTGGTTCG	GCAGCCCGGA	GGATCCCTTC	GGCTGGTATT	1000
ACAACCTGCT	GGCGCTGATG	ACCCATGTCA	GCGACGCCAG	TCTGTGGATG	1050
CGCCTGCCAG	ACCTGGCCCG	CGGGCTAGTG	TGCTGGCTGC	TGCTGTGCGG	1100
TGAGGTGCTG	CCCCGCCTCG	GGCCGGCGGT	GGAGGCCAGC	AAACCCGCCT	1150
ACTGGGCGGC	GGCCATGGTC	TTGCTGACCG	CGTGATGCC	GTTCAACAAC	1200
GGCCTGCGGC	CGGAGGGCAT	CATCGCGCTC	GGCTCGCTGG	TCACCTATGT	1250
GCTGATCGAG	CGGTCCATGC	GGTACAGCCG	GCTCACACCG	GCGGCGCTGG	1300
CCGTCGTTAC	CGCCGCATTC	ACACTGGGTG	TGCAGCCAC	CGGCCTGATC	1350
GCGGTGGCCG	CGCTGGTGGC	CGGCGGCCGC	CCGATGCTGC	GGATCTTGTT	1400
GCGCCGYCAT	CGCCTGGTCG	GCACGTTGCC	GTTGGTGTCT	CCGATGCTGG	1450
CCGCCGGCAC	CGTCATCCTG	ACCGTGGTGT	TCGCCGACCA	GACCCTGTCA	1500
ACGGTGTTGG	AAGCCACCAG	GGTTCGCGCC	AAAATCGGGC	CGAGCCAGGC	1550
GTGGTATACC	GAGAACCTGC	GTTACTACTA	CCTCATCCTG	CCCACCGTCG	1600
ACGGTTCGCT	GTCGCGGCGC	TTGCGCTTTT	TGATCACCGC	GCTATGCCTG	1650
TTACCCGCGG	TGTTTCATCAT	GTTGCGGCGC	AAGCGAATTC	CCAGCGTGGC	1700
CCGCGGACCG	GCGTGGCGGC	TGATGGGCGT	CATCTTCGGC	ACCATGTTCT	1750
TCCTGATGTT	CACGCCACCC	AAGTGGGTGC	ACCACTTCGG	GCTGTTTCGCC	1800
GCCGTAGGGG	CGGCGATGGC	CGCGCTGACG	ACGGTGTTGG	TATCCCCATC	1850
GGTGCTGCGC	TGGTCGCGCA	ACCGGATGGC	GTTCTTGCGG	GCGTTATTCT	1900
TCCTGCTGGC	GTTGTGTTGG	GCCACCACCA	ACGGCTGGTG	GTATGTCTCC	1950
AGCTACGGTG	TGCCGTTCAA	CAGCGCGATG	CCGAAGATCG	ACGGGATCAC	2000
AGTCAGCACA	ATCTTTTTCG	CCCTGTTTGC	GATCGCCGCC	GGCTATGCGG	2050
CCTGGCTGCA	CTTCGCGCCC	CGCGGCGCCG	GCGAAGGGCG	GCTGATCCGC	2100
GCGCTGACGA	CAGCCCCGGT	ACCGATCGTG	GCCGGTTTCA	TGGCGGCGGT	2150
GTTCGTCGCG	TCCATGGTGG	CCGGGATCGT	GCGACAGTAC	CCGACCTACT	2200
CCAACGGCTG	GTCCAACGTG	CGGGCGTTTG	TCGGCGGCTG	CGGACTGGCC	2250
GACGACGTAC	TCGTCGAGCC	TGATACCAAT	GCGGGTTTCA	TGAAGCCGCT	2300
GGACGGCGAT	TCGGGTTCCT	GGGGCCCCCT	GGGGCCGCTG	GGTGGAGTCA	2350
ACCCGGTCCG	CTTCACGCCC	AACGGCGTAC	CGGAACACAC	GGTGGCCGAG	2400
GCGATCGTGA	TGAAACCCAA	CCAGCCCGGC	ACCGACTACG	ACTGGGATGC	2450
GCCGACCAAG	CTGACGAGTC	CTGGCATCAA	TGGTTCTACG	GTGCCGCTGC	2500
CCTATGGGCT	CGATCCCGCC	CGGGTACCGT	TGGCAGGCAC	CTACACCACC	2550
GGCGCACAGC	AACAGAGCAC	ACTCGTCTCG	GCGTGGTATC	TCCTGCCTAA	2600
GCCGGACGAC	GGGCATCCGC	TGGTCGTGGT	GACCGCCGCG	GGCAAGATCG	2650
CCGGCAACAG	CGTGCTGCAC	GGGTACACCC	CCGGGCAGAC	TGTGGTGCTC	2700
GAATACGCCA	TGCCGGGACC	CGGAGCGCTG	GTACCCGCCG	GGCGGATGGT	2750
GCCCCAGGAC	CTATACGGAG	AGCAGCCCAA	GGCGTGGCGC	AACCTGCGCT	2800
TCGCCCCGAGC	AAAGATGCCC	GCCGATGCCG	TCGCGGTCCG	GGTGGTGGCC	2850
GAGGATCTGT	CGCTGACACC	GGAGGACTGG	ATCGCGGTGA	CCCCGCCGCG	2900
GGTACCGGAC	CTGCGCTCAC	TGCAGGAATA	TGTGGGCTCG	ACGCAGCCGG	2950
TGCTGCTGGA	CTGGGCGGTC	GGTTTGGCCT	TCCCGTGCCA	GCAGCCGATG	3000
CTGCACGCCA	ATGGCATCGC	CGAAATCCCG	AAGTTCCGCA	TCACACCGGA	3050
CTACTCGGCT	AAGAAGCTGG	ACACCGACAC	GTGGGAAGAC	GGCACTAACG	3100
GCGGCCTGCT	CGGGATCACC	GACCTGTTGC	TGCGGGCCCA	CGTCATGGCC	3150
ACCTACCTGT	CCCCGCGACTG	GGCCCGCGAT	TGGGGTTCCC	TGCGCAAGTT	3200
CGACACCCTG	GTCGATGCCC	CTCCCGCCCA	GCTCGAGTTG	GGCACC GCGA	3250
CCCCGAGCGG	CCTGTGGTCA	CCGGGCAAGA	TCCGAATTGG	TCCATAG	3297

2) INFORMATION FOR SEQ ID NO: 2106

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2106

GCGAGCAGAG CACGCCCTCC TCGCCGCTCG C

31

2) INFORMATION FOR SEQ ID NO: 2107

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2107

GCGAGCTCCC CATCTCTGGT TGGCACGCTC GC

32

2) INFORMATION FOR SEQ ID NO: 2108

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 41 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2108

GCGGGCAACT TCRTCAAGAA GGTTGGTTAC AACCCGCCCG C

41

2) INFORMATION FOR SEQ ID NO: 2109

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

1088

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2109

GCGGGCCCCAA TCTCTGGTTG GAAYGGTGAC AAGCCCGC

38

2) INFORMATION FOR SEQ ID NO: 2110

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 41 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2110

GCGGGCCCTT AACGATTTC ACGAATCTGG ATTCAGCCCG C

41

2) INFORMATION FOR SEQ ID NO: 2111

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 41 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2111

GCGGGCATGA TTGAAGCCAC CACCAACGCT TCCTGGCCCG C

41

2) INFORMATION FOR SEQ ID NO: 2112

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 43 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2112

GCGGGCTTGA TGAAGTTTTG GGTTTCCTTG ACAATTTGCC CGC

43

2) INFORMATION FOR SEQ ID NO: 2113

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 41 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2113

GCGGGCACAA GGGTTGGACT AAGGAAACCA AGGCAGCCCG C

41

2) INFORMATION FOR SEQ ID NO: 2114

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 41 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2114

GCGGGCATCG ATGCTATTGA ACCACCTGTC AGACCGCCCG C

41

2) INFORMATION FOR SEQ ID NO: 2115

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2115

GCGGGCTTGA TGATTCCTC GAATCTAGAT TGGGCCCGC

39

2) INFORMATION FOR SEQ ID NO: 2116

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2116

GCGGGCGGTA AGTCCACCGG TAAGACCTTG TTGGCCCGC

39

2) INFORMATION FOR SEQ ID NO: 2117

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2117

GCGGGCGACG CCATTGAGCC ACCTTCGAGA GCCCCG

36

2) INFORMATION FOR SEQ ID NO: 2118

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 42 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2118

GCGGGCTCCT TGACAATTTC TTCGTATCTG TTCTTGCCCC GC

42

2) INFORMATION FOR SEQ ID NO: 2119

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2119

GCGGGCTTAC AACCCTAAGG CTGTTCCATT CGTTGCCCCG

40

2) INFORMATION FOR SEQ ID NO: 2120

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 41 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single

1091

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2120

GCGGGCAGAA ACCAAGGCTG GTAAGGTTAC CGGTAGCCCG C

41

2) INFORMATION FOR SEQ ID NO: 2121

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 31 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2121

CGACCGCIAG CCGCACACCA AGTTCCGGTC G

31

2) INFORMATION FOR SEQ ID NO: 2122

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 35 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2122

CCGAGCGAAT GTAGGAGTCC AGGGTCTCTG CTCGG

35

2) INFORMATION FOR SEQ ID NO: 2123

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 19 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2123

TCTACCACTG AAGCATTAC

19

2) INFORMATION FOR SEQ ID NO: 2124

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2124

TAGGTACTGT AGGTTTATTG

20

2) INFORMATION FOR SEQ ID NO: 2125

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2125

CACGCGGATT TTGAATCTCT TCCTCTAGTA GCGCGTG

37

2) INFORMATION FOR SEQ ID NO: 2126

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2126

ATATCAGAGA CTGATGAG

18

2) INFORMATION FOR SEQ ID NO: 2127

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single

1093

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2127

TAGCATATTC AGAGAATATT GT

22

2) INFORMATION FOR SEQ ID NO: 2128

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2128

CAACGCTGGA GAATCTATAT TTGTAGAAAC TGC GTT G

37

2) INFORMATION FOR SEQ ID NO: 2129

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8133 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Clostridium difficile*
- (B) STRAIN: VPI 10463
- (C) ACCESSION NUMBER: X51797

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2129

ATGTCTTTAA	TATCTAAAGA	AGAGTTAATA	AAACTCGCAT	ATAGCATTAG	50
ACCAAGAGAA	AATGAGTATA	AACTATACT	AACTAATTTA	GACGAATATA	100
ATAAGTTAAC	TACAAACAAT	AATGAAAATA	AATATTTGCA	ATTAAAAAAA	150
CTAAATGAAT	CAATTGATGT	TTTTATGAAT	AAATATAAAA	CTTCAAGCAG	200
AAATAGAGCA	CTCTCTAATC	TAAAAAAGA	TATATTAAAA	GAAGTAATTC	250
TTATTAAAAA	TTCCAATACA	AGCCCTGTAG	AAAAAAATTT	ACATTTTGTA	300
TGGATAGGTG	GAGAAGTCAG	TGATATTGCT	CTTGAATACA	TAAAACAATG	350
GGCTGATATT	AATGCAGAAT	ATAATATTAA	ACTGTGGTAT	GATAGTGAAG	400
CATTCTTAGT	AAATACACTA	AAAAAGGCTA	TAGTTGAATC	TTCTACCACT	450
GAAGCATTAC	AGCTACTAGA	GGAAGAGATT	CAAAATCCTC	AATTTGATAA	500
TATGAAATTT	TACAAAAAAA	GGATGGAATT	TATATATGAT	AGACAAAAAA	550
GGTTTATAAA	TTATTATAAA	TCTCAAATCA	ATAAACCTAC	AGTACCCTACA	600
ATAGATGATA	TTATAAAGTC	TCATCTAGTA	TCTGAATATA	ATAGAGATGA	650
AACTGTATTA	GAATCATATA	GAACAAATTC	TTTGAGAAAA	ATAAATAGTA	700
ATCATGGGAT	AGATATCAGG	GCTAATAGTT	TGTTTACAGA	ACAAGAGTTA	750
TTAAATATTT	ATAGTCAGGA	GTTGTAAAT	CGTGGAATTT	TAGCTGCAGC	800

ATCTGACATA	GTAAGATTAT	TAGCCCTAAA	AAATTTTGGC	GGAGTATATT	850
TAGATGTTGA	TATGCTTCCA	GGTATTCAC	CTGATTTATT	TAAAACAATA	900
TCTAGACCTA	GCTCTATTGG	ACTAGACCGT	TGGGAAATGA	TAAAATTAGA	950
GGCTATTATG	AAGTATAAAA	AATATATAAA	TAATTATACA	TCAGAAAAC	1000
TTGATAAACT	TGATCAACAA	TTAAAAGATA	ATTTTAAACT	CATTATAGAA	1050
AGTAAAAGTG	AAAAATCTGA	GATATTTTCT	AAATTAGAAA	ATTTAAATGT	1100
ATCTGATCTT	GAAATTAATA	TAGCTTTCGC	TTTAGGCAGT	GTTATAAATC	1150
AAGCCTTGAT	ATCAAAACAA	GGTTCATATC	TTACTAACCT	AGTAATAGAA	1200
CAAGTAAAAA	ATAGATATCA	ATTTTAAAC	CAACACCTTA	ACCCAGCCAT	1250
AGAGTCTGAT	AATAACTTCA	CAGATACTAC	TAAAATTTTT	CATGATTCAT	1300
TATTTAATTC	AGCTACCGCA	GAAAACCTCTA	TGTTTTTAAC	AAAAATAGCA	1350
CCATACTTAC	AAGTAGGTTT	TATGCCAGAA	GCTCGCTCCA	CAATAAGTTT	1400
AAGTGGTCCA	GGAGCTTATG	CGTCAGCTTA	CTATGATTTT	ATAAATTTAC	1450
AAGAAAATAC	TATAGAAAAA	ACTTTAAAAG	CATCAGATTT	AATAGAATTT	1500
AAATTCCCAG	AAAATAATCT	ATCTCAATTG	ACAGAACAAG	AAATAAATAG	1550
TCTATGGAGC	TTTGATCAAG	CAAGTGCAAA	ATATCAATTT	GAGAAATATG	1600
TAAGAGATTA	TACTGGTGGG	TCTCTTCTG	AAGACAATGG	GGTAGACTTT	1650
AATAAAAAATA	CTGCCCTCGA	CAAAAACCTAT	TTATTAAATA	ATAAAATTCC	1700
ATCAACAAT	GTAGAAGAAG	CTGGAAGTAA	AAATTATGTT	CATTATATCA	1750
TACAGTTACA	AGGAGATGAT	ATAAGTTATG	AAGCAACATG	CAATTTATTT	1800
TCTAAAAATC	CTAAAAATAG	TATTATTATA	CAACGAAATA	TGAATGAAAG	1850
TGCAAAAAGC	TACTTTTTAA	GTGATGATGG	AGAATCTATT	TTAGAATTAA	1900
ATAAATATAG	GATACCTGAA	AGATTAAAAA	ATAAGGAAAA	AGTAAAAGTA	1950
ACCTTTTATTG	GACATGGTAA	AGATGAATTC	AACACAAGCG	AATTTGCTAG	2000
ATTAAGTGTA	GATTCACCTT	CCAATGAGAT	AAGTTCATTT	TTAGATACCA	2050
TAAAATTAGA	TATATCACCT	AAAAATGTAG	AAGTAACTTT	ACTTGGATGT	2100
AATATGTTTA	GTTATGATTT	TAATGTTGAA	GAAACTTATC	CTGGGAAGTT	2150
GCTATTAAGT	ATTATGGACA	AAATTACTTC	CACCTTACCT	GATGTAAATA	2200
AAAATTCTAT	TACTATAGGA	GCAAATCAAT	ATGAAGTAAG	AATTAATAGT	2250
GAGGGAAGAA	AAGAACTTCT	GGCTCACTCA	GGTAAATGGA	TAAATAAAGA	2300
AGAAGCTATT	ATGAGCGATT	TATCTAGTAA	AGAATACATT	TTTTTTGATT	2350
CTATAGATAA	TAAGCTAAAA	GCAAAGTCCA	AGAATATTC	AGGATTAGCA	2400
TCAATATCAG	AAGATATAAA	AACATTATTA	CTTGATGCAA	GTGTTAGTCC	2450
TGATACAAAA	TTTATTTTAA	ATAATCTTAA	GCTTAATATT	GAATCTTCTA	2500
TTGGGGATTA	CATTTATTAT	GAAAAATTAG	AGCCTGTAA	AAATATAATT	2550
CACAATTCTA	TAGATGATTT	AATAGATGAG	TTCAATCTAC	TTGAAAATGT	2600
ATCTGATGAA	TTATATGAAT	TAAAAAAATT	AAATAATCTA	GATGAGAAGT	2650
ATTTAATATC	TTTTGAAGAT	ATCTCAAAAA	ATAATTCAAC	TTACTCTGTA	2700
AGATTTATTA	ACAAAAGTAA	TGGTGAGTCA	GTTTATGTAG	AAACAGAAAA	2750
AGAAATTTTT	TCAAAATATA	GCGAACATAT	TACAAAAGAA	ATAAGTACTA	2800
TAAAGAATAG	TATAATTACA	GATGTTAATG	GTAATTTATT	GGATAATATA	2850
CAGTTAGATC	ATACTTCTCA	AGTTAATACA	TTAAACGCAG	CATTCTTTAT	2900
TCAATCATTA	ATAGATTATA	GTAGCAATAA	AGATGTACTG	AATGATTTAA	2950
GTACCTCAGT	TAAGGTTCAA	CTTTATGCTC	AACATTTTAG	TACAGGTTTA	3000
AATACTATAT	ATGACTCTAT	CCAATTAGTA	AATTTAATAT	CAAATGCAGT	3050
AAATGATACT	ATAAATGTAC	TACCTACAAT	AACAGAGGGG	ATACCTATTG	3100
TATCTACTAT	ATTAGACGGA	ATAAACTTAG	GTGCAGCAAT	TAAGGAATTA	3150
CTAGACGAAC	ATGACCCATT	ACTAAAAAAA	GAATTAGAAG	CTAAGGTGGG	3200
TGTTTTAGCA	ATAAATATGT	CATTATCTAT	AGCTGCAACT	GTAGCTTCAA	3250
TTGTTGGAAT	AGGTGCTGAA	GTTACTATTT	TCTTATTACC	TATAGCTGGT	3300
ATATCTGCAG	GAATACCTTC	ATTAGTTAAT	AATGAATTAA	TATTGCATGA	3350
TAAGGCAACT	TCAGTGGTAA	ACTATTTTAA	TCATTTGTCT	GAATCTAAAA	3400
AATATGGCCC	TCTTAAAACA	GAAGATGATA	AAATTTTAGT	TCCTATTGAT	3450
GATTTAGTAA	TATCAGAAAT	AGATTTTAAT	AATAATTCGA	TAAAAC TAGG	3500
AACATGTAAT	ATATTAGCAA	TGGAGGGGGG	ATCAGGACAC	ACAGTGACTG	3550
GTAATATAGA	TCACTTTTTC	TCATCTCCAT	CTATAAGTTC	TCATATTCCT	3600
TCATTATCAA	TTTATTCTGC	AATAGGTATA	GAAACAGAAA	ATCTAGATTT	3650

TTCAAAAAA	ATAATGATGT	TACCTAATGC	TCCTTCAAGA	GTGTTTTTGGT	3700
GGGAAACTGG	AGCAGTTCCTA	GGTTTAAGAT	CATTGGAAAA	TGACGGAACT	3750
AGATTACTTG	ATTCAATAAG	AGATTTATAC	CCAGGTAAAT	TTTACTGGAG	3800
ATTCTATGCT	TTTTTCGATT	ATGCAATAAC	TACATTAAAA	CCAGTTTATG	3850
AAGACACTAA	TATTAATAAT	AAACTAGATA	AAGATACTAG	AAACTTCATA	3900
ATGCCAACTA	TAACTACTAA	CGAAATTAGA	AACAAATTAT	CTTATTCATT	3950
TGATGGAGCA	GGAGGAACTT	ACTCTTTATT	ATTATCTTCA	TATCCAATAT	4000
CAACGAATAT	AAATTTATCT	AAAGATGATT	TATGGATATT	TAATATTGAT	4050
AATGAAGTAA	GAGAAATATC	TATAGAAAAT	GGTACTATTA	AAAAAGGAAA	4100
GTTAATAAAA	GATGTTTTAA	GTAAAATTGA	TATAAATAAA	AATAAACTTA	4150
TTATAGGCAA	TCAAACAATA	GATTTTTTCAG	GCGATATAGA	TAATAAAGAT	4200
AGATATATAT	TCTTGACTTG	TGAGTTAGAT	GATAAAATTA	GTTTAATAAT	4250
AGAAATAAAT	CTTGTTGCAA	AATCTTATAG	TTTGTTATTG	TCTGGGGATA	4300
AAAATTATTT	GATATCCAAT	TTATCTAATA	CTATTGAGAA	AATCAATACT	4350
TTAGGCCTAG	ATAGTAAAAA	TATAGCGTAC	AATTACACTG	ATGAATCTAA	4400
TAATAAATAT	TTTGGAGCTA	TATCTAAAAC	AAGTCAAAAA	AGCATAATAC	4450
ATTATAAAAA	AGACAGTAAA	AATATATTAG	AATTTTATAA	TGACAGTACA	4500
TTAGAATTTA	ACAGTAAAGA	TTTTATTGCT	GAAGATATAA	ATGTATTTAT	4550
GAAAGATGAT	ATTAATACTA	TAACAGGAAA	ATACTATGTT	GATAATAATA	5000
CTGATAAAAG	TATAGATTTC	TCTATTTCTT	TAGTTAGTAA	AAATCAAGTA	5050
AAAGTAAATG	GATTATATTT	AAATGAATCC	GTATACTCAT	CTTACCTTGA	5100
TTTTGTGAAA	AATTCAGATG	GACACCATAA	TACTTCTAAT	TTTATGAATT	5150
TATTTTTTGA	CAATATAAGT	TTCTGGAAAT	TGTTTGGGTT	TGAAAATATA	5200
AATTTTGTA	TCGATAAATA	CTTTACCCTT	GTTGGTAAAA	CTAATCTTGG	5250
ATATGTAGAA	TTTATTTGTG	ACAATAATAA	AAATATAGAT	ATATATTTTG	5300
GTGAATGGAA	AACATCGTCA	TCTAAAAGCA	CTATATTTAG	CGGAAATGGT	5350
AGAAATGTTG	TAGTAGAGCC	TATATATAAT	CCTGATACGG	GTGAAGATAT	5400
ATCTACTTCA	CTAGATTTTT	CCTATGAACC	TCTCTATGGA	ATAGATAGAT	5450
ATATAAATAA	AGTATTGATA	GCACCTGATT	TATATACAAG	TTTAATAAAT	5500
ATTAATACCA	ATTATTATTC	AAATGAGTAC	TACCCTGAGA	TTATAGTTCT	5550
TAACCCAAAT	ACATTCCACA	AAAAAGTAAA	TATAAATTTA	GATAGTTCTT	5600
CTTTTGAGTA	TAAATGGTCT	ACAGAAGGAA	GTGACTTTAT	TTTAGTTAGA	5650
TACTTAGAAG	AAAGTAATAA	AAAAATATTA	CAAAAAATAA	GAATCAAAGG	5700
TATCTTATCT	AATACTCAAT	CATTTAATAA	AATGAGTATA	GATTTTAAAG	5750
ATATTAAAAA	ACTATCATT	GGATATATAA	TGAGTAATTT	TAAATCATT	5800
AATTCTGAAA	ATGAATTAGA	TAGAGATCAT	TTAGGATTTA	AAATAATAGA	5850
TAATAAAACT	TATTACTATG	ATGAAGATAG	TAAATTAGTT	AAAGGATTAA	5900
GCAAGTAATT	GACAATAATA	AGTATTATTT	CAATCCTGAC	ACTGCTATCA	5950
TCTCAAAAGG	TTGGCAGACT	GTTAATGGTA	GTAGATACTA	CTTTGATACT	6000
GATACCGCTA	TTGCCTTTAA	TGGTTATAAA	ACTATTGATG	GTAAACACTT	6050
TTATTTTGAT	AGTGATTGTG	TAGTGAAAAT	AGGTGTGTTT	AGTACCTCTA	6100
ATGGATTTGA	ATATTTTGCA	CCTGCTAATA	CTTATAATAA	TAACATAGAA	6150
GGTCAGGCTA	TAGTTTATCA	AAGTAAATTC	TTAACTTTGA	ATGGTAAAAA	6200
ATATTACTTT	GATAATAACT	CAAAAGCAGT	TACCGGATTG	CAAACATTG	6250
ATAGTAAAAA	ATATTACTTT	AATACTAACA	CTGCTGAAGC	AGCTACTGGA	6300
TGGCAAACTA	TTGATGCTAA	AAAAATATTAC	TTTAATACTA	ACACTGCTGA	6350
AGCAGCTACT	GGATGGCAAA	CTATTGATGG	TAAAAAATAT	TACTTTAATA	6400
CTAACACTGC	TATAGCTTCA	ACTGGTTATA	CAATTATTAA	TGGTAAACAT	6450
TTTTATTTTA	ATACTGATGG	TATTATGCAG	ATAGGAGTGT	TTAAAGGACC	6500
TAATGGATTT	GAATATTTTG	CACCTGCTAA	TACGGATGCT	AACAACATAG	6550
AAGGTCAAGC	TATACTTTAC	CAAAATGAAT	TCTTAACCTT	GAATGGTAAA	6600
AAATATTACT	TTGGTAGTGA	CTCAAAAGCA	GTTACTGGAT	GGAGAATTAT	6650
TAACAATAAG	AAATATTACT	TTAATCCTAA	TAATGCTATT	GCTGCAATTC	6700
ATCTATGCAC	TATAAATAAT	GACAAGTATT	ACTTTAGTTA	TGATGGAATT	6750
CTTCAAAATG	GATATATTAC	TATTGAAAGA	AATAATTTCT	ATTTTGATGC	6800
TAATAATGAA	TCTAAAATGG	TAACAGGAGT	ATTTAAAGGA	CCTAATGGAT	6850
TTGAGTATTT	TGCACCTGCT	AATACTCACA	ATAATAACAT	AGAAGGTCAG	6900

GCTATAGTTT	ACCAGAACAA	ATTCTTAACT	TTGAATGGCA	AAAAATATTA	6950
TTTTGATAAT	GACTCAAAAG	CAGTTACTGG	ATGGCAAACC	ATTGATGGTA	7000
AAAAATATTA	CTTTAATCTT	AACACTGCTG	AAGCAGCTAC	TGGATGGCAA	7050
ACTATTGATG	GTAAAAAATA	TTACTTTAAT	CTTAACACTG	CTGAAGCAGC	7100
TACTGGATGG	CAAACTATTG	ATGGTAAAAA	ATATTACTTT	AATACTAACA	7150
CTTTCATAGC	CTCAACTGGT	TATACAAGTA	TTAATGGTAA	ACATTTTTTAT	7200
TTTAATACTG	ATGGTATTAT	GCAGATAGGA	GTGTTTAAAG	GACCTAATGG	7250
ATTTGAATAC	TTTGCACCTG	CTAATACGGA	TGCTAACAAC	ATAGAAGGTC	7300
AAGCTATACT	TTACCAAAAT	AAATTCTTAA	CTTTGAATGG	TAAAAAATAT	7350
TACTTTGGTA	GTGACTCAAA	AGCAGTTACC	GGACTGCGAA	CTATTGATGG	7400
TAAAAAATAT	TACTTTAATA	CTAACACTGC	TGTTGCAGTT	ACTGGATGGC	7450
AAACTATTAA	TGGTAAAAAA	TACTACTTTT	ATACTAACAC	TTCTATAGCT	7500
TCAACTGGTT	ATACAATTAT	TAGTGGTAAA	CATTTTTTATT	TTAATACTGA	7550
TGGTATTATG	CAGATAGGAG	TGTTTAAAGG	ACCTGATGGA	TTTGAATACT	7600
TTGCACCTGC	TAATACAGAT	GCTAACAAATA	TAGAAGGTCA	AGCTATACGT	7650
TATCAAAATA	GATTCTTATA	TTTACATGAC	AATATATATT	ATTTTGGTAA	7700
TAATTCAAAA	GCGGCTACTG	GTTGGGTAAC	TATTGATGGT	AATAGATATT	7750
ACTTCGAGCC	TAATACAGCT	ATGGGTGCGA	ATGGTTATAA	AACTATTGAT	7800
AATAAAAATT	TTTACTTTAG	AAATGGTTTA	CCTCAGATAG	GAGTGTTTAA	7850
AGGGTCTAAT	GGATTTGAAT	ACTTTGCACC	TGCTAATACG	GATGCTAACA	7900
ATATAGAAGG	TCAAGCTATA	CGTTATCAAA	ATAGATTCCT	ACATTTACTT	7950
GGAAAAATAT	ATTACTTTGG	TAATAATTCA	AAAGCAGTTA	CTGGATGGCA	8000
AACTATTAAT	GGTAAAGTAT	ATTACTTTAT	GCCTGATACT	GCTATGGCTG	8050
CAGCTGGTGG	ACTTTTCGAG	ATTGATGGTG	TTATATATTT	CTTTGGTGTT	8100
GATGGAGTAA	AAGCCCCTGG	GATATATGGC	TAA		8133

2) INFORMATION FOR SEQ ID NO: 2130

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 7101 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Clostridium difficile*
- (B) STRAIN: VPI 10463
- (C) ACCESSION NUMBER: X53138

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2130

ATGAGTTTAG	TTAATAGAAA	ACAGTTAGAA	AAAATGGCAA	ATGTAAGATT	50
TCGTACTCAA	GAAGATGAAT	ATGTTGCAAT	ATTGGATGCT	TTAGAAGAAT	100
ATCATAATAT	GTCAGAGAAT	ACTGTAGTCG	AAAAATATTT	AAAAATTAAAA	150
GATATAAATA	GTTTAACAGA	TATTTATATA	GATACATATA	AAAAATCTGG	200
TAGAAATAAA	GCCTTAAAAA	AATTTAAGGA	ATATCTAGTT	ACAGAAGTAT	250
TAGAGCTAAA	GAATAATAAT	TTAACTCCAG	TTGAGAAAAA	TTTACATTTT	300
GTTTGGATTG	GAGGTCAAAT	AAATGACACT	GCTATTAATT	ATATAAATCA	350
ATGGAAAGAT	GTAAATAGTG	ATTATAATGT	TAATGTTTTT	TATGATAGTA	400
ATGCATTTTT	GATAAACACA	TTGAAAAAAA	CTGTAGTAGA	ATCAGCAATA	450
AATGATACAC	TTGAATCATT	TAGAGAAAAC	TTAAATGACC	CTAGATTTGA	500
CTATAATAAA	TTCTTCAGAA	AACGTATGGA	AATAATTTAT	GATAAACAGA	550
AAAATTTTCAT	AAACTACTAT	AAAGCTCAAA	GAGAAGAAAA	TCCTGAACTT	600

ATAATTGATG	ATATTGTAAA	GACATATCTT	TCAAATGAGT	ATTCAAAGGA	650
GATAGATGAA	CTTAATACCT	ATATTGAAGA	ATCCTTAAAT	AAAATTACAC	700
AGAATAGTGG	AAATGATGTT	AGAAACTTTG	AAGAATTTAA	AAATGGAGAG	750
TCATTCAACT	TATATGAACA	AGAGTTGGTA	GAAAGGTGGA	ATTTAGCTGC	800
TGCTTCTGAC	ATATTAAGAA	TATCTGCATT	AAAAGAAATT	GGTGGTATGT	850
ATTTAGATGT	TGATATGTTA	CCAGGAATAC	AACCAGACTT	ATTTGAGTCT	900
ATAGAGAAAC	CTAGTTCAGT	AACAGTGGAT	TTTTGGGAAA	TGACAAAGTT	950
AGAAGCTATA	ATGAAATACA	AAGAATATAT	ACCAGAATAT	ACCTCAGAAC	1000
ATTTTGACAT	GTTAGACGAA	GAAGTTCAAA	GTAGTTTGA	ATCTGTTCTA	1050
GCTTCTAAGT	CAGATAAATC	AGAAATATTC	TCATCACTTG	GTGATATGGA	1100
GGCATCACCA	CTAGAAGTTA	AAATTGCATT	TAATAGTAAG	GGTATTATAA	1150
ATCAAGGGCT	AATTTCTGTG	AAAGACTCAT	ATTGTAGCAA	TTTAATAGTA	1200
AAACAAATCG	AGAATAGATA	TAAAATATTG	AATAATAGTT	TAAATCCAGC	1250
TATTAGCGAG	GATAATGATT	TTAATACTAC	AACGAATACC	TTTATTGATA	1300
GTATAATGGC	TGAAGCTAAT	GCAGATAATG	GTAGATTTAT	GATGGAACTA	1350
GGAAAGTATT	TAAGAGTTGG	TTTCTTCCCA	GATGTTAAAA	CTACTATTAA	1400
CTTAAGTGGC	CCTGAAGCAT	ATGCGGCAGC	TTATCAAGAT	TTATTAATGT	1450
TTAAAGAAGG	CAGTATGAAT	ATCCATTTGA	TAGAAGCTGA	TTTAAGAAAC	1500
TTTGAAATCT	CTAAACTAA	TATTTCTCAA	TCAACTGAAC	AAGAAATGGC	1550
TAGCTTATGG	TCATTTGACG	ATGCAAGAGC	TAAAGCTCAA	TTTGAAGAAT	1600
ATAAAAGGAA	TTATTTTGAA	GGTTCCTCTG	GTGAAGATGA	TAATCTTGAT	1650
TTTTCTCAAA	ATATAGTAGT	TGACAAGGAG	TATCTTTTAG	AAAAAATATC	1700
TTCATTAGCA	AGAAGTTCAG	AGAGAGGATA	TATACACTAT	ATTGTTTCACT	1750
TACAAGGAGA	TAAAATTAGT	TATGAAGCAG	CATGTAACCT	ATTTGCAAAG	1800
ACTCCTTATG	ATAGTGTACT	GTTTCAGAAA	AATATAGAAG	ATTCAGAAAT	1850
TGCATATTAT	TATAATCCTG	GAGATGGTGA	AATACAAGAA	ATAGACAAGT	1900
ATAAAATTCC	AAGTATAAT	TCTGATAGAC	CTAAGATTAA	ATTAACATTT	1950
ATTGGTCATG	GTAAAGATGA	ATTTAATACT	GATATATTTG	CAGGTTTGA	2000
TGTAGATTCA	TTATCCACAG	AAATAGAAGC	AGCAATAGAT	TTAGCTTAAAG	2050
AGGATATTTT	TCCTAAGTCA	ATAGAAATAA	ATTTATTAGG	ATGTAATATG	2100
TTTAGCTACT	CTATCAACGT	AGAGGAGACT	TATCCTGGAA	AATTATTACT	2150
TAAAGTTAAA	GATAAAATAT	CAGAATTAAT	GCCATCTATA	AGTCAAGACT	2200
CTATTATAGT	AAGTGCAAAT	CAATATGAAG	TTAGAATAAA	TAGTGAAGGA	2250
AGAAGAGAAT	TATTGGATCA	TTCTGGTGAA	TGGATAAATA	AAGAAGAAAG	2300
TATTATAAAG	GATATTTTCA	CAAAAGAATA	TATATCATTT	AATCCTAAAG	2350
AAAATAAAAT	TACAGTAAAA	TCTAAAAATT	TACCTGAGCT	ATCTACATTA	2400
TTACAAGAAA	TTAGAAATAA	TTCTAATTCA	AGTGATATTG	AACTAGAAGA	2450
AAAAGTAATG	TTAACAGAAT	GTGAGATAAA	TGTTATTTC	AATATAGATA	2500
CGCAAATTGT	TGAGGAAAGG	ATTGAAGAAG	CTAAGAATTT	AACTTCTGAC	2550
TCTATTAAAT	ATATAAAAGA	TGAATTTAAA	CTAATAGAAT	CTATTTCTGA	2600
TGCACTATGT	GACTTAAAAC	AACAGAATGA	ATTAGAAGAT	TCTCATTTTA	2650
TATCTTTTGA	GGACATATCA	GAGACTGATG	AGGGATTAG	TATAAGATTT	2700
ATTAATAAAG	AAACTGGAGA	ATCTATATTT	GTAGAACTG	AAAAACAAT	2750
ATTCTCTGAA	TATGCTAATC	ATATAACTGA	AGAGATTCT	AAGATAAAAG	2800
GTAATATATT	TGATACTGTA	AATGGTAAGT	TAGTAAAAAA	AGTAAATTTA	2850
GATACTACAC	ACGAAGTAAA	TACTTTAAAT	GCTGCATTTT	TTATACAATC	2900
ATTAATAGAA	TATAATAGTT	CTAAAGAATC	TCTTAGTAAT	TTAAGTGTAG	2950
CAATGAAAGT	CCAAGTTTAC	GCTCAATTAT	TTAGTACTGG	TTTAAATACT	3000
ATTACAGATG	CAGCCAAAGT	TGTTGAATTA	GTATCAACTG	CATTAGATGA	3050
AACTATAGAC	TTACTTCCTA	CATTATCTGA	AGGATTACCT	ATAATTGCAA	3100
CTATTATAGA	TGGTGTAAGT	TTAGGTGCAG	CAATCAAAGA	GCTAAGTGAA	3150
ACGAGTGACC	CATTATTAAG	ACAAGAAATA	GAAGCTAAGA	TAGGTATAAT	3200
GGCAGTAAAT	TTAACAACAG	CTACAACCTG	AATCATTTACT	TCATCTTTGG	3250
GGATAGCTAG	TGGATTTAGT	ATACTTTTAG	TTCTTTTAGC	AGGAATTTCA	3300
GCAGGTATAC	CAAGCTTAGT	AAACAATGAA	CTTGTAATTC	GAGATAAGGC	3350
AACAAAGGTT	GTAGATTATT	TTAAACATGT	TTCATTAGTT	GAAACTGAAG	3400
GAGTATTTAC	TTTATTAGAT	GATAAAATAA	TGATGCCACA	AGATGATTTA	3450

GTGATATCAG	AAATAGATTT	TAATAATAAT	TCAATAGTTT	TAGGTAAATG	3500
TGAAATCTGG	AGAATGGAAG	GTGGTTCAGG	TCATACTGTA	ACTGATGATA	3550
TAGATCACTT	CTTTTCAGCA	CCATCAATAA	CATATAGAGA	GCCACACTTA	3600
TCTATATATG	ACGTATTGGA	AGTACAAAAA	GAAGAACTTG	ATTTGTCAAA	3650
AGATTTAATG	GTATTACCTA	ATGCTCCAAA	TAGAGTATTT	GCTTGGGAAA	3700
CAGGATGGAC	ACCAGGTTTA	AGAAGCTTAG	AAAATGATGG	CACAAAAC TG	3750
TTAGACCGTA	TAAGAGATAA	CTATGAAGGT	GAGTTTATT	GGAGATATTT	3800
TGCTTTTATA	GCTGATGCTT	TAATAACAAC	ATTAAAACCA	AGATATGAAG	3850
ATACTAATAT	AAGAATAAAT	TTAGATAGTA	ATACTAGAAG	TTTATAGTT	3900
CCAATAATAA	CTACAGAATA	TATAAGAGAA	AAATTATCAT	ATTCTTTCTA	3950
TGGTTCAGGA	GGAACTTATG	CATTGTCTCT	TTCTCAATAT	AATATGGGTA	4000
TAAATATAGA	ATTAAGTGAA	AGTGATGTTT	GGATTATAGA	TGTTGATAAT	4050
GTTGTGAGAG	ATGTAAC TAT	AGAATCTGAT	AAAATTAAAA	AAGGTGATTT	4100
AATAGAAGGT	ATTTTATCTA	CACTAAGTAT	TGAAGAGAAT	AAAATTATCT	4150
TAAATAGCCA	TGAGATTAAT	TTTTCTGGTG	AGGTAAATGG	AAGTAATGGA	4200
TTTGTTTCTT	TAACATTTTC	AATTTTAGAA	GGAATAAATG	CAATTATAGA	4250
AGTTGATTTA	TTATCTAAAT	CATATAAATT	ACTTATTTCT	GGCGAATTAA	4300
AAATATTGAT	GTTAAATTCA	AATCATATTC	AACAGAAAAT	AGATTATATA	4350
GGATTCAATA	GCGAATTACA	GAAAAATATA	CCATATAGCT	TTGTAGATAG	4400
TGAAGGAAAA	GAGAATGGTT	TTATTAATGG	TTCAACAAAA	GAAGGTTTAT	4450
TTGTATCTGA	ATTACCTGAT	GTAGTCTCTA	TAAGTAAGGT	TTATATGGAT	4500
GATAGTAAGC	CTTCATTTGG	ATATTATAGT	AATAATTTGA	AAGATGTCAA	4550
AGTTATAACT	AAAGATAATG	TTAATATATT	AACAGGTTAT	TATCTTAAGG	4600
ATGATATAAA	AATCTCTCTT	TCTTTGACTC	TACAAGATGA	AAAAACTATA	4650
AAGTTAAATA	GTGTGCATTT	AGATGAAAGT	GGAGTAGCTG	AGATTTTGAA	4700
GTTTCATGAAT	AGAAAAGGTA	ATACAAATAC	TTCAGATTCT	TTAATGAGCT	4750
TTTTAGAAAG	TATGAATATA	AAAAGTATTT	TCGTTAATTT	CTTACAATCT	4800
AATATTAAGT	TTATATTAGA	TGCTAATTTT	ATAATAAGTG	GTACTACTTC	4850
TATTGGCCAA	TTTGAGTTTA	TTTGTGATGA	AAATGATAAT	ATACAACCAT	4900
ATTTTCATTAA	GTTTAATACA	CTAGAAACTA	ATTATACTTT	ATATGTAGGA	4950
AATAGACAAA	ATATGATAGT	GGAACCAAAT	TATGATTTAG	ATGATTCTGG	5000
AGATATATCT	TCAACTGTTA	TCAATTTCTC	TCAAAAGTAT	CTTTATGGAA	5050
TAGACAGTTG	TGTTAATAAA	GTTGTAATTT	CACCAAATAT	TTATACAGAT	5100
GAAATAAATA	TAACGCCTGT	ATATGAAACA	AATAATACTT	ATCCAGAAGT	5150
TATTGTATTA	GATGCAAAAT	ATATAAATGA	AAAAATAAAT	GTTAATATCA	5200
ATGATCTATC	TATACGATAT	GTATGGAGTA	ATGATGGTAA	TGATTTTATT	5250
CTTATGTCAA	CTAGTGAAGA	AAATAAGGTG	TCACAAGTTA	AAATAAGATT	5300
CGTTAATGTT	TTTAAAGATA	AGACTTTGGC	AAATAAGCTA	TCTTTTAACT	5350
TTAGTGATAA	ACAAGATGTA	CCTGTAAGTG	AAATAATCTT	ATCATTTACA	5400
CCTTCATATT	ATGAGGATGG	ATTGATTGGC	TATGATTTGG	GTCTAGTTTC	5450
TTTATATAAT	GAGAAATTTT	ATATTAATAA	CTTTGGAATG	ATGGTATCTG	5500
GATTAATATA	TATTAATGAT	TCATTATATT	ATTTTAAACC	ACCAGTAAAT	5550
AATTTGATAA	CTGGATTTGT	GACTGTAGGC	GATGATAAAT	ACTACTTTAA	5600
TCCAATTAAT	GGTGGAGCTG	CTTCAATTGG	AGAGACAATA	ATTGATGACA	5650
AAAATTATTA	TTTCAACCAA	AGTGGAGTGT	TACAAACAGG	TGTATTTAGT	5700
ACAGAAGATG	GATTTAAATA	TTTTGCCCCA	GCTAATACAC	TTGATGAAAA	5750
CCTAGAAGGA	GAAGCAATTG	ATTTTACTGG	AAAATTAATT	ATTGACGAAA	5800
ATATTTATTA	TTTTGATGAT	AATTATAGAG	GAGCTGTAGA	ATGGAAAGAA	5850
TTAGATGGTG	AAATGCACTA	TTTTAGCCCA	GAAACAGGTA	AAGCTTTTAA	5900
AGGTCTAAAT	CAAATAGGTG	ATTATAAATA	CTATTTCAAT	TCTGATGGAG	5950
TTATGCAAAA	AGGATTTGTT	AGTATAAATG	ATAATAAACA	CTATTTTGAT	6000
GATTCTGGTG	TTATGAAAGT	AGGTTACACT	GAAATAGATG	GCAAGCATTT	6050
CTACTTTGCT	GAAAACGGAG	AAATGCAAAAT	AGGAGTATTT	AATACAGAAG	6100
ATGGATTTAA	ATATTTTGCT	CATCATAATG	AAGATTTAGG	AAATGAAGAA	6150
GGTGAAGAAA	TCTCATATTC	TGGTATATTA	AATTTCAATA	ATAAAATTTA	6200
CTATTTTGAT	GATTCATTTA	CAGCTGTAGT	TGGATGGAAA	GATTTAGAGG	6250
ATGGTTCAAA	GTATTATTTT	GATGAAGATA	CAGCAGAAGC	ATATATAGGT	6300

TTGTCATTAA	TAAATGATGG	TCAATATTAT	TTTAATGATG	ATGGAATTAT	6350
GCAAGTTGGA	TTTGTCACTA	TAAATGATAA	AGTCTTCTAC	TTCTCTGACT	6400
CTGGAATTAT	AGAATCTGGA	GTACAAAACA	TAGATGACAA	TTATTTCTAT	6450
ATAGATGATA	ATGGTATAGT	TCAAATTGGT	GTATTTGATA	CTTCAGATGG	6500
ATATAAATAT	TTTGCACCTG	CTAATACTGT	AAATGATAAT	ATTTACGGAC	6550
AAGCAGTTGA	ATATAGTGGT	TTAGTTAGAG	TTGGGGAAGA	TGTATATTAT	6600
TTTGGAGAAA	CATATACAAT	TGAGACTGGA	TGGATATATG	ATATGGAAAA	6650
TGAAAGTGAT	AAATATTATT	TCAATCCAGA	AACTAAAAAA	GCATGCAAAG	6700
GTATTAATTT	AATTGATGAT	ATAAAATATT	ATTTTGATGA	GAAGGGCATA	6750
ATGAGAACGG	GTCTTATATC	ATTTGAAAAT	AATAATTATT	ACTTTAATGA	6800
GAATGGTGAA	ATGCAATTTG	GTTATATAAA	TATAGAAGAT	AAGATGTTCT	6850
ATTTTGGTGA	AGATGGTGTC	ATGCAGATTG	GAGTATTTAA	TACACCAGAT	6900
GGATTTAAAT	ACTTTGCACA	TCAAAATACT	TTGGATGAGA	ATTTTGAGGG	6950
AGAATCAATA	AACTATACTG	GTTGGTTAGA	TTTAGATGAA	AAGAGATATT	7000
ATTTTACAGA	TGAATATATT	GCAGCAACTG	GTTTCAGTTAT	TATTGATGGT	7050
GAGGAGTATT	ATTTTGATCC	TGATACAGCT	CAATTAGTGA	TTAGTGAATA	7100
G					7101

2) INFORMATION FOR SEQ ID NO: 2131

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2131

AAGCMATTGT TGTAATTTT GAAAG

25

2) INFORMATION FOR SEQ ID NO: 2132

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2132

TCATATCCAT AGCAATAGTT CTA

23

2) INFORMATION FOR SEQ ID NO: 2133

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 42 bases
- (B) TYPE: Nucleic acid

1100

- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2133

CCACGCACAW AAACCTTGTTT TAGAAGTAGC AGCWCAGCGT GG

42

2) INFORMATION FOR SEQ ID NO: 2134

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2134

CGCGTGAAGC TTCTGTG

17

2) INFORMATION FOR SEQ ID NO: 2135

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2135

TCTCGCCGTT ATTCAGTTTC

20

2) INFORMATION FOR SEQ ID NO: 2136

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 44 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2136

CCAACGCGTC CTCAATCATT TCTAACTTCT ATGGCCGGCG TTGG

44

2) INFORMATION FOR SEQ ID NO: 2137

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 889 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Pseudomonas putida*
- (C) ACCESSION NUMBER: Genome project

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2137

ATGATCACCG	GTGCTGCCCA	GATGGACGGC	GCGATCCTGG	TTTGCTCGGC	50
CGCCGATGGT	CCGATGCCrC	AAACCCGTGA	GCACATCCTG	CTGTCCCCTC	100
AGGTAGGCGT	TCCGTACATC	GTGGTCTTCC	TGAACAAGGC	CGACCTGGTA	150
GACGACGCTG	AGCTGCTGGA	ACTGGTCGAG	ATGGAAGTTC	GCGACCTGCT	200
GTCCACCTAC	GACTTCCCAG	GCGACGACAC	TCCGATCATC	ATCGGTTCCG	250
CTCGTATGGC	CCTGGAAGGC	AAAGACGACA	ACGAAATGGG	CACTACCGCT	300
GTCAAGAAGC	TGGTAGAAAC	TCTGGATGCC	TACATCCCTG	AGCCAGTTCCG	350
TGCCATCGAC	CAGCCGTTCC	TGATGCCGAT	CGAAGACGTG	TTCTCGATCT	400
CGGGTCGTGG	TACCGTTGTT	ACCGGTCGTA	TCGAGCGTGG	CATCGTTCGC	450
GTTTCAGGATC	CGCTGGAAAT	CGTTGGTCTG	CGTGACACCA	CCACCACCAC	500
CTGCACCGGT	GTTGAGATGT	TCCGCAAGCT	GCTGGACGAA	GGTCGTGCTG	550
GCGAGAAGT	CGGCGTTCTG	CTGCGTGGTA	CCAAGCGTGA	CGACGTTGAG	600
CGTGGCCAGG	TTCTGGTCAA	GCCAGGTTCC	GTCAAGCCGC	ACACCAAGTT	650
CACCGCAGAA	GTCTACGTCC	TGTCGAAGGA	AGAAGGCGGC	CGTCACACTC	700
CGTTCTTCAA	AGGCTACCGT	CCACAGTTCT	ACTTCCGTAC	CACTGACGTG	750
ACCGGTAAC	GCGAACTGCC	GGAAGGCGTT	GAAATGGTAA	TGCCAGGTGA	800
CAACATTGAG	ATGACTGTTA	CCCTGATCAA	GACCATCGCA	ATGGAAGACG	850
GTCTGCGCTT	CGCTATCCGT	GAAGGCGGTC	GTACCGTCCG		889

2) INFORMATION FOR SEQ ID NO: 2138

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 900 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Pseudomonas aeruginosa*
- (B) STRAIN: PAO-1
- (C) ACCESSION NUMBER: Genome project

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2138

AACATGATCA	CCGGTGCTGC	CCAGATGGAC	GGCGCGATCC	TGGTTTGCTC	50
GGCTGCCGAC	GGCCCCATGC	CGCAGACCCG	CGAGCACATC	CTGCTGTCCC	100
GCCAGGTAGG	CGTTCCCTAC	ATCGTCGTGT	TCCTGAACAA	GGCCGACATG	150
GTCGACGACG	CCGAGCTGCT	GGAAGTGGTC	GAGATGGAAG	TTCGCGATCT	200
GCTGAACACC	TACGACTTCC	CGGGCGACGA	CACTCCGATC	ATCATCGGTT	250
CCGCGCTGAT	GGCGCTGGAA	GGCAAGGATG	ACAACGGCAT	CGGCGTAAGC	300
GCCGTGCAGA	AGCTGGTAGA	GACCCTGGAC	TCCTACATTC	CGGAGCCGGT	350
TCGTGCCATC	GACCAGCCGT	TCCTGATGCC	GATCGAAGAC	GTGTTCTCGA	400
TCTCCGGCCG	CGGTACCGTG	GTAACCGGTC	GTGTAGAGCG	CGGCATCATC	450
AAGGTCCAGG	AAGAAGTGGA	AATCGTCGGC	ATCAAGGCCA	CCACCAAGAC	500
TACCTGCACC	GGCGTTGAAA	TGTTCCGCAA	GCTGCTCGAC	GAAGGTCGTG	550
CTGGTGAGAA	CGTTGGTATC	CTGCTGCGTG	GCACCAAGCG	TGAAGACGTA	600
GAGCGTGGCC	AGGTTCTGGC	CAAGCCGGGC	ACCATCAAGC	CGCACACCAA	650
GTTTCGAGTGC	GAAGTGTACG	TGCTGTCCAA	GGAAGAAGGT	GGTCGTCACA	700
CCCCGTTCTT	CAAGGGCTAC	CGTCCGCAGT	TCTACTTCCG	TACCACCGAC	750
GTGACCGGTA	ACTGCGAACT	GCCGGAAGGC	GTAGAGATGG	TAATGCCGGG	800
CGACAACATC	AAGATGGTTG	TCACCCTGAT	CGCTCCGATC	GCCATGGAAG	850
ATGGCCTGCG	CTTCGCGATC	CGCGAAGGCG	GCCGTACCGT	TGGCGCCGGC	900

2) INFORMATION FOR SEQ ID NO: 2139

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1398 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Campylobacter jejuni*
- (B) STRAIN: NCTC 11168
- (C) ACCESSION NUMBER: AL139074

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2139

ATGCAAGGAT	TTATTTTACA	GGTATTAGGT	CCGGTTGTTG	ATGTAGATTT	50
TAACGACTAT	TTGCCTCAAA	TTAATGAAGC	AATTGTTGTA	AATTTTGAAA	100
GCGAAGGAAA	AAAACATAAA	CTTGTTTTAG	AAGTAGCAGC	TCATTTAGGA	150
GATAATAGAG	TTAGAACTAT	TGCTATGGAT	ATGACAGATG	GTTTGGTAAG	200
GGGCTTAAAA	GCTGAGGCTT	TAGGTGCTCC	CATTAGTGTT	CCTGTTGGTG	250
AGAAAGTTTT	AGGAAGAATT	TTCAATGTTA	CTGGAGATTT	GATCGATGAA	300
GGTGAAGAAA	TTTCTTTCGA	TAAAAAATGG	GCAATTCATA	GAGATCCACC	350
AGCTTTTGAA	GATCAAAGCA	CAAAAAGTGA	GATTTTGTGA	ACAGGGATTA	400
AAGTTGTAGA	TTTACTTGCT	CCTTATGCAA	AAGGTGGTAA	AGTAGGTCTT	450
TTTGGTGGTG	CAGGTGTTGG	TAAAACTGTT	ATTATTATGG	AGCTTATTCA	500
CAATGTTGCA	TTTAAGCATA	GCGGCTATTC	TGTATTTGCA	GGTGTGGGTG	550
AGAGAACTCG	TGAAGGAAAT	GACCTTTATA	ATGAAATGAA	AGAAAGTAAT	600
GTTTTAGACA	AAGTTGCTCT	ATGTTATGGA	CAAATGAATG	AACCACCAGG	650
GGCAAGAAAT	CGTATTGCTT	TAACAGGTTT	AACAATGGCT	GAGTATTTTA	700
GAGATGAAAT	GGGTCTTGAT	GTGCTTATGT	TTATTGATAA	TATCTTTAGA	750
TTTTTACAAT	CAGGTTCTGA	AATGTCAGCA	CTTTTAGGAA	GAATTCCATC	800
AGCTGTGGGT	TATCAACCAA	CCTTAGCAAG	TGAAATGGGT	AAATTCCAAG	850
AAAGAATTAC	TTCAACTAAA	AAAGGCTCAA	TCACTTCAGT	TCAAGCTGTT	900
TACGTTCCAG	CTGATGACTT	AACAGACCCA	GCTCCAGCAA	CTGTTTTTGC	950

TCACCTTAGAT	GCTACAACGG	TTTTAAATAG	AGCTATTGCT	GAAAAGGGTA	1000
TTTATCCTGC	AGTTGACCCA	CTTGACTCAA	CTTCAAGAAT	GCTTGACCCA	1050
AATATCATTG	GAGAAGAACA	TTATAAAGTT	GCTCGTGGTG	TTCAATCAGT	1100
GCTTCAAAAA	TACAAAGATT	TACAAGATAT	CATCGCCATT	TTAGGTATGG	1150
ATGAGCTTAG	CGAAGAGGAT	AAACTTGTAG	TTGAAAGAGC	AAGAAAGATT	1200
GAAAAATTCT	TATCACAACC	ATTTTTCGTT	GCAGAAGTTT	TCACAGGTAG	1250
CCCAGGAAAA	TATATAAGCC	TTGAAGATAC	AATAGCAGGA	TTTAAGGGAA	1300
TTTTAGAAGG	TAAATATGAT	CATTTACCAG	AAAATGCTTT	CTATATGGTT	1350
GGAAATATAG	ATGAAGCTAT	TGCAAAAGCG	GATAAATTAA	AAGGTTAA	1398

2) INFORMATION FOR SEQ ID NO: 2140

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2157 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
- (B) STRAIN: 670
- (C) ACCESSION NUMBER: X67867

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2140

ATGAACAAAC	CAACGATTCT	GCGCCTAATC	AAGTATCTGA	GCATTAGCTT	50
CTTAAGCTTG	GTTATCGCAG	CCATTGTCTT	AGGCGGAGGA	GTTTTTTTCT	100
ACTACGTTAG	CAAGGCTCCT	AGCCTATCCG	AGAGTAAACT	AGTTGCAACA	150
ACTTCTAGTA	AAATCTACGA	CAATAAAAAT	CAACTCATTG	CTGACTTGGG	200
TTCTGAACGC	CGCGTCAATG	CCCAAGCTAA	TGATATTCCC	ACAGATTTGG	250
TTAAGGCAAT	CGTTTCTATC	GAAGACCATC	GCTTCTTCGA	CCACAGGGGG	300
ATTGATTCCA	TCCGTATCCT	GGGAGCTTTC	TTGCGCAATC	TGCAAAGTAA	350
TTCCCTCCAA	GGTGGATCAA	CTCTCACCCA	ACAGTTGATT	AAGTTGACTT	400
ACTTTTCAAC	CTCGACTTCC	GACCAGACTA	TTTCTCGTAA	GGCTCAGGAA	450
GCTTGGTTAG	CGATTCAAGT	AGAACAAAAA	GCAACCAAAC	AGGAAATCTT	500
GACCTACTAT	ATAAATAAGG	TCTACATGTC	TAATGGCAAC	TATGGAATGC	550
AGACAGCAGC	TCAAACTAC	TATGGTAAAG	ACCTCAATAA	TTTAAGTTTA	600
CCTCAGTTAG	CCTTGCTGGC	TGGAATGCCT	CAGGCACCAA	ACCAATATGA	650
CCCCTATTCA	CATCCAGAAG	CAGCCCAAGA	CCGCCGAAAC	TTGGTCTTAT	700
CTGAAATGAA	AAATCAAGGT	TACATCTCTG	CTGAACAGTA	TGAGAAAGCA	750
GTCAATACAC	CAATTACTGA	TGGACTACAA	AGTCTCAAAT	CAGCAAGTAA	800
TTACCCTGCT	TACATGGATA	ATTACCTCAA	GGAGGTCATC	AATCAAGTAG	850
AACAAGAAAC	TGGCTATAAC	CTTCTAACTA	CTGGGATGGA	TGTTTACACA	900
AATGTAGACC	AAGAAGCTCA	AAAACATCTG	TGGGATATCT	ACAACCTCCGA	950
TCAATACGTC	TCTTACCCTG	ACGATGATTT	GCAAGTCGCA	TCTACGGTCG	1000
TAGATGTTTC	AAATGGTAAA	GTCATCGCCC	AACCTGGAGC	TCGTCAACCA	1050
GCAAGTAACG	TTTCATTTGG	TACCAACCAA	GCTGTGGAAA	CCAATCGTGA	1100
CTGGGGTTCT	GCTATGAAAC	CAATCACCGA	TTATGCACCT	GCCATAGAAT	1150
ACGGTGTTTA	TGATTCCACT	GCAACTATGG	TTAATGATAT	TCCTTATAAC	1200
TATCCGGGAA	CAAGCACACC	TGTCTACAAC	TGGGATAGAG	CATATTTTCGG	1250
TAATATTACT	CTGCAATATG	CTCTTCAACA	ATCACGAAAT	GTCACAGCCG	1300
TTGAGACTTT	GAATAAGGTC	GGTCTAGATA	GAGCTAAAAC	CTTCCTTAAT	1350
GGTCTTG GTA	TCGACTATCC	AAGCATGCAT	TATGCAAACG	CCATTTCAAG	1400

TAATACAACA	GAATCTAATA	AACAATACGG	AGCAAGTAGT	GAAAAAATGG	1450
CTGCTGCTTA	TGCTGCCTTT	GCCAACGGTG	GAATTTACCA	CAAACCCATG	1500
TATATCAATA	AGGTCGTCTT	CAGTGACGGT	AGTAAAAAAG	AATTTTCAGA	1550
TGTAGGTACA	CGAGCTATGA	AAGAAACAAC	TGCTTACATG	ATGACCGAAA	1600
TGATGAAAAC	TGTCTTGGCA	TACGGAAC TG	GTCGTGGAGC	CTATCTCCCA	1650
TGGTTAGCGC	AAGCTGGTAA	GACAGGTACT	TCTAACTACA	CAGATGATGA	1700
AATTGAAAAA	CACATCAAGA	ACACTGGCTA	TGTAGCTCCA	GATGAAATGT	1750
TTGTTGGTTA	TACTCGTAAG	TATTCTATGG	CTGTATGGAC	AGGTTATTCTG	1800
AATCGTTTAA	CTCCTATCGT	TGGAGATGGT	TTCCTAGTTG	CAGCTAAAGT	1850
TTATCGCTCA	ATGATAACGT	ATCTATCAGA	AGATACTCAT	CCAGAAAGACT	1900
GGACGATGCC	AGACGGACTT	TTCAGAAACG	GGGAATTTGT	ATTCAAAAAT	1950
GGAGCTCGTT	CTACGTGGAG	CTCACCTGCT	CCACAACAAC	CCCCATCAAC	2000
TGAAAGTTCA	AGCTCATCAT	CAGATAGTTC	AACTTCACAG	TCTAGCTCAA	2050
CCACTCCAAG	CACAAATAAT	AGTACGACTA	CCGATCCTAA	CAATAATACG	2100
CAACAATCAA	ATACAACCCC	TGATCAACAA	AATCAGAATC	CTCAACCAGC	2150
ACAACCA					2157

2) INFORMATION FOR SEQ ID NO: 2141

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2141

CACCAGTCAC AGAAAAGC

18

2) INFORMATION FOR SEQ ID NO: 2142

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2142

GCCTTAATTT CGGATAGTGC

20

2) INFORMATION FOR SEQ ID NO: 2143

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single

1105

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2143

GAGAAAGAGC CCAATTATCT AATGT

25

2) INFORMATION FOR SEQ ID NO: 2144

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3075 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus aureus*
- (B) STRAIN: J2870
- (C) ACCESSION NUMBER: X75439

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2144

TTGACAAAGA	AATATTTAAA	CACCCAGAAT	GAAATATCAG	CATTTTGGAA	50
TACTCAAAAG	ATATTTAAAA	AATCAATTGA	CAATAGAAAA	GGACAGGAAA	100
GTTTTGTTTT	TTATGACGGC	CCCCCAACTG	CAAATGGCCT	TCCTCATGCT	150
GGCCATGTTC	TTGGAAGAGT	AATCAAGGAT	TTAGTTGCAA	GATTAAAAAC	200
TATGCAAGGT	TTTTATGTAG	AAAGAAAAGC	AGGATGGGAT	ACCCATGGCT	250
TACCAGTTGA	ATTAGAGGTT	GAAAAAATAA	TTGGAATTAA	AGGAAAACAA	300
GACATTGAAA	AGTATGGAAT	AGAAAATTTT	ATAAATGAAT	GTAAAAAAG	350
TGTATTTAAT	TATGAAAAAG	AATGGCGGGA	TTTTTCTAAA	GATTTAGGAT	400
ACTGGGTGTA	CATGGACTCC	CCCTATATAA	CTCTTGAGAA	TAATTATATT	450
GAAAGTGTAT	GGAATATATT	ATCTACATTC	CATAAAAAAG	GACTATTATA	500
TAAGGGACAT	AAGGTGACTC	CTTATTGTAC	ACATGATCAA	ACCGCTTTAA	550
GTTCTCATGA	AGTAGCGCAA	GGCTATAAAA	ACGTTAAAGA	TTTATCAGCT	600
GTTGTAAAT	TTCAACTTAC	AAATAGTAAA	GATACTTATT	TCTTAAGTTG	650
GACTACCACT	CCCTGGACTT	TGCCTGCAAA	TGTAGCATT	GCTATAAATA	700
AAGATCTTAA	TTATTCAAAA	ATTCGGGTAG	AAAAATGAGTA	TTATATCTTA	750
GCTACAGATC	TAATTAATTC	TATAATAACT	GAAAAATACG	AAATTATTGA	800
TACCTTTTCA	GGAAGTAATT	TAATTAATTT	AAAAATACATT	CCTCCTTTTG	850
AAAGCGACGG	TTTAGTTAAT	GCATATTACG	TTGTTGATGG	AGAATTTGTT	900
ACTAACTCAG	AAGGAACTGG	TATTGTTTAT	ATAGCACCAG	CTCATGGGGA	950
AGATGACTAC	CAATTGGTTT	TAGAGCGTGA	TTTGATTTC	TTAAATGTTA	1000
TAACAAGAGA	AGGAGTATAT	AATGATAGGT	TCCCTGAATT	AGTTGGTAAT	1050
AAAGCTAAAA	ATAGTGATAT	AGAAATCATA	AAATTATTAT	CCAAAAACA	1100
ACTTTTATAT	AAAAAACAAA	AATATGAGCA	TAATTATCCT	CATTGTTGGA	1150
GATGTGGTAA	TCCTTTGATA	TATTATGCGA	TGGAAGGTTG	GTTTATTAAA	1200
ACAATAATT	TTAAGAATGA	AATTATTAAC	AATAATAATA	ATATAGAGTG	1250
GTTTCCTTCT	CATATTAAGG	AAGGGAGAAT	GGGAAATTTT	TTAGAAAATA	1300
TGGTTGATTG	GAACATTGGT	AGAAATAGAT	ATTGGGGAAC	ACCATTAAAT	1350
GTATGGATTT	GCAATGATTG	TAATCACGAA	TACGCACCAA	GTAGTATTAA	1400
GGATTTACAA	AATAATTCCA	TCAATAAAAT	TGATGAAGAT	ATTGAGTTGC	1450
ATAGACCTTA	TGTTGATAAT	ATCACTCTTA	GTTGCCCTAA	GTGTAATGGG	1500

1106

AAAATGTCTC	GAGTAGAAGA	AGTAATCGAT	TTTTGGTTTG	ATAGCGGCTC	1550
TATGCCGTTT	GCTCAGCATC	ATTATCCTTT	TGATAACCAG	AAAATTTTAA	1600
ATCAACACTT	TCCAGCTGAT	TTTATTGCAG	AAGGAGTTGA	TCAAACGAGA	1650
GGCTGGTTTT	ACAGTTTACT	AGTAATTTCT	ACTATTCTAA	AAGGAAAATC	1700
TTCTTATAAA	CGTGCTTTAT	CTTTAGGACA	TATTCTAGAC	AGTAATGGTA	1750
AAAAAATGTC	TAAAAGTAAA	GGAAACGTTA	TTAATCCAAC	TGAATTAATT	1800
AATAAGTACG	GAGCCGATTC	TTTAAGATGG	GCCTTAATTT	CGGATAGTGC	1850
TCCATGGAAT	AACAAAAGAT	TCTCAGAAAA	TATAGTAGCT	CAGACCAAAT	1900
CGAAATTTAT	AGATACGCTT	GATAATATTT	ATAAATTTTA	TAATATGTAT	1950
AATAAAATAG	ATCACTATAA	TCCTAATAAT	GAAATTACAA	AAAGTAGAAA	2000
TACATTAGAT	AATTGGGCTC	TTTCTCGCTT	AAACACCTTA	ATAAAAGAAA	2050
GTAATATTTA	TGTAAATAAT	TACGATTTCA	CTTCCGCAGC	CAGATTAATT	2100
AACGAATATA	CCAATACAAT	AAGTAATTGG	TATATCGGAG	ATTCGAGAGG	2150
ACGATTTTGG	GAACAAGGAA	TTTCTAACGA	TAAAAAAGAT	GCGTACAATA	2200
CGCTTTATGA	AATTTTAACA	ACTTTATCAA	GACTAGTGGC	TCCATTTGTT	2250
CCATTTATAT	CTGAAAAAAT	CCATTATAAT	TTGACTGGAA	AAAGTGTGCA	2300
TTTACAAGAT	TATCCACAAT	ATAAAGAAAG	TTTTATTAAT	CAAGCATTGG	2350
AAGATGAAAT	GCATACCGTT	ATAAAAATTG	TAGAATTATC	TAGACAGGCT	2400
CGCAAAAATG	CAGATTTAAA	AATTAAGCAA	CCTTTATCGA	AAATGGTGAT	2450
TAAACCTAAT	AGTCAATTAA	ACTTAAGTTT	TTTACCTAAT	TACTATTCAA	2500
TAATAAAAGA	CGAATTAAAT	ATAAAAAACA	TTGAATTAAC	TGATAATATT	2550
AATGACTATA	TTACCTATGA	GCTTAAATTG	AATTTTCTT	CTGTGGGACC	2600
AAAAC TAGGG	AACAAAACGA	AAAATATTCA	AACATTGATA	GACTCCCTAT	2650
CAGAGTATGA	TAAAAAAGT	TTAATTGAGT	CTAATAACTT	CAAAAGTTTA	2700
TCTTCTGATG	CTGAGTTAAC	TAAGGATGAT	TTTATAATTA	AAACCTTACC	2750
TAAGGATAGT	TATCAACTCA	GTGAAGATAA	TGACTGCGTT	ATATTATTAG	2800
ATAAAAATTT	ATCTCCTGAA	TTAATTCGCG	AAGGACATGC	TAGAGAGCTC	2850
ATTAGATTAA	TTCAACAATT	AAGAAAAAAG	AAAAATTTAC	CAATAAATCA	2900
ACGTATTGAT	ATTTATATCG	GTGTAAGTGG	GGAATTATTA	GAATCAATAA	2950
AAACCAATAA	AAATATGTTT	AAAGAAAATT	TCGTGATTAA	AAATATACAC	3000
TTAAATGTTA	TAGATGAATA	TGAAAATACT	ATTCATTTTA	ATAATAAAGA	3050
AATAAAAATT	TCCTTATTAT	ATTAA			3075

2) INFORMATION FOR SEQ ID NO: 2145

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2145

GCAAGATGTG GCGTGTTACG GT

22

2) INFORMATION FOR SEQ ID NO: 2146

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single

1107

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2146

GGGGCGAAGA AGTTGTCCAT ATT

23

2) INFORMATION FOR SEQ ID NO: 2147

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 660 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Escherichia coli*
- (C) ACCESSION NUMBER: V00622

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2147

ATGGAGAAAA	AAATCACTGG	ATATAACCACC	GTTGATATAT	CCCAATGGCA	50
TCGTAAAGAA	CATTTTGAGG	CATTTCAGTC	AGTTGCTCAA	TGTACCTATA	100
ACCAGACCGT	TCAGCTGGAT	ATTACGGCCT	TTTTAAAGAC	CGTAAAGAAA	150
AATAAGCACA	AGTTTTATCC	GGCCTTTATT	CACATTCTTG	CCCGCCTGAT	200
GAATGCTCAT	CCGGAATTCC	GTATGGCAAT	GAAAGACGGT	GAGCTGGTGA	250
TATGGGATAG	TGTTACCCCT	TGTTACACCG	TTTTCCATGA	GCAAAC TGAA	300
ACGTTTTTCAT	CGCTCTGGAG	TGAATACCAC	GACGATTTC	GGCAGTTTCT	350
ACACATATAT	TCGCAAGATG	TGGCGTGTTA	CGGTGAAAAC	CTGGCCTATT	400
TCCCTAAAGG	GTTTATTGAG	AATATGTTTT	TCGTCTCAGC	CAATCCCTGG	450
GTGAGTTTCA	CCAGTTTGA	TTTAAACGTG	GCCAATATGG	ACAACTTCTT	500
CGCCCCCGTT	TTCACCATGG	GCAAATATTA	TACGCAAGGC	GACAAGGTGC	550
TGATGCCGCT	GGCGATTCAG	GTTTCATCATG	CCGTCTGTGA	TGGCTTCCAT	600
GTCGGCAGAA	TGCTTAATGA	ATTACAACAG	TACTGCGATG	AGTGGCAGGG	650
CGGGGCGTAA					660

2) INFORMATION FOR SEQ ID NO: 2148

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2148

CAGATTAAAT GCGGATTCAG CC

22

2) INFORMATION FOR SEQ ID NO: 2149

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2149

ATCAGGTAAA TCATCAGCGG ATA

23

2) INFORMATION FOR SEQ ID NO: 2150

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 642 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Escherichia coli*
- (B) STRAIN: K12
- (C) ACCESSION NUMBER: X53796

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2150

ATGAATTTTA	CCCGGATTGA	CCTGAATACC	TGGAATCGCA	GGGAACACTT	50
TGCCCTTTAT	CGTCAGCAGA	TTAAATGCGG	ATTCAGCCTG	ACCACCAAAC	100
TCGATATTAC	CGCTTTGCGT	ACCGCACTGG	CGGAGACAGG	TTATAAGTTT	150
TATCCGCTGA	TGATTTACCT	GATCTCCCGG	GCTGTTAATC	AGTTTCCGGA	200
GTTCCGGATG	GCACTGAAAG	ACAATGAACT	TATTTACTGG	GACCAGTCAG	250
ACCCGGTCTT	TACTGTCTTT	CATAAAGAAA	CCGAAACATT	CTCTGCACTG	300
TCCTGCCGTT	ATTTTCCGGA	TCTCAGTGAG	TTTATGGCAG	GTTATAATGC	350
GGTAACGGCA	GAATATCAGC	ATGATACCAG	ATTGTTTCCG	CAGGGAAATT	400
TACCGGAGAA	TCACCTGAAT	ATATCATCAT	TACCGTGCGT	GAGTTTTGAC	450
GGATTTAACC	TGAACATCAC	CGGAAATGAT	GATTATTTTG	CCCCGGTTTT	500
TACGATGGCA	AAGTTTCAGC	AGGAAGGTGA	CCGCGTATTA	TTACCTGTTT	550
CTGTACAGGT	TCATCATGCA	GTATGTGATG	GCTTTCATGC	AGCACGGTTT	600
ATTAATACAC	TTCAGCTGAT	GTGTGATAAC	ATACTGAAAT	AA	642

2) INFORMATION FOR SEQ ID NO: 2151

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid

1109

- (C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2151

ATATTTTCAGC ATTACCTTGG GTT

23

2) INFORMATION FOR SEQ ID NO: 2152

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2152

TACACAAC TC TTGTAGCCGA TTA

23

2) INFORMATION FOR SEQ ID NO: 2153

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 642 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

- (vi) ORIGINAL SOURCE:
(A) ORGANISM: *Shigella flexneri*
(C) ACCESSION NUMBER: X07848

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2153

ATGAACTATA	CAAAATTTGA	TGTAAAAAAT	TGGGTTTCGCC	GTGAGCATT	50
TGAGTTTAT	CGGCATCGTT	TACCATGTGG	TTTAGCTTA	ACAAGCAAAA	100
TTGATATCAC	GACGTTAAAA	AAGTCATTGG	ATGATTCAGC	GTATAAGTTT	150
TATCCGGTAA	TGATCTATCT	GATTGCTCAG	GCCGTGAATC	AATTTGATGA	200
GTTGAGAATG	GCGATAAAAG	ATGATGAATT	GATCGTATGG	GATTCAGTCG	250
ACCCACAATT	CACCGTATTC	CATCAAGAAA	CAGAGACATT	TTCAGCACTG	300
AGTTGCCCAT	ACTCATCCGA	TATTGATCAA	TTTATGGTGA	ATTATTTATC	350
GGTAATGGAA	CGTTATAAAA	GTGATACCAA	GTTATTTTCT	CAAGGGGTAA	400
CACCAGAAAA	TCATTTAAAT	ATTTCAGCAT	TACCTTGGGT	TAATTTTGAT	450
AGCTTTAATT	TAAATGTTGC	TAATTTTACC	GATTATTTTG	CACCCATTAT	500
AACAATGGCA	AAATATCAGC	AAGAAGGGGA	TAGACTGTTA	TTGCCGCTCT	550
CAGTACAGGT	TCATCATGCA	GTTTGTGATG	GCTTCCATGT	TGCACGCTTT	600
ATTAATCGGC	TACAAGAGTT	GTGTAACAGT	AAATTTAAAT	AA	642

2) INFORMATION FOR SEQ ID NO: 2154

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2154

CGCCATTCAG AGTTTAGGAC

20

2) INFORMATION FOR SEQ ID NO: 2155

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2155

TTCCATACCG TTGCGTATCA CTT

23

2) INFORMATION FOR SEQ ID NO: 2156

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 624 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Clostridium perfringens*
- (B) STRAIN: CP590
- (C) ACCESSION NUMBER: M74769

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2156

ATGGTATTTG	AAAAAATTGA	TAAAAATAGT	TGGAACAGAA	AAGAGTATTT	50
TGACCACTAC	TTTGCAAGTG	TACCTTGTA	ATACAGCATG	ACCGTTAAAG	100
TGGATATCAC	ACAAATAAAG	GAAAAGGGAA	TGAAACTATA	TCCTGCAATG	150
CTTTATTATA	TTGCAATGAT	TGTAAACCGC	CATTCAGAGT	TTAGGACGGC	200
AATCAATCAA	GATGGTGAAT	TGGGGATATA	TGATGAGATG	ATACCAAGCT	250

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ATACAATATT	TCACAATGAT	ACTGAAACAT	TTTCCAGCCT	TTGGACTGAG	300
TGTAAGTCTG	ACTTTAAATC	ATTTTTAGCA	GATTATGAAA	GTGATACGCA	350
ACGGTATGGA	AACAATCATA	GAATGGAAGG	AAAGCCAAAT	GCTCCGGAAA	400
ACATTTTAA	TGTATCTATG	ATACCGTGGT	CAACCTTCGA	TGGCTTTAAT	450
CTGAATTTGC	AGAAAGGATA	TGATTATTTG	ATTCCTATTT	TTACTATGGG	500
GAAATATTAT	AAAGAAGATA	ACAAAATTAT	ACTTCCTTTG	GCAATTCAAG	550
TTCATCACGC	AGTATGTGAC	GGATTTTACA	TTTGCCGTTT	TGTAAACGAA	600
TTGCAGGAAT	TGATAAATAG	TTAA			624

2) INFORMATION FOR SEQ ID NO: 2157

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2157

CCACAGAAAT TGATATTAGT GTTTTAT

27

2) INFORMATION FOR SEQ ID NO: 2158

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2158

TCGCTATTGT AACCAGTTCT A

21

2) INFORMATION FOR SEQ ID NO: 2159

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 651 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus aureus*
- (C) ACCESSION NUMBER: V01277

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2159

ATGAACTTTA	ATAAAATTGA	TTTAGACAAT	TGGAAGAGAA	AAGAGATATT	50
TAATCATTAT	TTGAACCAAC	AAACGACTTT	TAGTATAACC	ACAGAAATTG	100
ATATTAGTGT	TTTATACCGA	AACATAAAAC	AAGAAGGATA	TAAATTTTAC	150
CCTGCATTTA	TTTTCTTAGT	GACAAGGGTG	ATAAACTCAA	ATACAGCTTT	200
TAGAACTGGT	TACAATAGCG	ACGGAGAGTT	AGGTTATTGG	GATAAGTTAG	250
AGCCACTTTA	TACAATTTTT	GATGGTGTAT	CTAAAACATT	CTCTGGTATT	300
TGGACTCCTG	TAAAGAATGA	CTTCAAAGAG	TTTTATGATT	TATACCTTTC	350
TGATGTAGAG	AAATATAATG	GTTCGGGGAA	ATTGTTTCCC	AAAACACCTA	400
TACCTGAAAA	TGCTTTTTTCT	CTTTCTATTA	TTCCATGGAC	TTCATTTACT	450
GGGTTTAACT	TAAATATCAA	TAATAATAGT	AATTACCTTC	TACCCATTAT	500
TACAGCAGGA	AAATTCATTA	ATAAAGGTAA	TTCAATATAT	TTACCGCTAT	550
CTTTACAGGT	ACATCATTCT	GTTTGTGATG	GTTATCATGC	AGGATTGTTT	600
ATGAACTCTA	TTCAGGAATT	GTCAGATAGG	CCTAATGACT	GGCTTTTATA	650
A					651

2) INFORMATION FOR SEQ ID NO: 2160

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2160

TTTTGAACAC TATTTTAACC AGC

23

2) INFORMATION FOR SEQ ID NO: 2161

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2161

GATTTAACTT ATCCCAATAA CCT

23

2) INFORMATION FOR SEQ ID NO: 2162

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 648 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double

1113

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Staphylococcus aureus*

(C) ACCESSION NUMBER: X02166

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2162

ATGACTTTTA	ATATTATCAA	ATTAGAAAAT	TGGGATAGAA	AAGAATATTT	50
TGAACACTAT	TTTAACCAGC	AAACTACGTA	TAGCATTACT	AAAGAAATTG	100
ATATTACTTT	GTTTAAAGAT	ATGATAAAAA	AGAAAGGATA	TGAAATTTAT	150
CCTTCTTTGA	TTTATGCAAT	TATGGAAGTT	GTAAATAAAA	ATAAAGTGTT	200
TAGAACAGGA	ATTAATAGTG	AGAATAAATT	AGGTTATTGG	GATAAGTTAA	250
ATCCTTTGTA	TACAGTTTTT	AATAAGCAAA	CTGAAAAAAT	TACTAACATT	300
TGGACTGAAT	CTGATAACAA	CTTCACTTCT	TTTTATAATA	ATTATAAAAA	350
TGACTTGCTT	GAATATAAAG	ATAAAGAAGA	AATGTTTCCT	AAAAAACCGA	400
TACCTGAAAA	CACCATACCG	ATTTCAATGA	TTCCTTGGAT	TGATTTTAGT	450
TCATTTAATT	TAAACATTGG	TAACAATAGC	AACCTTTTAT	TGCCTATTAT	500
TACGATAGGT	AAATTTTATA	GTGAGAATAA	TAAAATTTAT	ATACCAGTTG	550
CTTTGCAGCT	TCATCATGCT	GTATGTGATG	GTTACCATGC	TTCATTATTT	600
ATGAATGAAT	TTCAAGATAT	AATTCATAAG	GTAGATGATT	GGATTTAG	648

2) INFORMATION FOR SEQ ID NO: 2163

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2163

ACCTTCATCC TACCGATGTG GGT

24

2) INFORMATION FOR SEQ ID NO: 2164

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2164

CAACGACACC AGCACTGCCA TTG

23

2) INFORMATION FOR SEQ ID NO: 2165

1114

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1215 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Salmonella typhimurium*
- (B) STRAIN: H3380
- (C) ACCESSION NUMBER: AF071555

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2165

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ATGACCACCA CACGCCCCGC GTGGGCCTAT ACGCTGCCGG CAGCACTGCT      50
GCTGATGGCT CCTTTCGACA TCCTCGCTTC ACTGGCGATG GATATTTATC      100
TCCCTGTCGT TCCAGCGATG CCCGGCATCC TGAACACGAC GCCCGCTATG      150
ATCCAACTCA CGTTGAGCCT CTATATGGTG ATGCTCGGCG TGGGCCAAGT      200
GATTTTTGGT CCGCTCTCAG ACAGAATCGG GCGACGGCCA ATTCTACTTG      250
CGGGCGCAAC GGCTTTCGTC ATTGCGTCTC TGGGAGCAGC TTGGTCTTCA      300
ACTGCACCGG CCTTTGTCGC TTTCCGTCTA CTTCAAGCAG TGGGCGCGTC      350
GGCCATGCTG GTGGCGACGT TCGCGACGGT TCGCGACGTT TATGCCAACC      400
GTCCTGAGGG TGTGTCATC TACGGCCTTT TCAGTTCGAT GCTGGCGTTC      450
GTGCCTGCGC TCGGCCCTAT CGCCGGAGCA TTGATCGGCG AGTTCTTGGG      500
ATGGCAGGCG ATATTCATTA CTTTGGCTAT ACTGGCGATG CTCGCACTCC      550
TAAATGCGGG TTTCAGGTGG CACGAAACCC GCCCTCTGGA TCAAGTCAAG      600
ACGCGCCGAT CTGTCTTGCC GATCTTCGCG AGTCCGGCTT TTTGGGTTTA      650
CACTGTCGGC TTTAGCGCCG GTATGGGCAC CTTCTTCGTC TTCTTCTCGA      700
CGGCTCCCCG TGTGCTCATA GGCCAAGCGG AATATTCCGA GATCGGATTC      750
AGCTTTGCCT TCGCCACTGT CGCGCTTGTA ATGATCGTGA CAACCCGTTT      800
CGCGAAGTCC TTTGTGCTCA GATGGGGCAT CGCAGGATGC GTGGCGCGTG      850
GGATGGCGTT GCTTGTTTGC GGAGCGGTCC TGTTGGGGAT CGGCGAACTT      900
TACGGCTCGC CGTCATTCCT CACCTTCATC CTACCGATGT GGGTTGTCGC      950
GGTCGGTATT GTCTTCACGG TGTCCGTAC CGCGAACGGC GCTTTGGCAG     1000
AGTTCGACGA CATCGCGGGA TCAGCGGTGC CGTTCTACTT CTGCATCCAA     1050
AGCCTGATAG TCAGTATCGT CGGGACATTG GCGGTGACGC TGTAAACGG      1100
CGATACAGCG TGGCCCGTGA TTTGTTACGC CACGGCAATG GCAGTGCTGG      1150
TGTCGTTGGG GCTGGCGCTC CTTGATCCC GTGATGCTGC CACCGAGAAG      1200
TCGCCAGTCG TCTAG                                     1215

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2) INFORMATION FOR SEQ ID NO: 2166

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2166

GACAAACCAT TCCTGCTG

2) INFORMATION FOR SEQ ID NO: 2167

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2167

CAGCAGCTGG GCGGCGGT

18

2) INFORMATION FOR SEQ ID NO: 2168

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2168

CATCAAAGTT GGTGAAGAAG TTG

23

2) INFORMATION FOR SEQ ID NO: 2169

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2169

CCCGTTTGCG AAAGGTGG

18

2) INFORMATION FOR SEQ ID NO: 2170

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single

1116

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2170

ACGTGACGTT GACAAACCA

19

2) INFORMATION FOR SEQ ID NO: 2171

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2171

TCGTTGGATT AACTGAAGAA

20

2) INFORMATION FOR SEQ ID NO: 2172

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2172

GTGTTGAAAT GTTCCGTAAA

20

2) INFORMATION FOR SEQ ID NO: 2173

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2173

AAGAAAAAAT CTTCGAACTG GCTA

24

2) INFORMATION FOR SEQ ID NO: 2174

1117

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 15 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2174

TCTACACGGC CGGTG

15

2) INFORMATION FOR SEQ ID NO: 2175

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 16 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2175

CCGCCATACC CCGTTT

16

2) INFORMATION FOR SEQ ID NO: 2176

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2176

CGGCATTACC ATTTCCACAC CTTT

24

2) INFORMATION FOR SEQ ID NO: 2177

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 49 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2177

GGCACGGACA AACCATTCCT GCTGCCTATC GAAGACGTGT TCCCGTGCC

49

2) INFORMATION FOR SEQ ID NO: 2178

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2178

GGCACGACAA ACCATTCCTG CTGCCTATCG AACGTGCC

38

2) INFORMATION FOR SEQ ID NO: 2179

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2179

GGCAGCTCTA CTTCCGTACC ACTGACGTAA CCGGCTGCC

39

2) INFORMATION FOR SEQ ID NO: 2180

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2180

TTCGCCGGCG TGGGC

15

2) INFORMATION FOR SEQ ID NO: 2181

(i) SEQUENCE CHARACTERISTICS:

1119

- (A) LENGTH: 15 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2181

AGCGCCACGC GCAGG

15

2) INFORMATION FOR SEQ ID NO: 2182

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 42 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2182

GCGCGCCAAC GACTTCTACC ACGAAATGGA AGAGTCGCGC GC

42

2) INFORMATION FOR SEQ ID NO: 2183

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 817 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Alcaligenes faecalis* subsp. *faecalis*
- (B) STRAIN: ATCC 8750

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2183

TATCTTGTT	WGCTCGGCCG	CTGACGGCCC	AATGCCTCAG	ACTCGCGAGC	50
ACATCCTGCT	GAGCCGTCAG	GTTGGCGTTC	CTTACATCAT	CGTGTTCTTG	100
AACAAGGCCG	ACATGGTTGA	TGACGAAGAG	CTGATCGAAC	TGGTTGAAAT	150
GGAAGTTCGC	GAGCTGTTGT	CCAAGTACGA	CTTCCCTGGC	GACGACACCC	200
CGATCATCAA	GGGTTGCGCC	AAACTGGCTC	TGGAAGGCCA	CGAAGGCCCA	250
CTGGGCAGCC	AAGCCGTTCT	GGCTCTGGCC	GAAGCGCTGG	ACAACCTACAT	300
TCCTACGCCT	GAGCGTGCCG	TTGACGGTAC	GTTCCCTGATG	CCTGTTGAAG	350
ACGTGTTCTC	GATCTCCGGC	CGTGGTACGG	TTGTGACCGG	TCGTATTGAG	400
CGCGGCATCA	TCAAGGTCGG	CGAAGAAATC	GAAATCGTGG	GTATCAAAGA	450
CACGGTCAAG	ACCATTGTGA	CCGGCGTTGA	AATGTTCCGC	AAACTGCTGG	500
ACCAGGGCGA	AGCTGGCGAT	AACGTCCGTC	TGCTGCTGCG	TGGTACCAAG	550
CGTGAAGACG	TGGAACGTGG	TCAAGTCTTG	GCCAAGCCAG	GCTCGATCAA	600
GCCACACACT	GACTTCGACG	CCGAGGTGTA	CATTCTGTCC	AAAGAAGAAG	650
GTGGTCGTCA	CACTCCTTTC	TTCAAGGGCT	ACCGTCCTCA	GTTCTACTTC	700

1120

CGTACAAC	CTG	ACCGG	CACCATC	GAG	CTGCCAGA	AAG	ACAAGGAA	AT	750
GGTTCTG	CCA	GGCGACA	ACA	TTTCGAT	GAA	AGTGTC	CCTG	ATCGCTC	800
TCGCCAT	GGA	AGAAGGT							817

2) INFORMATION FOR SEQ ID NO: 2184

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1652 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Campylobacter coli*
 (B) STRAIN: ATCC 43479

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2184

TACAATTGAA	GTTGAAAGAT	CTATGCGTGT	TCTTGATGGT	GCTGTTGCGG	50
TATTTTGTTC	AGTGGGTGGG	GTGCAGCCTC	AAAGTGAAAC	AGTTTGGAGA	100
CAAGCAAATA	AATATGGTGT	TCCAAGAATA	GTATTTGTAA	ATAAAATGGA	150
TAGAATCGGT	GCAAATTTCT	ACAATGTAGA	AGATCAAATT	CGCAACCGTT	200
TAAAAGCTAA	TCCAGTTCCA	CTTCAAATTC	CAATCGGTGC	TGAGGATAAT	250
TTTAAAGGCG	TAATCGATCT	TGTAACATG	AAAGCTTTAG	TTTGGGAAGA	300
TGATACTAAG	CCAACGGATT	ATGTAGAAAA	AGAAATCCA	GCTGAACTTA	350
AAGAAAAGGC	AGAAGAATAT	CGCACAAAAA	TGATAGAAGC	AGTTTCTGAA	400
ACTTCAGATG	AGTTGATGGA	AAAATATTTA	GGTGGAGAAG	AATTAAGCCT	450
TGAAGAGATT	AAAACAGGGA	TTAAAGCAGG	ATGTTTAAGT	CTTCTATCG	500
TTCTATGCT	TTGCGGTACA	GCGTTTAAAA	ATAAAGGGGT	TCAACCTTTG	550
CTTGATGCTG	TTGTGGCTTA	TTTACCAGCT	CCTGATGAAG	TTGCTAATAT	600
CAAAGGGGAA	TATGAAGACG	GCACAGAAGT	TTCTGTAAAA	TCAACTGATG	650
ATGGCGAATT	TGCAGGACTT	GCATTTAAAA	TTATGACAGA	TCCATTTGTA	700
GGACAACCTA	CTTTCGTGCG	TGTTTATCGT	GGATGTTTAG	AAAGCGGTTT	750
TTATGCTTAT	AACTCAACCA	AAGATAAAAA	AGAAAGAAAT	GGTCGTTTGT	800
TAAAAATGCA	CTCTAATAAA	AGAGAAGAAA	TTAAAGTTCT	TTACGCAGGA	850
GAAATCGGTG	CAGTTGTAGG	ACTTAAAGAT	ACTTTAACAG	GGGATACTCT	900
TGCAAGTGAA	AAAGATAAAG	TAATTCTTGA	AAGAATGGAT	TTCCCAGACC	950
CAGTTATTTT	TGTTGCAGTA	GAMCCAAAAA	CTAAAGCAGA	TCAAGAAAAA	1000
ATGTCTATTG	CACTAAATAA	ATTAGCTCAA	GAAGATCCAA	GCTTTAGAGT	1050
TTCTACGGAT	GAAGAAAGTG	GTCAAACCTAT	CATTTTCAGG	ATGGGTGAAT	1100
TACACCTTGA	AATTATTGTT	GATCGTATGC	TTCGTGAATT	TAAAGTGGA	1150
GCTGAAGTGG	GACAACCTCA	AGTTGCTTAT	CGTGAAACTA	TCAGAAAAAC	1200
TGTTGAGCAA	GAATACAAAT	ACGCTAAGCA	ATCAGGCGGT	CGTGGTCAGT	1250
ATGGACATGT	ATTCTTACGC	CTTGAGCCAC	TTGAGCCAGG	AAGTGGATAC	1300
GAGTTTGTTA	ACGACATCAA	AGGTGGGGTA	ATTCCAAAAG	AATATATTCC	1350
TGCAGTAGAT	AAGGGTGTTC	AAGAAGCATT	GCAAAATGGT	GTTTTAGCAG	1400
GTTATCCAGT	AGAAGATGTT	AAAGTAACTG	TTTATGATGG	AAGTTATCAC	1450
GAGGTGGATT	CATCTGAGAT	GGCATTTAAA	CTTGCTGCTT	CTATGGGATT	1500
TAAAGAGGGT	GCTAGAAAAAG	CAGGTGCTGT	GATCTTAGAG	CCTATGATGA	1550
AAGTTGAAGT	AGAACTCCT	GAAGATTACA	TGGGCGATGT	TATTGGCGAT	1600
CTTAATAAGC	GTCGTGGTCA	AGTAAATAGC	ATGGATGAAA	GAGGTGGTAA	1650
TA					1652

2) INFORMATION FOR SEQ ID NO: 2185

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 820 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Succinivibrio dextrinosolvens*
- (B) STRAIN: ATCC 19716

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2185

GCTATTCTAG	TAGTAGCAGC	AACTGATGGT	CCTATGCCAC	AGACCCGTGA	50
GCACATCCTA	TTAGCACGTC	AGGTAGGCGT	ACCATACATC	ATCGTATTCC	100
TAAACAAGTG	CGATATGGTT	GACGACGAGG	AATTATTAGA	GTTAGTTGAG	150
ATGGACGTAC	GTGATCTATT	AAATCAGTAC	CAGTTCCCAG	GCGACGACAC	200
TCCAATCATC	CGTGGTTCAG	CACTAGGTGC	ATTAAACGGC	GAAGAGAAGT	250
GGAAAGAGGC	AATCTATCAG	TTAGCAGACA	CTCTAGATTC	ATACATTCCA	300
GAGCCAAAGC	GTGATATCGA	TGATCCATTC	CTATTACCAA	TCGAAGATAT	350
CTTCTCAATC	TCAGGTCGTG	GTACTGTAGT	AACCGGCCGT	GTAGAGCGTG	400
GTATTGTACA	CGTAGGTGAC	GAAGTTGAAA	TCGTTGGTAT	TCGTCCAACC	450
ACCAAGACCA	CTGTAAGTGG	CGTTGAAATG	TTCCGTAAGT	TACTAGACGA	500
AGGTCGTGCA	GGTGATAACG	TTGGTGTTCT	ACTACGTGGT	ACCAAGCGTG	550
ATGAGGTTGA	GCGTGGTGAG	GTTCTAGCTG	CTCCAGGCAC	AATCACTCCA	600
CACACCAAGT	TCACTGGTCA	GTTTACGTA	CTAAGCAAGG	ATGAAGGTGG	650
TCGTCACT	CCATTCTTCA	AGGGCTACCG	TCCACAGTTC	TTCTTCCGTA	700
CAACCGATAT	TACCGGTTCT	ATCGATCTGA	AAGAGGGCGT	AGAGATGGTA	750
ATGCCAGGTG	ATAACACCGA	CATGACCGTA	ACCCTAATCC	ACCCAGTAGC	800
TATGGCTGAA	GCGGAGAGAT				820

2) INFORMATION FOR SEQ ID NO: 2186

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 44 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2186

ACGCGCTCAA AGCAGAAGTA TACGTATTAT CAAAAGACGC GCGT

44

2) INFORMATION FOR SEQ ID NO: 2187

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1612 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Campylobacter jejuni* subsp. *jejuni*
- (B) STRAIN: ATCC 33292

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2187

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CAGTGGGTGG GGTGCAGCCT CAAAGTGAAA CAGTTTGGAG ACAAGCAAAT      50
AAATATGGTG TTCCAAGAAT AGTATTTGTA AACAAAATGG ATAGAATCGG      100
TGCAAATTTT TACAATGTAG AAGATCAAAT TCGCAACCGT TTAAAAGCTA      150
ATCCAGTTCC ACTTCAAATT CCAATCGGTG CTGAGGATAA TTTTAAAGGC      200
GTAATCGATC TTGTAAGTAT GAAAGCTTTA GTTTGGGAAG ATGATACTAA      250
GCCAACGGAT TATGTAGAAA AAGAAATTCC AGCTGAACTT AAAGAAAAGG      300
CAGAAGAATA TCGCACAAAA ATGATAGAAG CAGTTTCTGA AACTTCAGAT      350
GAGTTGATGG AAAAATATTT AGGCGGAGAA GAATTAAGCC TTGAAGAGAT      400
TAAACAGGG ATTAAAGCAG GATGTTTAAG TCTTCTATC GTTCCTATGC      450
TTTGCGGTAC AGCGTTTAAA AATAAAGGGG TTCAACCTTT ACTTGATGCT      500
GTTGTGGCTT ATTTACCAGC TCCTGATGAA GTGGCAAATA TCAAGGGTGA      550
ATATGAAGAT GGCACAGAAG TTTCTGTAAA ATCAACTGAT GATGGCGAGT      600
TTGCAGGACT TGCATTTAAA ATTATGACAG ATCCATTTGT AGGACAACCT      650
ACTTTCGTGC GTGTTTATCG CGGTTGTTTA GAAAGTGTTT CTTATGCTTA      700
TAACTCAACT AAAGATAAAA AAGAAAGAAT TGGTCGTTTG TTAAAAATGC      750
ACTCTAACCA AAGAGAAGAG ATTAAAGTGC TTTACGCAGG CGAAATTGGT      800
GCTGTTGTAG GACTTAAAGA TACTTTAACA GGGGATACTC TTGTAAGTGA      850
AAAAGATAAG GTAATCCTTG AAAGAATGGA TTTTCCAGAT CCAGTTATTT      900
CTGTTGCAGT TGAGCCAAAA ACTAAAGCAG ATCAAGAAAA AATGTCTATT      950
GCTTTAAATA AATTAGCACA AGAAGATCCA AGTTTtagag TTTCTACAGA     1000
TGAAGAAAGT GGCCAAACTA TCATTTcagg TATGGGTGAG TTACACCTTG     1050
AAATTATCGT TGATAGAATG CTTCGTGAAT TTAAAGTTGA AGCTGAAGTA     1100
GGTCAACCAC AAGTTGCTTA TCGCGAAACT ATTAGAAAAA CTGTTGAACA     1150
AGAATACAAA TACGCTAAAC AATCAGGTGG TCGTGgTCAG TATGGACATG     1200
TATTCTTACG CCTTGAACCA CTTGAGCCAG GTAGTGGATA TGAATTTGTT     1250
AATGATATCA AAGGTGGAGT AATTCCAAAA GAATACATTC CTGCAGTTGA     1300
TAAAGGTGTT CAAGAAGCAT TACAAAATGG TGTTTTAGCA GGTATCCTG     1350
TGGAAGATGT TAAAGTAACT GTTTATGATG GAAGTTATCA CGAGGTGGAT     1400
TCATCTGAGA TGGCGTTTAA ACTTGCTGCT TCTATGGGCT TTAAAGAAGG     1450
TGCTAGAAAA GCAGGTGCTG TGATCTTAGA GCCTATGATG AAAGTTGAAG     1500
TAGAACTCC TGAAGATTAC ATGGGTGATG TTATTGGAGA TCTTAACAAA     1550
CGCCGTGGTC AAGTAAATAG CATGGATGAG CGTGGTGGAA ATAAATCAT     1600
CACAGCATTT TG                                     1612

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2) INFORMATION FOR SEQ ID NO: 2188

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1667 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Campylobacter jejuni* subsp. *jejuni*
 (B) STRAIN: ATCC 33560

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2188

ACAATTGAAG	TTGAAAGATC	TATGCGTGTT	CTTGATGGTG	CTGTTGCGGT	50
ATTTTGTTC	GTGGGTGGG	TGCAGCCTCA	AAGTGAAACA	GTTTGGAGAC	100
AAGCAAATA	ATATGGTGTT	CCAAGAATAG	TATTTGTAAA	TAAAATGGAT	150
AGAATCGGT	CAAATTTCTA	CAATGTAGAA	GATCAAATTC	GCAACCGTTT	200
AAAAGCTAA	CCAGTTCCAC	TTCAAATTC	AATTGGTGCT	GAGGATAATT	250
TTAAAGGCG	AATCGATCTT	GTAACATGA	AAGCTTTAGT	TTGGGAAGAT	300
GATACTAAG	CAACGGATTA	TGTAGAAAAA	GAAATTCAG	CTGAACCTTA	350
AGAAAAGGC	GAAGAATATC	GCACAAAAAT	GATAGAAGCA	GTTTCTGAAA	400
CTTCAGATG	GTTGATGGAA	AAATATTTAG	GCGGAGAAGA	ATTAAGCCTT	450
GAAGAGATTA	AAACAGGGAT	TAAAGCAGGA	TGTTTAAGTC	TTTCTATCGT	500
TCCTATGCTT	TGCGGTACAG	CGTTTAAAAA	TAAAGGGGTT	CAACCTTTGC	550
TTGATGCTGT	TGTGGCTTAT	TTACCAGCTC	CTGATGAAGT	GGCAAATATC	600
AAGGGTGAAT	ATGAAGATGG	CACAGAAGTT	TCTGTAAAAT	CAACTGATGA	650
TGGCGAGTTT	GCAGGACTTG	CATTTAAAAAT	CATGACAGAT	CCATTTGTAG	700
GACAACTTAC	TTTCGTGCGT	GTTTATCGCG	GTTGTTTAGA	AAGCGGTTCT	750
TATGCGTATA	ACTCAACTAA	AGATAAAAAA	GAAAGAATTG	GTCGTTTGTT	800
AAAAATGCAC	TCTAACAAAA	GAGAAGAGAT	TAAAGTGCTT	TACGCAGGCG	850
AAATTGGTG	TGTTGTAGGA	CTTAAAGATA	CTTTAACAGG	GGATACTCTT	900
GCAAGTGA	AAGATAAGGT	AATCCTTGAA	AGAATGGATT	TTCCAGATCC	950
AGTTATTTCT	GTTGCAGTTG	AGCCAAAAAC	TAAAGCTGAT	CAAGAAAAAA	1000
TGTCTATTGC	TTTAAATAAA	TTAGCACAA	AAGATCCAAG	TTTTAGAGTT	1050
TCTACAGATG	AAGAAAGTGG	TCAAATATC	ATTTCAGGTA	TGGGTGAGTT	1100
ACACCTTGAA	ATTATCGTTG	ATAGAATGCT	TCGTGAATTT	AAAGTTGAAG	1150
CTGAAGTAGG	TCAACCACAA	GTTGCTTATC	GCGAAACTAT	TAGAAAAACT	1200
GTTGAACAAG	AATACAAATA	CGCTAAACAA	TCAGGTGGTC	GTGGTCAGTA	1250
TGGACATGTA	TTCTTACGCC	TTGAACCACT	TGAGCCAGGT	AGTGGATATG	1300
AATTTGTAA	TGATATCAAA	GGTGGGGTAA	TTCCAAAAGA	ATACATTCTT	1350
GCAGTTGATA	AAGGTGTTCA	AGAAGCATT	CAAAATGGTG	TTTTAGCAGG	1400
TTATCCTGTG	GAAGATGTTA	AAGTAACTGT	TTATGATGGA	AGTTATCACG	1450
AGGTGGATT	ATCTGAGATG	GCGTTTAAAC	TTGCTGCTTC	TATGGGCTTT	1500
AAAGAAGGTG	CTAGAAAAGC	AGGCGCTGTG	ATCTTAGAGC	CTATGATGAA	1550
AGTTGAAGTA	GAAACTCCTG	AAGATTATAT	GGGTGATGTT	ATTGGAGATC	1600
TTAACAAACG	CCGTGGTCAA	GTAATAGCA	TGGATGAGCG	TGGTGGAAT	1650
AAAATCATCA	CAGCATT				1667

2) INFORMATION FOR SEQ ID NO: 2189

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1255 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Leishmania guyanensis*

(B) STRAIN: ATCC 50126

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2189

TGACGGCGCT	GGACGTGACG	GAGGACCTCG	GCCGCGATGA	GCCGCTGACG	50
CTGGAGATCG	TGCAGCACTT	GGATGCGAAC	ACCGGCCGCT	GCATTGCGAT	100
GCAGACGACG	GACCTGCTGA	AGCTGAAGTC	GAAGGTTGTG	TCGACCGGCG	150
GCAACATCTC	CGTGCCGGTG	GGCCGCGAGA	CACTGGGCCG	CATCTTCAAC	200
GTGCTGGGCG	ACGCGATTGA	CCACCGCGGC	CCCGTGTGCG	AGAAGATGCG	250
CATGGCGATC	CACGCCGAGG	CGCCGAAGCT	GGCGGACCAG	GCTGCGGAGG	300
ACACGATCCT	GACGACCGGC	ATCAAGGTGA	TCGACCTGAT	TCTGCCCTAC	350
TGCAAGGGCG	GCAAGATCGG	CCTGTTCTGGC	GGTGCCGGTG	TGGGCAAGAC	400
TGTGATCATC	ATGGAGCTGA	TCAACAACGT	CGCGAAGGGG	CACGGCGGCT	450
TCTCCGTGTT	CGCCGGCGTT	GGCGAGCGCA	CGCGCGAGGG	CACGGACCTG	500
TACCTGGAGA	TGATGCAGTC	AAAGGTGATT	GACCTGAAGG	GCGAGTCGAA	550
GTGCGTGCTT	GTGTACGGGC	AGATGAACGA	GCCCCCGGGT	GCGCGCGCGC	600
GCGTTGCGCA	GTCTGCGCTG	ACGATGGCCG	AGTACTTCCG	CGACGTGGAG	650
GGCCAGAACG	TGCTGCTGTT	CATCGACAAC	ATCTTCCGCT	TCACGCAGGC	700
GAACTCCGAG	GTGTCTGCGC	TGCTGGGCCG	CATCCCGGCC	GCCGTGGGTT	750
ACCAGCCGAC	GCTTGCGGAG	GATCTTGCGA	TGCTGCAGGA	GCGCATTACG	800
TCGACGACGA	AGGGATCGAT	TACGTCTGTG	CAGGCTGTGT	ACGTGCCTGC	850
GGATGATATC	ACGGACCCCG	CGCCCGCGAC	GACGTTCTCG	CACCTGGACG	900
CGACGACTGT	GCTGGACCGC	GCGGTGGCGG	AGTCGGGCAT	CTACCCTGCC	950
GTGAACCCGC	TGGAGTGCGC	GTCGCGCATC	ATGGACCCCG	ATGTGATCGA	1000
CGTGGACCAT	TACAACGTTG	CACAGGATAT	CGTCCAGATG	CTGACCAAGT	1050
ACAAGGAGCT	GCAGGACATC	ATTGCGGTGC	TTGGCATCGA	CGAGCTGAGC	1100
GAGGAGGACA	AGGTCGTGGT	GGACCGCGCG	CGCAAGGTGA	CGCGGTTCCCT	1150
GTCGCAGCCG	TTCCAGGTTG	CGGAGGTGTT	CACCGGCATG	ACGGGCCACT	1200
ACGTGCAGCT	GAGCGACACG	GTGGAGTCGT	TCTCTGGCCT	GCTGATGGGG	1250
TCGTA					1255

2) INFORMATION FOR SEQ ID NO: 2190

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1248 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Trypanosoma brucei* subsp. *brucei*
- (B) STRAIN: EATRO 795

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2190

GCCCTTGACG	TTGTTGACAA	ACTTGGCCGT	GATGAGCCTC	TTACTCTTGA	50
GATCGTGACG	CATCTTGACG	CCCACACGGG	CCGCTGTATC	GCGATGCAAA	100
CGACGGATCT	CCTCAAACCTG	AAGGCAAAGG	TCGTTTCGAC	AGGTGGCAAC	150
ATTTCCGTTC	CTGTCGGCCG	GGAAACACTA	GGTCGTATCT	TCAACGTGCT	200
TGGAGACGCT	ATTGACCAGC	GCGGCCCCGT	TGGTGAGAAA	CTGCGCATGC	250
CCATCCATGC	CGTGGCTCCC	AAGCTTGCGG	ACCAGGCCGC	TGAGGATGCG	300
GTGCTCACAA	CTGGTATTAA	GGTGATTGAT	CTCATTCTCC	CTTACTGCAA	350

AGGTGGA AAA	ATTGGCCTCT	TTGGGGGTGC	GGGTGTGGGC	AAAACCGTCA	400
TTATTATGGA	GCTCATTAAC	AACGTTGCCA	AGGGTCACGG	TGGTTTCTCT	450
GTCTTCGCTG	GTGTTGGTGA	GCGTACCCGT	GAGGGAACGG	ATTTGTATCT	500
TGAGATGATG	CAGTCTAAGG	TTATTGACCT	TAAGGGTGAG	TCCAAATGTG	550
TGTTGGTGTA	CGGTCAGATG	AACGAGCCCC	CAGGTGCCCCG	TGCGCGTGTT	600
GCGCAGTCGG	CTCTGACGAT	GGCTGAGTAC	TTCCGTGATG	TGGAGGGCCA	650
AGATGTGCTT	CTTTTTATCG	ACAATATTTT	TCGTTTCACT	CAGGCTAACT	700
CCGAGGTGTC	GGCGCTTCTG	GGTCGTATTC	CCGCCGCTGT	TGGCTACCAG	750
CCTACCCTCG	CTGAGGATCT	AGGGCAGTTG	CAGGAGCGTA	TTACCTCAAC	800
AACGAAAGGC	TCCATTACTT	CTGTGCAGGC	CGTATACGTG	CCGGCCGATG	850
ACATTACCGA	TCCAGCTCCA	GCAACAACCT	TCTCACATCT	GGACGCCACA	900
ACTGTGTTGG	ACCGTGCTGT	TGCCGAGTCT	GGTATCTACC	CCGCTGTAA	950
CCCACTGGAA	TGCGCCTCGC	GTATCATGGA	CCCCGACGTT	ATCAGTGTGG	1000
ATCACTACAA	TGTTGCACAA	GATGTGGTAC	AGATGCTCAC	CAAGTACAGG	1050
GAATTACAGG	ATATCATTGC	TGTCCTTGGT	ATCGACGAGC	TAAGCGAGGA	1100
GGACAAACTT	ATCGTGGACC	GTGCGCGTAA	GTTGGTGAAG	TTCCTCTCCC	1150
AGCCATTCCA	AGTTGCTGAG	GTCTTCACAG	GAATGACTGG	CCATTACGTG	1200
CAGTTGGATG	ACACCATCGA	TTCCTTTTCT	GGTCTCCTCA	TGGGTACG	1248

2) INFORMATION FOR SEQ ID NO: 2191

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 440 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Aspergillus nidulans*
- (B) STRAIN: WSA-176

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2191

GAGCTGATTG	TAAGTCATCG	ACCACTTGAT	ATATGAATAC	ATCTAACAGT	50
AGTAGAACAA	CATCGCCAAG	GCTCACGGTG	GTTACTCCGT	CTTCACTGGT	100
GTCGGTGAGC	GTACTCGTGA	GGGTAACGAT	CTGTACCACG	AAATGCAGGA	150
GACTGGTGTC	ATTGAGCTCG	ACGGCGAATC	CAAGGTGTCT	CTTGTGTTCTG	200
GTCAGATGAA	CGAGCCCCCA	GGTGCTCGTG	CCCGTGTCGC	CCTTACTGGT	250
CTGACCATCG	CCGAATACTT	CCGTGACGAG	GAGGGTCAGG	ACGTGCTGCT	300
CTTCATTGAC	AACATTTTCC	GTTTCACCCA	GGCCGGTTCC	GAGGTGTCTG	350
CCCTTCTTGG	TCGTATCCCC	TCTGCCGTCG	GTTACCAGCC	CACTCTGGCC	400
GTCGACATGG	GTGGTATGCA	GGAACGTATT	ACCACCACCA		440

2) INFORMATION FOR SEQ ID NO: 2192

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1262 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Leishmania panamensis*

(B) STRAIN: ATCC 50158

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2192

GCTGACGGCG	CTGGACGTGA	CGGAGGACCT	CGGCCGCGAT	GAGCCGCTGA	50
CGCTGGAGAT	CGTGCAGCAC	TTGGATGCGA	ACACCGGCCG	CTGCATTGCG	100
ATGCAGACGA	CGGACCTGCT	GAAGCTGAAG	TCTGAAGGTTG	TGTCGACCGG	150
CGGCAACATC	TCCGTGCCCG	TGGGCCGCGA	GACGCTGGGC	CGCATCTTCA	200
ACGTGCTGGG	CGACGCGATT	GACCACCGCG	GCCCCGTGTG	CGAGAAGATG	250
CGCATGGCGA	TCCACGCCGA	GGCGCCGAAG	CTGGCGGACC	AGGCTGCGGA	300
GGACACGATC	CTGACGACCG	GCATCAAGGT	GATCGACCTG	ATTCTGCCCT	350
ACTGCAAGGG	CGGCAAGATC	GGCCTGTTCG	GCGGTGCCCG	TGTGGGCAAG	400
ACTGTGATCA	TCATGGAGCT	GATCAACAAC	GTCGCGAAGG	GGCACGGCGG	450
CTTCTCCGTG	TTCGCCGGCG	TTGGCGAGCG	CACGCGCGAG	GGCACGGACC	500
TGTACCTGGA	GATGATGCAG	TCAAAGGTGA	TTGACCTGAA	GGGCGAGTCG	550
AAGTGCCTGC	TTGTGTACGG	GCAGATGAAC	GAGCCCCCGG	GTGCGCGCGC	600
GCGCGTTGCG	CAGTCTGCGC	TGACGATGGC	CGAGTACTTC	CGCGACGTGG	650
AGGGCCAGAA	CGTGCTGCTG	TTCATCGACA	ACATCTTCCG	CTTCACGCAG	700
GCGAACTCCG	AGGTGTCTGC	GCTGCTGGGC	CGCATCCCCG	CCGCCGTGGG	750
TTACCAGCCG	ACGCTTGCGG	AGGATCTTGG	CATGCTGCAG	GAGCGCATTG	800
CGTCGACGAC	GAAGGGATCG	ATTACGTCTG	TGCAGGCTGT	GTACGTGCCT	850
GCGGATGATA	TCACGGACCC	CGCGCCCGCG	ACGACGTTCT	CGCACCTGGA	900
CGCGACGACT	GTGCTGGACC	GCGCGGTGGC	GGAGTCGGGC	ATCTACCCTG	950
CCGTGAACCC	GCTGGAGTGC	GCGTCGCGCA	TCATGGACCC	CGATGTGATC	1000
GACGTGGACC	ATTACAACGT	TGCACAGGAT	ATCGTCCAGA	TGCTGACCAA	1050
GTACAAGGAG	CTGCAGGACA	TCATTGCGGT	GCTTGGCATC	GACGAGCTGA	1100
GCGAGGAGGA	CAAGGTCGTG	GTGGACCGCG	CGCGCAAGGT	GACGCGGTTC	1150
CTGTCGCAGC	CGTTCCAGGT	TGCGGAGGTG	TTCACCGGCA	TGACGGGCCA	1200
CTACGTGCAG	CTGAGCGACA	CGGTGGAGTC	GTTCTCTGGC	CTGCTGATGG	1250
GGTCGTACGA	CC				1262

2) INFORMATION FOR SEQ ID NO: 2193

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 912 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Aspergillus nidulans*

(B) STRAIN: WSA-176

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2193

TTCCGATGGT	CAAATGTACG	ATTGATATTC	CTTCCAGCCA	GTCAGGATAA	50
CAGCTGATAC	CAGTTGCAAA	TAGGCCCCAG	ACTCGTGAGC	ACTTGTTGCT	100
TGCCCCGTCAG	GTTGGTGTCC	AGAAGATCGT	TGTCTTCGTC	AACAAGGTTG	150
ACGCTGTCTGA	TGACCCTGAG	ATGTTGGAGC	TTGTTGAGCT	CGAGATGCGT	200

GAGCTCCTCA	ACACTTACGG	TTTCGAGGGA	GAGGAGACCC	CTATCATCTT	250
CGGTTCCGCC	CTGTGCGCTC	TCGAAGGCCG	CCGCGAGGAC	ATTGGTACTC	300
AGCGTATTGA	CTCCCTCCTC	GAGGCCGTTG	ACACTTGGAT	CCCTACCCCC	350
CAGCGTGACT	TGGACAAGCC	CTTCCTGATG	TCCATTGAGG	AAGTTTTCTC	400
CATTGGTGGT	CGTGGTACCG	TCGCCTCTGG	TCGTGTCGAG	CGTGGTCTCC	450
TCAAGAAGGA	TACCGAAGTT	GAAATTCACG	GTGCTGATGG	TATTCTGAAG	500
ACCAAGGTCA	CCGACATTGA	GACCTTCAAG	AAGAGCTGCG	ATGAGTCTCG	550
TGCTGGTGAC	AACTCCGGTC	TTCTCCTCCG	TGGTATCCGT	CGTGAGGATG	600
TTCGTCTGGG	TATGGTCATC	GCTGCCCTCG	GCTCCATCAA	GGCCTCCAAG	650
AAGTTCATGG	TCTCCATGTA	CGTCTTGACT	GAGGCTGAAG	GTGGCCGCAA	700
GAACGGCTTC	GGTGCCAACT	ACCGCCCCCA	GGCTTTCATC	CGCACTGCTG	750
GTAAGTTTCG	AACTATTTGA	TTCATTGATC	ACGTCCCTAA	CTGTTACTTT	800
AGACGAGGCT	TGCGACCTTC	ATTTCCCTGA	TGAGGCCGAC	AAGGACCGCC	850
ACGTCATGCC	CGGTGACAAC	GTCGAAATGG	TCCTCAACCT	CAACAACCCC	900
GTTGCTGCTG	AG				912

2) INFORMATION FOR SEQ ID NO: 2194

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 887 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Aureobasidium pullulans*
- (B) STRAIN: WSA-234

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2194

TCATCGTCGT	CGCCGCTTCT	GACGGTCAGA	TGCCCCAGAC	CAGAGAGCAC	50
TTGCTTCTCG	CCCGTCAGGT	CGGTATCCAG	AAGATTGTCT	TCTTCGTCAA	100
CAAGGTCGAC	GCCATCGAGG	ACAAGGAGAT	GCTTGAGCTC	GTCGAGATGG	150
AGATGCGTGA	GCTCCTCAGC	AGCTACGGCT	TCGAGGGTGA	CGAGACCCCC	200
ATCGTCATGG	GTTCCGCTCT	TTGTGCCCTT	GAGAACCGCC	AGCCCGAGAT	250
TGGAACCACC	CAGATCGACA	ACCTGATGAA	CGCTGTCGAC	GAGTGGATCC	300
CCACTCCCCA	GAGAGATCTT	GAGAAGCCCT	TCCTCATGTC	CGTTGAGGAT	350
GTCTTCTCTA	TCCCCGGTCT	TGGTACTGTC	GTTTCTGGCC	GTGTTGAGCG	400
TGGTACCCTG	AAGAAGGATT	CCGAAATCGA	GCTTGTCGGC	AAGAACAAGG	450
TCCCCATCAA	GACCAAGGTC	ACCGACATCG	AGACCTTCAA	GAAGTCTTGC	500
GACGAGTCCC	GCGCTGGTGA	CAACTCCGGT	CTTCTGCTCC	GTGGTATCAA	550
GCGTGAGGAT	GTCAACCGTG	GTATGGTTGT	CGTCAAGCCC	GGTACCGTCA	600
CCTCGCACAA	GAAGTTCCTC	GTCTCCATGT	ACGTCTTGAC	CAAGGAGGAG	650
GGTGGTCGTC	AACTGGTTT	CCACGGAAAC	TACCGTCCCC	AGATCTTCAT	700
CCGTACCGCT	GGTAAGTCCT	GACTTTGAAC	TGCTGACCAA	TTTTCGCATC	750
TCTAACATGT	TTTACAGACG	AGGCTGCCGC	TATTGACTGG	CCCGAAGGCA	800
CCGAGGACGC	TGACTCCAAG	ATGGTCATGC	CCGGTGACAA	CGTCGAGATG	850
GTCTGCTCTC	TTACAGACC	TCTTGCCGTT	GAACAGG		887

2) INFORMATION FOR SEQ ID NO: 2195

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 984 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Emmonsia parva*
- (B) STRAIN: ATCC 10784

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2195

TGACGGCCAA	ATGTAGGACT	CTTGCGCGGG	ACTGACTGAT	TGGGGGGAAT	50
CCATTTTTC	TTTTTCTTT	TTCTTTTGA	GTACATGATT	ATACTAATAT	100
TTGGATAACG	TACCAGGCCT	CAAACACGTG	AACATTACT	CCTTGCCCGA	150
CAAGTCGGTG	TCCAGAAGAT	CGTCGTTTTC	GTAAACAAGG	TCGATGTTCT	200
CGAAGATAAG	GAGATGTTGG	AGCTTGTCGA	GTTGGAAATG	AGAGAGCTCT	250
TGAACACCTA	CGGATTCGAG	GGTGAGGAAA	CGCCCATCAT	CTTCGGTTCT	300
GCCCTTTGTG	CCATGGAGGG	CCGCGAGCCT	GAGCTGGGCG	AGAAGAGAAT	350
TGATGAATTG	CTCGACGCTG	TTGATAGCTG	GATCCCTACG	CCGCAACGTG	400
ATACGGAAAA	ACCCTTCCTA	ATGTCCATTG	AGGAAGTGTT	CTCCATCTCC	450
GGTCGTGGAA	CCGTTGCCTC	CGGCCGTGTT	GAGCGTGGTG	TCCTCAAGAA	500
GGATTCCGAA	GTCGAGCTTG	TTGGCGGCGG	CGTCGCCCCA	ATCAGGACCA	550
AGGTAACCGA	TATCGAAACC	TTCAAGAAGT	CCTGCGACGA	GTCCAGGGCT	600
GGAGACAAC	CTGGCCTTTT	GTTGCGTGGT	GTCAAGCGTG	AGGATATCCG	650
CCGTGGTATG	GTCGTTGTCG	TTCTTGGCAG	CGTCAAGGCC	CACGACAAGT	700
TCTTGGTGTC	CATGTATGTT	CTGACCGAAG	CCGAGGGTGG	TCGCCGAAC	750
GGATTCCGCC	AAACTATCG	TCCTCAAATG	TTTATCCGCA	CAGCTGGTAC	800
GTAACGTATA	ATGCCTCTCC	TCTTCATATA	TACCACCCCC	CCCACCACTG	850
ACTCCCTGAC	TCTTCGATTA	CAGACGAGGC	CGCCGATCTC	AGCTTCCCTG	900
ACGCAGCAGA	CGAAACCAAA	CTGGTTATGC	CCGGTGACAA	CGTCGAGATG	950
ATCCTCAAGA	CACACCGCCC	CATAGCTGCC	GAAG		984

2) INFORMATION FOR SEQ ID NO: 2196

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 806 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Exserohilum rostratum*
- (B) STRAIN: WSA-215

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2196

GCCGCCTCTG	ACGGCCAAAT	GCCCCAGACC	CGTGAGCACT	TGCTGCTTGC	50
TCGCCAGGTC	GGTGTTTACA	AGATTGTTGT	TTTTGTCAAC	AAGGTCGATG	100
CCGTCGAGGA	CAAGGAGATG	TTGGAGCTCG	TTGAGATGGA	GATGCGTGAG	150
TTGCTCAGCA	GCTATGGCTT	CGAGGGCGAT	GAGACTCCCA	TTGTCATGGG	200

CTCCGCTCTC	TGCGCCATCG	AGGGCCGTGA	GCCCGAAATT	GGTGTCAACC	250
GTATTGATGA	GCTGCTCGAG	GCTGTCGACA	CCTGGATCCC	CACCCCTCAG	300
CGTGATAACG	ACAAGCCCTT	CCTCATGGCT	GTTGAGGACG	TCTTCTCCAT	350
TGCTGGCCGT	GGTACCGTCG	TTTCTGGCCG	TGTCGAGCGA	GGTGTCTTGA	400
AGCGCGATGC	CGAAGTCGAG	CTGGTTGGCA	AGGGCACTGC	GCCCATCAAG	450
ACCAAGGTTA	CCGACATTGA	AACCTTCAAG	AAGTCGTGTG	AAGAGTCTCG	500
CGCCGGTGAC	AACTCGGGTC	TCCTCCTCCG	TGGTGTCAAG	CGTGACGACG	550
TCCGCCGTGG	CATGGTCGTT	TCTGTTCTTG	GACAAGTCAA	GGCCACAAAG	600
AAGTTCCTCG	TCTCCATGTA	TGTGTTGAGC	AAAGAGGAAG	GTGGCCGCCA	650
CACGGGCTTC	GGCGAGAACT	ACAGGCCACA	AATGTTTCATC	CGTACTGCTG	700
ACGAGTCATG	CGCGCTGCAC	TGGCCAGAAG	GTACCCCAAG	TGCTCACGAC	750
AAGCTTGTTA	TGCCTGGTGA	TAACGTTGAG	ATGGTTTGTG	AGCTTCACGT	800
GCCACA					806

2) INFORMATION FOR SEQ ID NO: 2197

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 799 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Fusarium moniliforme*
- (B) STRAIN: WSA-213

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2197

ACCCGTGAAC	ACTTGCTCCT	CGCTCGTCAG	GTTGGTGTTT	AGCGAATTGT	50
CGTCTTTGTC	AACAAGGTCG	ATGCCATTGA	TGACCCCGAG	ATGCTTGAGC	100
TCGTGAGAT	GGAGATGCGC	GAGCTTCTTA	ACACCTATGG	CTTCGAAGGC	150
GACGACACTC	CCGTCATCAT	GGGCTCGGCT	CTCATGTCTC	TCCAGAACCA	200
GCGCCCTGAG	ATTGGCACCG	AGAAGATTGA	TGAGCTTCTT	GCTGCCGTCG	250
ACGAGTGGAT	CCCAACCCCC	GAGCGTGACC	TTGACAAGCC	CTTCCTTATG	300
TCCGTCGAGG	ATGTCTTCTC	CATTGCTGGC	CGTGGTACCG	TCGTGTCTGG	350
CCGTGTGGAG	CGTGGTGTTT	TGAAGCGTGA	CCAGGAGATC	GAGCTTGTTG	400
GAAAGGGTCA	GGAGGTTATC	AAGACCAAGG	TTACCGACAT	CGAGACCTTC	450
AAGAAGTCTT	GTGAGCAGTC	CCAGGCTGGT	GACAACTCTG	GTCTCCTCAT	500
CCGAGGTGTT	CGCCGTGAGG	ATGTCCGCCG	TGGTATGGTC	GTCTGCGCTC	550
CTGGCACCGT	GAAGTCTCAC	ACCCAGTTCC	TCGCTTCCCT	CTATGTCCTC	600
TCCAAGGAGG	AGGGTGGCCG	ACACACCGGT	TTCCAGGAGC	ACTACCGACC	650
CCAGCTCTAC	CTCCGAACCG	CAGATGAGTC	CATTGACCTG	ACTTTCCTTG	700
AGGGTACTGA	GGATGCCTCC	AGCAAGATGG	TCATGCCTGG	CGACAACACC	750
GAGATGGTTG	TCACCATGGG	TCACCCCAAT	GCCATCGAGG	TTGGTCAGC	799

2) INFORMATION FOR SEQ ID NO: 2198

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 819 bases
- (B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Fusarium solani*

(B) STRAIN: ATCC 32793

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2198

CTCTGACGGT	CAGATGCCCC	AGACCCGTGA	GCACTTGCTG	CTTGCCCCGTC	50
AGGTCGGTGT	CCAGAAGATT	GTCGTCTTCG	TCAACAAGGT	CGATGCCATT	100
GACGACCCCTG	AGATGCTTGA	GCTCGTCGAG	ATGGAGATGC	GTGAGCTCCT	150
CAACACCTAC	GGCTTCGAGG	GTGACGAGAC	CCCTGTCATC	ATGGGCTCTG	200
CTCTCATGTC	CCTCCAGAAC	CAGCGCCCCG	AGATCGGTAG	CCAGAAGATT	250
GACGAGCTCC	TTGCCGCCGT	TGACGAGTGG	ATCCCTACCC	CCGAGCGTGA	300
CCTTGACAAG	CCCTTCCTCA	TGTCCGTTGA	GGATGTCTTC	TCCATTGCCG	350
GCCGTGGTAC	CGTCGTCTCT	GGCCGTGTCG	AGCGTGGTGT	CCTGAAGCGC	400
GACCAGGAGA	TTGAGCTCGT	CGGCAAGGGT	AACGAGGTCA	TCAAGACCAA	450
GGTCACCGAC	ATTGAGACCT	TCAAGAAGTC	TTGCGAGCAG	TCCCAGGCTG	500
GTGACAACTC	TGGTCTCCTC	ATCCGAGGTG	TCCGCCGTGA	GGATGTCCGC	550
CGTGGTATGG	TCGTCTGCGC	CCCCGGCACT	GTCAAGTCCC	ACACTCAGTT	600
CCTTTCTTCC	CTCTACGTCC	TCACCAAGGA	GGAGGGTGGC	CGACACACTG	650
GCTTCCAGGA	GCACTACCGA	CCCCAGCTCT	ACCTCCGAAC	TGCTGATGAG	700
TCCATCGACC	TGACCTTCCC	CGAGGGTACC	GAGGACGCCA	GCAGCAAGAT	750
GGTCATGCCC	GGTGACAACA	CCGAGATGGT	CATCACCATG	GGCCACCCCA	800
ACGCCATTGA	GGTCGGTCA				819

2) INFORMATION FOR SEQ ID NO: 2199

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1025 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Histoplasma capsulatum*

(B) STRAIN: WSA-377

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2199

TGCTGACGGC	CAAATGTAAG	ACGCCGCGAG	GGAGTGCTGA	AGGTTTTATG	50
CTTTTTAGGC	CCTTTGTTTC	TGAGAGCATG	ATGATACTAA	TACTCGGAAA	100
CGTATCTATT	AGGCCTCAAA	CACGTGAGCA	TTTGCTCCTT	GCCCCACAGG	150
TCGGTGTCCA	AAAGATCGTC	GTTTTTCGTGA	ACAAAGTCGA	CGCCCTTGAG	200
GACAAGGAGA	TGTTGGAGCT	TGTCGAGTTA	GAAATGAGAG	AGCTCTTAAA	250
CACCTACGGA	TTTGAGGGTG	AAGAGACACC	CATCATCTTT	GGTTCTGCCC	300
TTTGCGCCAT	GGAAGGCCGT	GAGCCTGAGT	TGGGAGAAAA	GAAAATTGAT	350
GAATTGCTGG	AGGCTGTTGA	TACTTGATC	CCAACACCAC	AACGTGATAC	400
CGAAAAACCT	TTCTTGATGT	CCGTTGAGGA	AGTATTCTCT	ATCTCCGGTC	450
GTGGAACCGT	TGCCTCCGGT	CGTGTTGAGC	GCGGTGTCCT	CAAGAAGGAT	500

TCAGAAAGTCG	AGCTAATTGG	GGGCGGCTCC	ACCCCCATCA	GGACGAAGGT	550
AACTGATATC	GAAACTTTCA	AGAAATCCTG	TGACGAGTCT	AGAGCTGGGG	600
ACAACTCCGG	TCTTTTATTG	CGTGGTATCA	AGCGTGAAGA	TATCCGCCGT	650
GGTATGGTAG	TTGCCGTTCC	TGGCAGCGTC	AAGGCCACG	ACAAGTTCTT	700
GGTGTGATG	TATGTCCTGA	CCGAAGCTGA	GGGTGGTCGC	CGAACCGGAT	750
TCGGCCAGAA	CTATCGTCCT	CAAAATGTTCA	TCCGCACAGC	TGGTATGTCA	800
AAATGGGGCC	CCTTTTCATA	ATCCTTTCTT	TTTTTCCTTT	TCCTCTCTCT	850
ATCTCTCTCT	CTGTTTCTTT	TCAACTCGCC	TGATTCACGA	AATTAATAA	900
CCCCTTTGAT	TATAGACGAA	GCCGCCCATC	TCAGCTTCCC	TAGTGGAGCA	950
GATGAAAGCA	AACTCGTTAT	GCCTGGTGAC	AACGTCGAGA	TGATCCTCCA	1000
GACACACCGC	CCCGTGGCTG	CTGAG			1025

2) INFORMATION FOR SEQ ID NO: 2200

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 667 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Kocuria kristinae*
- (B) STRAIN: ATCC 27570

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2200

AGCACGTGCT	GCTCGCCCGC	CAGGTCGGCG	TGCCGACCCT	GCTGGTCGCC	50
CTGAACAAGG	CCGACATGGT	CGAGGACGAG	GAGCTGCTGG	ACCTCGTCGA	100
GATGGAGGTC	CGCGAGCTGC	TGTCCTCCCA	GGAGTTCGAC	GGCGACAACG	150
CCCCCGTCAT	CCGCGTCTCC	GCGCTGAAGG	CGCTGGAGGG	CGACGAGAAG	200
TGGGTCAAGT	CCATCGAGGA	GCTCATGGAG	GCCGTGGACG	AGTACATCCC	250
GGACCCCGTG	CGCGACAAGG	ACAAGCCGTT	CCTGATGCCC	ATCGAGGACG	300
TCTTCACCAT	CACCGGGCGC	GGCACCGTGG	TGACCGGTCG	CGCCGAGCGC	350
GGGACCCTGG	CCCTGAACTC	CGAGGTCGAG	ATCGTCGGCA	TCCGCCCGAT	400
CCAGAAGACC	ACGGTCACCG	GGATCGAGAT	GTTCCACAAG	CAGCTCGACG	450
AGGCCTGGGC	CGGCGAGAAC	TGCGGTCTGC	TGCTGCGCGG	CCTGAAGCGC	500
GACGACGTCG	AGCGCGGCCA	GGTCGTGGTG	AAGCCGGGTT	CCATCACCCC	550
GCACACCAAC	TTCGAGGCGA	ACGTCTACAT	CCTGTCCAAG	GACGAGGGTG	600
GGCGTCACAA	CCCGTTCTAC	TCGAATAACC	GTCCGCAGTT	CTACTTCCGG	650
ACCACCGACG	TCACCGG				667

2) INFORMATION FOR SEQ ID NO: 2201

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 778 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Vibrio mimicus*
 (B) STRAIN: ATCC 33653

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2201

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TGCTGCAACA GATGGTCCAA TGCCACAAAC TCGTGAGCAC ATCCTGCTGG      50
GTCGCCAAGT AGGTATTCCT TACATCATCG TATTCATGAA CAAATGTGAC      100
ATGGTTGACG ATGAAGAGCT TCTAGAGCTG GTTGAGATGG AAGTTCGTGA      150
GCTTCTGTCT GAGTACGATT TCCCAGGTGA TGACCTGCCA GTAATCCAAG      200
GTTCAGCACT AGGCGCGCTA AACGGCGAAG CACAGTGGGA AGCGAAGATT      250
GTTGAACTAG CAGAAGCACT AGATTTCATAC ATTCCAGAGC CAGAGCGTGC      300
AGTAGACATG GCATTTCCTGA TGCCAATCGA AGACGTATTC TCAATCCAAG      350
GTCGTGGTAC AGTAGTAACT GGCCGTATCG AGCGCGGCAT CCTGAAAGTG      400
GGTGACGAAG TTGCGATCGT TGGTATCAAA GACACAGTAA AAACCTACCTG      450
TACAGGTGTA GAAATGTTCC GTAAGCTGCT TGACGAAGGT CGTGCAGGTG      500
AGAACGTTGG TGCACTGCTA CGTGGTACTA AGCGTGAAGA AGTAGAGCGT      550
GGTCAAGTAC TGGCGAAGCC AGGTTCAATC ACCCCACACA CTAAGTTCGA      600
ATCAGAAGTA TACGTACTGT CAAAAGACGA AGGTGGCCGT CATACTCCAT      650
TCTTCAAAGG TTACCGTCCA CAGTTCTACT TCCGTACAAC TGACGTAACA      700
GGCAGCATCG AGCTTCCAGA AGGCGTAGAA ATGGTAATGC CAGGCGACAA      750
CATCAAGATG GTTGTAGACC TGATTGCA      778

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2) INFORMATION FOR SEQ ID NO: 2202

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 412 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Citrobacter freundii*
 (B) STRAIN: ATCC 8090

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2202

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AACGCTGACC CTGCAGGTTA TTGCCGCTGC GCAGCGTGAA GGTAACACCT      50
GTGCATTTAT CGATGCAGAA CACGCACTGG ACCCGGTCTA TGCCCGTAAG      100
CTTGGCGTTG ATATCGATAA CCTGCTGTGT TCTCAGCCGG ATACCGGTGA      150
ACAAGCGCTG GAAATCTGTG ATGCACTGGC GCGCTCCGGT GCGGTTGACG      200
TTATCGTTGT CGACTCCGTT GCCGCATTGA CGCCGAAGGC AGAAATCGAA      250
GGCGAGATTG GCGACTCTCA CATGGGCCTT GCGGCGCGTA TGATGAGCCA      300
GGCGATGCGT AAGCTGGCCG GTAACCTGAA GCAGTCCAAC ACGCTGCTGA      350
TTTTCATCAA CCAGATCCGT ATGAAGATTG GCGTTATGTT CGGTAACCCG      400
GAAACCACCA CC      412

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2) INFORMATION FOR SEQ ID NO: 2203

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 337 bases

- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Clostridium botulinum*
- (B) STRAIN: 20:1.2

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2203

TTTAGATCCA	TCTTATGCTA	GAAATTTAGG	TGTTGATATA	GATAACCTAA	50
TAGTTTCTCA	ACCAGATACA	GGAGAACAGG	CTTTAGAGAT	AACAGAAGCT	100
TTAGTAAGAT	CAGGAGCAGT	AGATGTTATA	GTTGTAGACT	CTGTAGCAGC	150
TTTAGTTCCT	AGGGCAGAAA	TAGAAGGAGA	AATGGGAGAC	TCACATGTAG	200
GTCTTCAAGC	AAGACTTATG	TCTCAAGCCC	TAAGAAAATT	AGCAGGATCT	250
ATAAATAAAT	CTAAGTGTGT	AGCTATATTT	ATAAACCAAT	TAAGAGAAAA	300
GGTTGGTATA	ATGTTTGAA	ATCCAGAAAC	AACTCCT		337

2) INFORMATION FOR SEQ ID NO: 2204

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 379 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Francisella tularensis*
- (B) STRAIN: ATCC 29684

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2204

AAAGCAAGGC	GGTACTGCAG	CATTTGTTGA	TGCTGAGCAT	GCACTAGATC	50
CAAAATATGC	AAAGCTTTTA	GGTGTTGATG	TTGATAATCT	GATCGTGTCA	100
CAGCCGGATA	CGGGTGAGCA	AGCTTTAGAG	ATTGCTGATA	TGTTGGTACG	150
TTCTGGAGGA	GTTGATATTG	TAGTAATTGA	CTCTGTTGCT	GCACTTACGC	200
CAAAGGCAGA	GATTGAGGGT	GACATGGGCG	ACTCGCACAT	GGGCTTACAA	250
GCAAGATTAA	TGTCACAAGC	ACTAAGAAAA	CTAACGGCAA	ATATCAAGCG	300
CTCAAATACT	CTAGTGATAT	TCATTAACCA	AATTCGTATG	AAGATCGGGG	350
TTATGTTTGG	TAACCCTGAA	ACTACAAC			379

2) INFORMATION FOR SEQ ID NO: 2205

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 337 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Peptostreptococcus anaerobius*

(B) STRAIN: ATCC 27337

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2205

ACTTGACCCA GTATATGCAA GGGCTCTTGG AGTGGATATA GACAACCTAG-	50
TCATATCTCA GCCAGATACA GGAGAACAGG CCCTAGATAT AGCAGAGTCC-	100
CTTATAAGAT CAGGAGCTGT AGATATACTA GTAATAGACT CAGTAGCTGC-	150
CCTAGTACCT AAGGCAGAAA TAGAAGGTGA CATGGGAGAT TCTCACGTAG-	200
GTCTACAGGC TAGACTTATG TCACAGGCAC TTAGAAAATT GACTGGATCT-	250
ATAAAGAAGT CAAACTGTGT TGTTATATTT ATCAACCAGT TGAGAGAAAA-	300
AGTAGGGGTT ATGTTTCGGTA ATCCAGAGAC AACAAACA	337

2) INFORMATION FOR SEQ ID NO: 2206

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 337 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Peptostreptococcus asaccharolyticus*

(B) STRAIN: LSPQ 2639

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2206

TCTTGATGCT GGATATGCAA AAAACCTTGG AGTAGATGTA GAAAATTTAA-	50
TTATTTCTCA ACCTGATACA GGTGAGCAAG CCTTAGAAAT AACTGAAGCT-	100
CTTGTAAGAT CTAACGCTGT TGATTTAATT ATTATAGACT CAGTTGCCGC-	150
ACTTGTAACA AAAGCAGAAA TCGATGGTGA CATGGGAGCT GCACAAATAG-	200
GTCTTCAAGC AAGACTTATG TCTCAAGCTC TTAGAAAATT AACTGGGGCA-	250
ATCAACAAGT CAAAATGTAC CGTTGTATTT ATTAACCAAC TTAGAGAAAA-	300
AGTTGGTATC ATGTTTGGTA ACCCAGAAAC TACAACA	337

2) INFORMATION FOR SEQ ID NO: 2207

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 408 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Providencia stuartii*

1135

(B) STRAIN: ATCC 33672

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2207

CTCACGTTGC	AAGTTATTGC	AGCAGCACAA	CGTAGCGGAA	AAACCTGTGC	50
ATTTATCGAC	GCTGAACATG	CGCTAGATCC	AATCTATGCG	AAAAAACTGG	100
GTGTTGATAT	CGATAACCTT	CTATGTTCTC	AACCTGATAC	TGGTGAGCAA	150
GCATTAGAGA	TTTGTGATGC	ACTGACGCGT	TCAGGCGCTG	TTGATGTCAT	200
TATCGTTGAC	TCCGTGGCCG	CATTAACACC	AAAAGCTGAA	ATTGAAGGTG	250
AAATCGGTGA	CTCACACATG	GGCTTAGCGG	CTCGTATGAT	GAGCCAAGCG	300
ATGCGTAAAT	TAGCGGGTAA	CTTAAAGAAC	TCGAATACAC	TTTTAATCTT	350
CATTAACCAA	ATCCGTATGA	AGATTGGCGT	TATGTTTGGT	AACCCAGAAA	400
CCACTACA					408

2) INFORMATION FOR SEQ ID NO: 2208

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 403 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Salmonella choleraesuis* subsp. *choleraesuis*
serotype Paratyphi A
- (B) STRAIN: ATCC 9150

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2208

GCTGCAGGTG	ATTGCCGCTG	CGCAGCGTGA	AGGTAAAACC	TGTGCGTTTA	50
TCGATGCGGA	ACACGCGCTT	GACCCTGTTT	ACGCACGCAA	GCTGGGCGTC	100
GATATCGATA	ACCTGCTTTG	TTCTCAGCCG	GATACCGGCG	AGCAGGCGCT	150
GGAAATCTGT	GACGCGCTGG	CGCGTTCAGG	CGCGGTGGAC	GTCATTGTGG	200
TCGACTCCGT	AGCGGCGCTA	ACGCCGAAAG	CGGAAATCGA	AGGCGAAATT	250
GGCGACTCTC	ACATGGGCCT	CGCGGCGCGT	ATGATGAGCC	AGGCGATGCG	300
TAAGCTGGCG	GGGAACCTAA	AACAGTCCAA	CACGCTGTTG	ATTTTCATCA	350
ACCAGATCCG	TATGAAGATT	GGCGTGATGT	TCGGTAACCC	GGAAACCACC	400
ACC					403

2) INFORMATION FOR SEQ ID NO: 2209

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 412 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Salmonella choleraesuis* subsp. *choleraesuis*
 serotype Typhimurium
 (B) STRAIN: ATCC 14028

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2209

GACCCTGACG	CTGCAGGTGA	TTGCCGCTGC	GCAGCGTGAA	GGTAAACCT	50
GTGCGTTTAT	CGATGCGGAA	CACGCGCTTG	ACCCTGTTTA	CGCACGCAAG	100
CTGGGCGTCG	ATATCGATAA	CCTGCTCTGC	TCTCAGCCGG	ATACCGGCGA	150
GCAGGCGCTG	GAAATCTGTG	ACGCGCTGGC	GCGTTCAGGC	GCGGTGGACG	200
TCATTGTGGT	CGACTCCGTA	GCGGCGCTAA	CGCCGAAAGC	GGAAATCGAA	250
GGCGAAATCG	GCGACTCTCA	CATGGGCCTC	GCGGCGCGTA	TGATGAGCCA	300
GGCGATGCGT	AAGCTGGCGG	GGAACCTGAA	ACAGTCCAAC	ACGCTGTTGA	350
TTTTTCATCA	CCAGATCCGT	ATGAAGATTG	GCGTGATGTT	CGGTAACCCG	400
GAAACCACCA	CC				412

2) INFORMATION FOR SEQ ID NO: 2210

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 337 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Staphylococcus saprophyticus*
 (B) STRAIN: ATCC 15305

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2210

ATTAGATCCT	GTTTACGCAG	AAGCTTTAGG	CGTAGATATA	CAAAATTTAT-	50
ATTTATCTCA	ACCTGATCAT	GGGGAACAAG	GTTTAGAAAT	TGCCGAAGCA-	100
TTTGTTAGAA	GTGGCGCTGT	TGATATCGTT	GTGGTCGATT	CAGTTGCTGC-	150
GCTTACACCT	AAAGCTGAAA	TTGAAGGTGA	AATGGGAGAT	ACGCACGTTG-	200
GTTTGCAAGC	ACGTCTTATG	TCCCAAGCCT	TGAGAAAGCT	TTCCGGTGCA-	250
ATTTCAAAAT	CAAATACAAC	AGCAGTATTT	ATCAACCAAA	TCCGTGAAAA-	300
AGTTGGTGTG	ATGTTCCGTA	ATCCTGAAGT	TACACCA		337

2) INFORMATION FOR SEQ ID NO: 2211

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 412 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Yersinia pseudotuberculosis*
 (B) STRAIN: ATCC 29833

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2211

GACACTGACA	TTACAGGTTA	TCGCCGCCGC	ACAGCGTGAA	GGCAAAACGT	50
GTGCATTTAT	CGATGCCGAA	CATGCCCTTG	ACCCAATCTA	TGCCAAGAAA	100
TTGGGTGTAG	ATATTGATAA	CCTACTGTGT	TCTCAGCCAG	ATACTGGCGA	150
GCAGGCACTG	GAAATTGTG	ATGCGCTGAC	TCGCTCTGGT	GCGGTTGACG	200
TTATCATCGT	TGACTCCGTA	GCGGCATTGA	CACCAAAAGC	TGAAATTGAA	250
GGTGAAATTG	GCGATTCTCA	TATGGGCCTT	GCCGCGCGTA	TGATGAGCCA	300
GGCTATGCGT	AAGCTGGCGG	GTAACCTGAA	GAATGCGAAT	ACCTTACTGA	350
TTTTTATCAA	CCAAATCCGC	ATGAAAATTG	GCGTGATGTT	TGGTAACCCA	400
GAAACCACTA	CC				412

2) INFORMATION FOR SEQ ID NO: 2212

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 404 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Zoogloea ramigera*
- (B) STRAIN: ATCC 25935

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2212

CACGCTCACC	TTGCAAACCA	TCGCGGAAAT	GCAAAAACCTG	GGCGGCACCT	50
GCGCGTTTAT	CGACGCCGAG	CACGCACTGG	ACGTCACGTA	CGCGCAAAAG	100
CTGGGCGTCA	ACCTGAGCGA	TCTGCTGATC	TCGCAACCGG	ACACCGGCGA	150
ACAAGCGCTG	GAAATCTGCG	ACGCCCTGGT	GCGTTCCGGT	TCGGTGGACA	200
TGGTCGTGAT	CGACTCGGTC	GCCGCGCTGA	CCCCGCGCGC	CGAGATCGAA	250
GGCGACATGG	GCGATTGCT	GCCAGGTTTG	CAGGCACGTT	TGATGTGCGA	300
AGCACTGCGC	AAGCTTACCG	GTTTCGATCAA	CCGCACCAAC	ACCCTGGTCA	350
TCTTCATCAA	CCAGATCCGC	ATGAAAATCG	GCGTCATGTT	CGGCAGCCCG	400
GAAA					404

2) INFORMATION FOR SEQ ID NO: 2213

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 42 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2213

CGTGCCATTG	ACATGATTTC	CGAAGAAGAC	GCTGAAGGCA	CG	42
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2) INFORMATION FOR SEQ ID NO: 2214

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 125 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Abiotrophia adiacens*
- (B) STRAIN: ATCC 49175

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2214

CAACTACATT ACGTTCTGCA ACACAAGGTC GTGGTACTTT CAGTATGACA	50
TTTGACCACT ATGAAGATGT TCCTAAGAGC ATTGCAGAAG AAATCATCAA	100
GAAAAATGGC GGTAACGGAG AATAA	125

2) INFORMATION FOR SEQ ID NO: 2215

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 140 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Acinetobacter baumannii*
- (B) STRAIN: ATCC 19606

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2215

CGACTCAAAT GCGTTCTATG TCTCAAGGTC GTGCGACATA CTCAATGGAA	50
TTTGCTAAAT ATGCTGAAAC TCCACGTAAC GTGGCTGAAG GCATCATCGC	100
TAAATTCCAA GCTGGCGGTA AAAAAGGTGA CGACGAGTAA	140

2) INFORMATION FOR SEQ ID NO: 2216

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 119 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Actinomyces meyeri*
(B) STRAIN: ATCC 35568

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2216

CCGGTGACCT GCGTTCTAAG ACGCAGGGTC GCGCTGTCTA CTCCATGGAG	50
TTCGACAGCT ACGCCGAGGT TCCGCGCGCG GTCGCGGATG AGATCGTCGG	100
CAAGTCTCGG GGCAACTGA	119

2) INFORMATION FOR SEQ ID NO: 2217

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Clostridium difficile*
(B) STRAIN: ATCC 9689

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2217

CGACCGACGT TCGCTCCATG TCCCAGGGTC GCGCAAGCTA CTCTATGGAA	50
TTCAAAAAAT ACAACACAGC TCCGGCGCAC ATCGCTGAAA CTGTATCCAA	100
AAAACAAGGC TGA	113

2) INFORMATION FOR SEQ ID NO: 2218

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 119 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Corynebacterium diphtheriae*
(B) STRAIN: ATCC 27010

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2218

GCGACCTGCG TTCCCGTACC CAGGGCCGTG CAAACTACAC CATGATCTTC	50
GACTCCTACG CTGAGGTTCC TACCAACGTG GCAGCTGAGA TCGTGGCAGA	100
GCGCAACGGC ACTGCCTAA	119

2) INFORMATION FOR SEQ ID NO: 2219

1140

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 115 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterobacter cloacae*
- (B) STRAIN: ATCC 13047

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2219

AACTCAGCTG	CGTTCTCTGA	CCAAAGGTCG	TGCATCATAC	ACCATGGAAT	50
TCCTGAAGTA	TGATGATGCG	CCTAACACG	TTGCTCAGGC	CGTTATTGAA	100
GCCCGTGGTA	AGTAA				115

2) INFORMATION FOR SEQ ID NO: 2220

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 115 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Klebsiella pneumoniae pneumoniae*
- (B) STRAIN: ATCC 13883

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2220

AACTCAGCTG	CGTTCTCTGA	CCAAAGGTCG	TGCATCATAC	ACCATGGAAT	50
TCCTGAAGTA	TGATGATGCG	CCGAACAACG	TTGCTCAGGC	CGTTATTGAA	100
GCCCGTGGTA	AATAA				115

2) INFORMATION FOR SEQ ID NO: 2221

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Listeria monocytogenes*
- (B) STRAIN: ATCC 15313

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2221

CAACTCACCT TCGTTCAGGT ACGCAAGGTC GTGGTGTATA CACTATGCAA	50
TTTGACCACT ATGAAGAAGT TCCTAAATCT ATTGCTGAAG AAATCATTA	100
AGCTAATGGT GGA	113

2) INFORMATION FOR SEQ ID NO: 2222

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 118 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Mycobacterium avium*
- (B) STRAIN: ATCC 25291

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2222

CGGCGACCTG CGGTCCAAGA CCGAAGGCCG GGCGAACTAC TCCATGGTCT	50
TCGACTCCTA CGCCGAAGTG CCGGCCAACG TGTCGAAGGA GATCATCGCG	100
AAGGCGACGG GTCAGTGA	118

2) INFORMATION FOR SEQ ID NO: 2223

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 119 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Mycobacterium gordonae*
- (B) STRAIN: Mgor-1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2223

CCGGCGACCT GCGGTCCAAG ACGCAAGGCC GGGCGAACTA CTCCATGGTG	50
TTCGACTCGT ACGCCGAAGT TCCGGCGAAC GTGTGAAGG AGATCATCGC	100
GAAGGCGACG GGCGAATAG	119

2) INFORMATION FOR SEQ ID NO: 2224

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 118 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Mycobacterium kansasii*
(B) STRAIN: Mkan-1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2224

CGGCGACCTG	CGGTCCAAGA	CTCAAGGCCG	GGCGAACTAC	TCGATGGTGT	50
TCGATTCTTA	CGCCGAAGTG	CCGGCTCAGG	TGTCGAAGGA	GATCATCGCG	100
AAGGCGACTG	GCGAGTGA				118

2) INFORMATION FOR SEQ ID NO: 2225

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 118 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Mycobacterium terrae*
(B) STRAIN: Mter-1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2225

CGGAGACTTG	CGGTCGAAGA	CCCAGGGCCG	GGCGAACTAC	TCCATGGTGT	50
TCGACTCTTA	CGCCGAAGTG	CCGGCGCAGG	TGGCGAAGGA	GATTATCGCG	100
AAGGCAACGG	GCGAGTAA				118

2) INFORMATION FOR SEQ ID NO: 2226

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 115 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Neisseria polysaccharea*
(B) STRAIN: ATCC 43768

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2226

GACCGACCTG	CGTTCTGCAA	CCCAAGGCCG	CGCTACTTAC	TCTATGGAGT	50
TCAAGAAATA	TTCTGAAGCT	CCTGCCCCACA	TAGCTGCTGC	TGTAAGTAA	100
GCCCGTAAAG	GCTAA				115

2) INFORMATION FOR SEQ ID NO: 2227

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 118 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus epidermidis*
- (B) STRAIN: ATCC 14990

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2227

AACTTCATTA CGTTCTAACA CGCAAGGTCG CGGTACTTAC ACAATGTACT	50
TTGACCACTA TGCAGAAGTT CCTAAATCAA TTGCTGAAGA AATCATCAAG	100
AAAAATAAAG GTGAATAA	118

2) INFORMATION FOR SEQ ID NO: 2228

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 118 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus haemolyticus*
- (B) STRAIN: ATCC 29970

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2228

AACTTCATTA CGTTCTAACA CTCAAGGTCG CGGTACTTAC ACTATGTACT	50
TCGATCACTA TGCAGAAGTT CCAAATCAA TTGCTGATGA TATCATCAAA	100
AAAAATAAAG GTGAATAA	118

2) INFORMATION FOR SEQ ID NO: 2229

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1630 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Succinivibrio dextrinosolvens*
 (B) STRAIN: ATCC 19716

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2229

CGTTCAATGC	GTGTTCTAGA	CGGTGCAGTT	ATGGTTTACT	GTGCTGTGGG	50
TGGTGTTTCA	GCTCAGTCTG	AAACCGTTTG	GAGACAGGCT	CAGAAGTACA	100
AGGTTCTCTG	TATTGCTTTC	GTTAATAAGA	TGGACCGTAC	TGGTGCTAAT	150
TTCCTACGTG	TTGTAGAGCA	GATTAAGACC	CGTCTAAAGG	GTAACCTGT	200
TCCTCTAATG	TTACCTATCG	GTAAAGAGGA	CAGCTTTGTT	GGTGTAGTTG	250
ACCTAATCAA	GCGTAAGGCT	ATCGACTGGG	ATGAGGCATC	TCAGGGTATG	300
AAGTTTGAGT	ACGTTGACAT	TCCAGCAGAT	ATGGTTGAGG	AAGTTGAAGA	350
GTGGCGTGCA	AAGCTTGTAG	AAGCAGCTGC	AGAAGCTAAC	GACGAGCTGA	400
TGGATAAATT	CTTCGGTGGT	GAAGAGCTGA	CCGAGGAAGA	GATCAAGGCT	450
GCTCTACGTG	AGCGTACTCT	TCGCAACGAA	ATTATTCCTA	TGTGCTGCGG	500
TTCAGCATTT	AAGAACAAGG	GTGTTCAGGC	AATGCTTGAC	GCTGTTGTTG	550
AGTATCTTCC	ATCTCCAGCA	GATGTTCTTG	CTGTTGAGGG	TAAGACCCTA	600
ACCGGTGAAG	CTGATACTCG	TAAGGCTGAC	GATAAAGAGC	CATTCTCTGC	650
TTTAGCATTT	AAGCTAGCAA	ATGACCCATT	CGTAGGTAAC	TTAACATTCT	700
TACGTTGCTA	CTCAGGCTTT	ATTAAGTCTG	GTGACACTGT	AATGAACTCA	750
GATAAGCAGA	AGCGTGAGCG	TTTCGGCCGT	CTAGTTCAGA	TGCACGCTAA	800
TGCTCGTAAT	GAGGTTAGCG	AGGTTTATGC	AGGTGACATC	GTTGCTGCTA	850
TTGGTCTGAA	GGAAACCGTT	ACCGGTGATA	CCTTATGTGA	CCCAGAGCAT	900
CCAATCATTC	TTGAGTCAAT	CGACTTTGCA	GAGCCAGTTA	TCTCTGTAGC	950
AGTTGAGCCT	AAGACCAAGG	ACGATCAGGA	GAAGATGGCT	CTTGCTTTAC	1000
AGCGTTTAGC	AAAAGAAGAT	CCTTCATTCC	GCGTTCGTAC	AGACGAAGAG	1050
TCTGGCCAGA	CCATTATTTT	TGGTATGGGT	GAGCTTCACC	TAGACATCAT	1100
TGTTGACCGT	CTACGCCGTG	AGTTCAAGGT	TGAGTGTAAT	CAGGGTAAGC	1150
CACAGGTGTC	ATACCGTGAG	ACCATTAAGA	GCAAGGTTGA	ACAGCAAGGT	1200
AAGTTTGCTC	GTCAGTCTGG	TGGTCGTGGT	CAGTACGGTG	ACTGCTGGTT	1250
ACGTATGGAA	CCTCTTGAGC	CAGGTAAGGG	CTACGAATTC	GTGAATGAGA	1300
TTGTTGGTGG	TGTAATTCCT	AAGGAATATA	TCCCTGCAAT	TGATAAGGGC	1350
TGTCAGGAGC	AGATCGCTAA	CGGTGTTCTA	GCTGGTTTCC	CAGTTGTTGA	1400
CATCAAGATC	ACTGTATTCG	ATGGTCTTCA	CCACGAAGTT	GACTCTTCAG	1450
AAATGGCATT	CAAGATTGCT	GCTTCTATGG	CATTCAAAGA	GGGCTTCAAG	1500
AAGGCAAATC	CTGTTCTTCT	AGAGCCTTTA	ATGAAGGTAG	AAGTTGATAC	1550
TCCTGAAGAC	TACATGGGTG	ACGTTATTGG	TGACTTAAAC	CGTCGTCGTG	1600
CTATCGTTGA	AGGCATGGAA	GATGGTCCTA			1630

2) INFORMATION FOR SEQ ID NO: 2230

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1662 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Tetragenococcus halophilus*
 (B) STRAIN: ATCC 33315

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2230

TTGAAGTGCA	ACGTTTCATTG	CGTGTGCTAG	ACGGTTCAGT	TACTGTCTTG	50
GACTCACAAT	CAGGTGTTGA	ACCACAAACT	GAAACAGTTT	GGCGTCAAGC	100
AACAGAATAT	CAAGTACCTC	GTATTGTATT	CTGTAATAAA	ATGGATAAGG	150
TTGGCGCAGA	TTTCTTATAT	TCTGTCCGAT	CATTGCATGA	TCGTTTAGAA	200
GCTAATGCAC	AACCTATCCA	ATTGCCAATT	GGTGCTGAAG	ATAACTTTGA	250
AGGTATCATC	GACCTTGTGA	AGATGAAAGC	TGAATTTTAT	AAAGATGATT	300
TAGGGACTAC	TTTCTGAAGAA	ACTGAAATCC	CAGATGAATA	TAAAGAAACA	350
GCTCAAGAAT	GGCATAATAA	TTTGGTAGAA	TCTGTAGCTG	ATTTTGATGA	400
AGATATCATG	ATGAAATACT	TGGAAGGTGA	AGAAATTACA	CCTGAAGAGT	450
TACAAGCAGG	TATTCGTAAA	GCAACATTAT	CTGTTGAATT	TTACCCAGTA	500
TTATGTGGTT	CTGCATTTAA	AAACAAAGGT	GTTCAAATGA	TGTTGGATGC	550
AGTAATTGAT	TACTTGCCCTT	CTCCAACCGA	CGTTCCCCCA	ATTAAAGGGA	600
TCGATCCGAA	AACAGATGAA	GAAACTGAAC	ATCCTGCTGA	TGATAGTGAG	650
CCTTTTTTCAT	CACCTTGCTTT	TAAAGTTATG	TCAGACCCTT	ATGTTGGCCG	700
CTTAACCTTC	TTCCGTGTTT	ATTGAGGTGT	GTTGGATACA	GGTTCCTTATG	750
TATTGAATGC	TACTAAGGGT	TCACGTGAAC	GAATTGGTCG	TATTTTGCAA	800
ATGCATGCCA	ATTCTCGTTC	TGAGATCGAT	AAGGTTTATT	CAGGTGACAT	850
TGCAGCTGCT	GTAGGCTTGA	AGAACACTAC	AACAGGGGAT	ACCCTTTGTG	900
ATGAGAAAAA	TCCAGTTATT	TTGGAAACTA	TCAACTTCCC	TGAACCAGTA	950
ATTCAAGTTG	CTGTTGAACC	TAAGTCAAAA	GCTGACCAAG	ATAAAATGAG	1000
CGTAGCACTA	CAAAAACCTG	CAGAAGAAGA	CCCATCTTTT	AAAGTGGAAA	1050
CCAACGCTGA	AACTGGCGAA	ACTGTAATTG	CTGGTATGGG	TGAACCTCAA	1100
TTAGACGTTT	TTATTGACCG	TATGAAGACT	GAATTTAAAG	TGGATGCCAA	1150
TATTGGTGCA	CCACAAGTTT	CTTATCGTGA	AACTTTCCGT	TCATCAACTA	1200
AAGCTGAAGG	GAAATTTATC	CGCCAATCTG	GTGGTAGAGG	TCAATACGGT	1250
CACGTATGGG	TTGAATTTAC	TCCAAACGAA	GAAGGAGCAG	GATTCGAATT	1300
TAAAAACTCC	ATTGTTGGTG	GGGTTGTCCC	TCGTGACTAT	ATACCTGCAG	1350
TACAAAAAGG	ACTGGAAGAC	GCCATGGAAA	ATGGTGTGTT	AGCTGGTTAT	1400
CCATTAGTTG	ACGTAAAGGC	AGAAGTGTTC	GATGGTTCTT	ACCATGACGT	1450
CGACTCTAAT	GAAACAGCCT	TCCGTATTGC	GGCTTCAATG	TCTCTACGTG	1500
AAGCTGCGAA	AAAGGCAGAT	CCAGTTATTC	TTGAACCGAT	GATGAAAGTA	1550
ACAATTAGTA	TCCCTGAAGA	ATATCTAGGT	GATATTATGG	GACATGTTAC	1600
AGCTCGTCGT	GGTCGTGTTG	AAGGAATGGA	TGCTCACGGT	AATGCACAAA	1650
CTGTAAATGC	GT				1662

2) INFORMATION FOR SEQ ID NO: 2231

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1652 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Veillonella parvula*
- (B) STRAIN: ATCC 10790

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2231

AAGTAGAACG	TTCTCTACGT	GTAAGTGACG	GTTCTGTTGC	GGTGTTTCAGT	50
GCTAAAGGTG	GCGTTGAACC	TCAATCCGAA	ACAGTATGGC	GTCAGGCTTC	100
TAAGTACGGC	GTACCTCGTA	TCGCTTATGT	AAATAAGATG	GATACTGTAG	150

GTGCTGACTT	CTTCAACGTA	GTTGACATGA	TGAAAGCTCG	TTTGGGTGCA	200
AATTCCGTAG	CTATCCAAGT	ACCAATCGGT	GCTGAAGATA	CTTTCGAAGG	250
CATCATTGAC	TTGATGACTA	TGAAAGCGGA	AATTTATAAA	TCCGATGACG	300
GTAAAGAATA	TGAAATCACT	GATATCCCTG	CTGAATATCA	AGAAGTAGCA	350
GAAGCTCGTC	GCGAAATGAT	GATCGATGCT	ATCGCTGAAA	CAGATGATGA	400
TATCATGATG	AAATATTTGG	AAGGCGAAGA	AATTTCTGTG	GAAGAATTGA	450
AAGCGGCATT	GCGTAAAGCT	GTTATTGCTA	ACCAATTATT	CCCAGTTCTT	500
TGTGGTTCTT	CCTATAAAAA	TAAAGGTGTT	CAAATGTTAT	TGGATGCTGT	550
TATCGATTAC	ATGCCAGCTC	CAATCGACAT	CCCACCTATT	AAAGGTGTTG	600
TTCTCTGGTAC	TGAAGAAGAA	ACAACCTCGTC	CTTCTTCCGA	TGAAGAGCCA	650
TTCTCTGTCAT	TGGCATTCAA	AATCATGGCT	GACCCTTATG	TTGGTAAATT	700
AGCGTTCTTC	CGTGTGTA	CCGGTACATT	GGAATCTGGC	TCCTACGTTT	750
TCAACTCCAC	TAAAGGTAAA	AAAGAACGTA	TCGGTCGTAT	TCTTCAAATG	800
CACGCTAACT	CCCGTAAAGA	AATCGAACGC	GTATATTCTG	GTGACATCGC	850
TGCGGCGGTT	GGCTTAAAGG	ATACTACTAC	AGGCGACACA	TTGTGTGATG	900
AAAAATCTCC	TGTAATCCTT	GAGTCCATGG	AATTCCCTGA	ACCAGTTATC	950
TCCGTTGCTG	TTGAACCTAA	AACAAAAGCT	GACCAAGAAA	AAATGGGTAC	1000
AGCTCTTGCT	CGTTTGGCAG	AAGAAGATCC	TACTTTCAAA	GTTTCGTA	1050
ATGAAGAAAC	AGGTCAAAC	ATTATCTCTG	GTATGGGCGA	ACTTCACTTG	1100
GATATCATCG	TTGACCGTAT	GAACCGTGAA	TTCAAAGTAG	ATTGTAACGT	1150
AGGTAAACCT	CAAGTAGCAT	ACCGCGAAAC	TATCCGTAAA	GCTGTTAAGG	1200
CTGAAGGTAA	ATTCGTACGT	CAATCTGGTG	GTCGTGGTCA	ATATGGTCAC	1250
TGCTGGTTGG	AATTGATTCC	TCAAGAACCA	GGTGCTGGCT	TCGAGTTTGA	1300
AAACAAGGTT	GTAGGTGGTG	CGATTCCCTCG	TGAATACATC	GGACCTGTTG	1350
AAAGCGGTGT	TAAAGAAGCT	ATGGAATCCG	GTGTTATCGC	TGGGTACCCT	1400
ATGGTTGATG	TTAAAGTTAT	CGTATTTGAT	GGTTCTTACC	ATGACGTTGA	1450
CTCCAACGAA	ATGGCCTTCA	AAATTGCTGG	TTCTATGGGC	TTCAAAGAAG	1500
GTGCTCGCAA	AGCAGACCCT	GCATTGCTTG	AACCATATAT	GGCTGTAGAA	1550
GTAGACGTTT	CTGAAGAATA	CATGGGCGAC	GTTATCGGTG	ACTTGAAC	1600
TCGTCGTGGT	CGCATGGACG	GCATGGAAGC	TCGTAATGGT	TCCCAACATA	1650
TC					1652

2) INFORMATION FOR SEQ ID NO: 2232

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1624 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Yersinia pseudotuberculosis*
- (B) STRAIN: ATCC 29833

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2232

AGTAGAGCGT	TCCATGCGTG	TTCTTGACGG	CGCGGTAATG	GTTTACTGTG	50
CAGTTGGTGG	TGTTCAGCCA	CAGTCTGAAA	CCGTATGGCG	TCAGGCTAAT	100
AAATATAAAG	TTCCACGTAT	TGCGTTCGTT	AACAAAATGG	ACCGTATGGG	150
TGCGAACTTC	CTGCGCGTAG	TTGGTCAACT	GAAATCTCGC	CTTGGTGCGA	200
ACCCAGTTCC	ACTGCAGTTG	GCAATTGGCG	CAGAAGAAAA	ATTACCCGGT	250
ATTATCGATC	TGGTGAAAAT	GAAAGCGATC	AACTGGAACG	AAGCTGATCA	300
GGGCGTGACC	TTCGAATATG	AAGAAATCCC	TGCTGATATG	GCTGAACTGG	350

CTGCTGAATG	GCACCAGAAT	CTGGTTGAAT	CTGCGGCAGA	AGCGTCTGAC	400
GAGCTGATGG	ACAAATACTT	GGGTGGCGAA	GAGCTGACCG	AAGAAGAAAT	450
CAAGAAAGCT	TTACGTCAAC	GTGTTCTGAA	AAGCGAAATT	ATTCTTGTTA	500
CCTGTGGTTC	TGCGTTTAAA	AACAAAGGCG	TACAGGCAAT	GCTGGATGCG	550
GTTATTGAGT	ACCTGCCTGC	ACCAACTGAC	GTTGAATCAA	TCAACGGCAT	600
CTTGATGATG	GGCAAAGATA	CTCCGGCTGT	TCGTCATTCT	GACGACAAAG	650
AGCCGTTCTC	TGCTCTGGCG	TTCAAAATCG	CTACCGACCC	ATTCGTGGGT	700
AACCTGACGT	TCTTCCGCGT	GTACTCTGGT	ATTGTTAATT	CCGGTGATAC	750
CGTTCTGAAC	TCAGTGAAAT	CGCAACGTGA	ACGCTTAGGT	CGTATCGTAC	800
AGATGCACGC	TAACAAGCGT	GAAGAGATCA	AAGAAGTTCA	CGCCGGTGAT	850
ATCGCAGCCG	CTATCGGTCT	GAAAGATGTG	ACTACGGGTG	ACACTTTGTG	900
TGACCCGAAT	AATCCGATCA	TCTTGGAACG	TATGGAGTTC	CCAGAGCCGG	950
TAATCTCTGT	TGCTGTTGAA	CCAAAAACCA	AAGCTGACCA	AGAAAAAATG	1000
GGTATGGCTC	TGGGGCGTTT	GGCGAAAGAA	GATCCATCAT	TCCGCGTTTG	1050
GACTGACGAA	GAATCTGGTC	AGACTATCAT	CGCTGGTATG	GGTGAGTTGC	1100
ATTTGGATAT	CCTGGTTGAC	CGTATGCGCC	GCGAATTAA	CGTGGAAGCA	1150
AACGTCGGTA	AACCTCAGGT	TGCGTACCGT	GAAACTATCC	GCGAAACCGT	1200
TAAGGATGTG	GAAGGTAAGC	ACGCTAAGCA	GTCAGGCGGT	CGTGGTCAGT	1250
ATGGTCATGT	TGTTATCGAC	ATGTCTCCAT	TGCCACCGGG	TGGTGTTGGG	1300
TATGAATTCG	TCAACGAAAT	CGTTGGTGGT	TCTATTCCTA	AAGAATTCAT	1350
TCCGGCCGTT	GATAAAGGTA	TTCAAGAACA	GCTGAAATCT	GGCCCTCTGG	1400
CAGGTTACCC	AGTTGTTGAC	GTTAAAGTGC	GTCTGCACTA	CGGTTCTTAC	1450
CATGACGTTG	ACTCCTCAGA	ATTGGCATT	AAATTAGCTG	GTTCTATCGC	1500
CTTTAAAGAA	GGTTTCAAAC	GAGCTAAACC	AGTTCTGCTT	GAGCCAATCA	1550
TGAAGGTTGA	AGTCGAAACC	CCTGAAGATT	ACATGGGTGA	CGTAATGGGC	1600
GACCTGAACC	GTCGTCGCGG	TATC			1624

2) INFORMATION FOR SEQ ID NO: 2233

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1636 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Zoogloea ramigera*
- (B) STRAIN: ATCC 25935

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2233

GAACGCTCGA	TGCGCGTGCT	TGACGGTGCT	TGCATGGTTT	ACTGCGCAGT	50
GGGCGGTGTT	CAGCCACAGT	CGGAAACCGT	GTGGCGTCAG	GCTAACAAAGT	100
ACAAAGTGCC	ACGTCTGGCC	TTCGTCAACA	AGATGGACCG	TACCGGCGCC	150
AACTTCTTCA	AGGTGTACGA	GCAGATGCGT	GCTCGCCTGA	AGGCCAACCC	200
GGTCCTGATC	CAGATCCCTA	TCGGCGCTGA	AGACAACTTC	AAAGGCGTGA	250
TCGATCTGGT	CAAGATGAAG	GCTATCCTGT	GGGACGAAGC	GTCGCAAGGC	300
ATGAAATTCG	ACTACGTCGA	TATTCCTGCA	GAGCTGGCTG	ATTGCGCCGC	350
CGAGTGCGCG	GAAAAGATGG	TTGAAGCTGC	TGCTGAAGCC	ACCGAAGAGC	400
TGATGAACAA	GTACCTGGAA	GAAGGCGACC	TGACCGAAGC	CGAGATCAAG	450
CAGGCGCTGC	GTACCCGTAC	CATCGCTTCG	GAAATCGTTC	CGATGATGTG	500
CGGTACCGCC	TTCAAGAACA	AGGGCGTACA	GGCCATGCTG	GACGCGGTCA	550
TCGAATACCT	GCCATCGCCA	CTGGACATCG	ACGATGTCGG	CGGTACGGAC	600

GAAGACGACC	AGCCAACCAC	CCGTCGCGCA	GCTGACGACG	AGAAATTCTC	650
GGCGCTGGCC	TTCAAGATCA	TGACCGACCC	GTTCGTGCGT	CAATTGGCCT	700
TCTTCCGCGT	GTACTCGGGC	GCCGTCAATT	CGGGCGACAC	CGTGTACAAC	750
TCGGTCAAAG	GTCGTAAAGA	GCGTCTGGGC	CGTATTCTGC	AGATGCACGC	800
GAATCAGCGC	GAAGAGATCA	AAGAAGTGCG	CGCCGGCGAC	ATCGCCGCTG	850
CGGTTGGCCT	GAAAGACGTG	ACCACGGGCG	AAACCCTGTG	CGATCCGACC	900
GCCATCATCA	CGCTGAAAAA	AATGATCTTC	CCTGAGCCTG	TGATTCAACA	950
GGCAGTCGAG	CCAAAAACCA	AGGCCGACCA	GGAAAAAATG	GGCCTGGCAC	1000
TGAACCGCCT	GGCACAGGAA	GATCCTTCGT	TCCGCGTGAA	GACCGATGAA	1050
GAATCGGGCC	AGACCATCAT	CGGTGGWATG	GGCGAGCTGC	ACCTGGAAAT	1100
TATCGTTGAC	CGCATGAAGC	GCGAATTCGG	CGTGGAAGCA	ACCGTCGGCA	1150
AGCCACAAGT	GGCTTACCGC	GAAACGATCC	GTAAACCTG	CGAAGAATCG	1200
GAAGGCAAGT	TCGTCAAGCA	ATCCGGTGGT	CGTGGTCAAT	ACGGTCACGT	1250
TGTGCTGAAG	ATCGAGCCGC	AAGAACCAGG	CAAGGGCTTC	GAGTTCGTTG	1300
ACGCCATCAA	GGGCGGTACC	GTTCTTCGCG	AGTACATCCC	TGCGGTGGAA	1350
AAAGGCGTGC	GCGGCACCCT	GAACACCGGC	GTGCTGGCTG	GTTACCCGGT	1400
CGTGACGTC	AAGGTCACGC	TGTTCTTCGG	TTCGTACCAC	GATGTGGACT	1450
CGAACGAAAA	CGCGTTCCAG	ATGGCCGCTT	CGATGGCATT	CAAAGAAGGC	1500
TGCCGCAAAG	CATCGCCAGT	CATTCTGGAG	CCAATGATGG	CTGTGGAAGT	1550
GGAAACGCCG	GAAGACTACG	CCGGTACCGT	GATGGGCGAC	CTGTCGTCCC	1600
GCCGCGGTAT	GGTGCAGGGC	ATGGACGAAA	TCCCAG		1636

2) INFORMATION FOR SEQ ID NO: 2234

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1656 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Aeromonas hydrophila*
- (B) STRAIN: ATCC 7966

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2234

GGCACGAACG	ATCTTGCCGG	ACGGGCCATC	TTCCATACCT	TCGATCAGGC	50
CACGACGACG	GTTCAGGTCA	CCGATCACGT	CGCCCATATA	GTCTTCCGGA	100
GTCTCGACTT	CTACTTTCAT	GATCGGTTTCG	AGCAGAACCG	GGTTGGCCTT	150
CATGAAGCCA	GCCTTAAAGG	CCATGGAAGC	AGCGATCTTG	AACGCCAGTT	200
CGGAAGAGTC	GACATCGTGG	TAGGAACCGA	AGTGCAGACG	CACGCCCAGA	250
TCCATAACCG	GATAACCTGC	CAGCGGGCCG	GACTTCAGTT	GCTCGCGGAT	300
ACCCTTGTC	ACACCCGGGA	TGAACTCACC	AGGAATGACG	CCGCCCTTGA	350
TGTCGTTGAC	GAATTCGTAG	GCTTTGCCTT	CTTCCAGCGG	GTACATGTCTG	400
ATCACAACGT	GACCGTACTG	ACCACGACCA	CCGGACTGCT	TGGCGTGCTT	450
ACCTTCGATA	TCCTTGACGG	TGTTACGAAT	GGTTTCACGG	TAGGCAACCT	500
GCGGCTTACC	TACGTTTCGT	TCTACCTTGA	ACTCGCGACG	CATACGGTCA	550
ACGATGATGT	CCAGGTGCAG	CTCACCCATA	CCGGCGATGA	TGGTTTGGCC	600
AGACTCTTCG	TCAGTCCATA	CGCGGAAGGA	CGGGTCTTCC	TGAGCCAGAC	650
GGCCCAGAGC	CAGGCCCCATC	TTCTCTTGGT	CAGCCTTGGT	TTTCGGCTCA	700
ACTGCGATGG	AGATTACCGG	TTCCGGGAAT	TCCATACGCT	CGAGGATGAT	750
CGGCGCTTTT	TCGTCAACACA	GGGTGTCACC	GGTGGTCACG	TCTTTCAGAC	800
CAATGGCGGC	AGCGATGTCTG	CCTGCGCGAA	CTTCTTTGAT	CTCTTCACGC	850

TTGTTGGCGT	GCATCTGAAC	GATACGGCCA	AAACGCTCGC	GCTTCTCTTT	900
AACGGAGTTC	AGCACGGAGT	CACCGGAGTT	AACCACACCG	GAGTAAACGC	950
GGAAGAAGGT	CAGGTTGCCT	ACGAACGGGT	CGGTAGCAAT	CTTGAATGCC	1000
AGAGCAGCAA	ACGGCTCGTC	ATCAGAAGCA	TGACGCTCGT	CTTTGGTCTC	1050
GCCATCCAGC	TTCAGACCGT	CGATGGCTGC	TACGTCGGTC	GGCGCCGGCA	1100
GATAGTCAAC	CACGGCATCC	AGCATGGCCT	GTACGCCCTT	GTTCTTGAAC	1150
GCGGAGCCAC	AGGTAACCAG	GATGATTTTCG	TTGTTTCAGAA	CACGCTGACG	1200
AAGAGCTTTC	TTGATCTCTT	CCTCGGTCAG	TTCTTCACCA	CCCAGGTATT	1250
TTTCCATCAG	GTCTTCAGAC	GCTTCAGCAG	CGGCTTCAAC	CAGGGTCATG	1300
CGCATTTCTT	GCGCTTTTTC	CAGCAGCTCA	GCCGGGACGT	CTTCGTAATC	1350
GAAGGATACG	CCCTGGTCAG	CTTCGCTCCA	GTTGATGGCT	TTTATCTTGA	1400
CCAGGTCGAT	AACGCCCTTG	AAGTTCTCTT	CTGAACCGAT	GTTTCAGTTGC	1450
AGCGGAACCG	GGTTACCTTT	CAGACGGGTC	TTGATGTGCT	CAACGCAGCG	1500
CAGGAAGTTG	GCACCGGTAC	GGTCCATCTT	GTTGACGAAC	GCGATACGGG	1550
GAACCTTGTA	CTTGTTAGCC	TGACGCCATA	CGGTTTCAGA	CTGTGGCTGT	1600
ACGCCACHTA	CGGCACAGTA	CACCATCACG	GCGCCGTCCA	GAACACGCAT	1650
GGAACG					1656

2) INFORMATION FOR SEQ ID NO: 2235

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 155 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Abiotrophia adiacens*
- (B) STRAIN: ATCC 49175

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2235

TCTCCTCCCC	ATTTGATAAC	TACCAAATGA	ACGCTATCGA	CTGGTTATGT	50
CAGTCATAAC	CAGTTGATTT	TTAAGAGAGT	TCTTTGGTAT	AATTACAATC	100
GGTAGATACT	GTTATAGAAT	CTAACAAAAC	TCAATTAATA	GGAGGAATCA	150
TTTAA					155

2) INFORMATION FOR SEQ ID NO: 2236

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 94 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Acinetobacter baumannii*
- (B) STRAIN: ATCC 19606

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2236

TCTTTCGATT ACTATAAGCC CTAAC TAATT CTTAGTTAAA AACCAAGTGC	50
TCATGGAGCG ACCCTCCATG AGTAGTTAAT AAAGGAAGAT CATC	94

2) INFORMATION FOR SEQ ID NO: 2237

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 150 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Actinomyces meyeri*
- (B) STRAIN: ATCC 35568

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2237

GTCCCACCGG GGGTGAGTGG GGGCCGGGCA ATCGGCCCCCT GCGAGCCGCC	50
TCACACACCA GTAATCCCAG TAGGTCTCAT GCCCATGGG TGTAAAGTG	100
ACACCTAGCC GTAGGCTGAG AATTCTACC CGAGTCCAGG AGGACGAAAA	150

2) INFORMATION FOR SEQ ID NO: 2238

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Clostridium difficile*
- (B) STRAIN: ATCC 9689

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2238

TTCAGTCCTT TAGGCAAGGA GTTAATTGTC	30
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2) INFORMATION FOR SEQ ID NO: 2239

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 317 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Corynebacterium diphtheriae*
 (B) STRAIN: ATCC 27010

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2239

CAACTAGCCT	CTCGCTTATC	TCCCTATGCA	AAATTTCTAG	TCAGTTACAG	50
GGCATAGGGG	GAGCGTAGGC	GGGGGTAGCG	GCTTGCTGAG	CACTTCCTCT	100
ACATCAAAGG	GAATGTTGAG	CCGGCCGTTA	CCCTGTACGA	TCCCATCTGG	150
TTTCTTCGGT	GGTTTGATAA	ATACCCCGTT	GTGACCCTAG	GATCATGTAA	200
CTGGCACAAT	GTAAATAGCT	GTACTGCCAG	GCTGCCGAAT	TAGCAGTCAG	250
AAATGTACAG	CACTGTCAAC	TCGTGGCTGC	GAAATCGTAG	CCACCACGAA	300
GTCCAGGAGG	ACACACA				317

2) INFORMATION FOR SEQ ID NO: 2240

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 69 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterobacter cloacae*
 (B) STRAIN: ATCC 13047

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2240

TCCACAGGAT	TAAAACCTAA	GTCCCGTGCT	CTCTCCTGAG	GGGAGAGCAC	50
TATAGTAAGG	AATATAGCC				69

2) INFORMATION FOR SEQ ID NO: 2241

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 69 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Klebsiella pneumoniae* subsp. *pneumoniae*
 (B) STRAIN: ATCC 13883

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2241

TCCACAGGAT	TAAAACCTAA	GTCCCGTGCT	CTCTCCGAAG	GGGAGAGCAC	50
TATAGTAAGG	AATATAGCC				69

2) INFORMATION FOR SEQ ID NO: 2242

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 126 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Listeria monocytogenes*
- (B) STRAIN: ATCC 15313

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2242

AACAACAAAG AAGATTAATT GATTTTTTTC GCAACATCAA GTATAACTTT	50
AGTTAGAAGT ATTACTTAGT TTAAATTTAA GCTAAGTAAA AAATAATTAT	100
CGAATTATCG AGGAGGATAT TTTAAA	126

2) INFORMATION FOR SEQ ID NO: 2243

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 170 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Mycobacterium avium*
- (B) STRAIN: ATCC 25291

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2243

GTGTCAACTC ACTGGCTCGG AGCCGAGCAA TCGGCTCAGC GAAGGCGACG	50
GGTCAGTAGC TACTGGCAGC GGAGTAATCT TGCCGGGTCA TTGGAATGCC	100
TTGGGCGCGG CACAACTGAA AACACCAACA CTGCTTTAAC AAGCACCAAC	150
TAGTCCAGGA GGACACAGAA	170

2) INFORMATION FOR SEQ ID NO: 2244

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 103 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

1153

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Mycobacterium gordonae*
(B) STRAIN: Mgor-1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2244

```
GGCCGGCAAG CCTGCGAGTA AGCTGACGCG GTTAGCACCG CGGCAAAC 50
AAGAAAAATC AACACTGCTT TTTAAGCAC CAACAGTCCA GGAGGACAAC 100
AAA 103
```

2) INFORMATION FOR SEQ ID NO: 2245

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 101 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Mycobacterium kansasii*
(B) STRAIN: Mkan-1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2245

```
GCCGAGCGTT GCGCGTAAGC TAGCTCGGTT ACCACGGCGG CAAAACCTAGA 50
AAAACATCAA CACTGCTTTT ATAAGCACCA ACAGTCCAGG AGGACACAGA 100
A 101
```

2) INFORMATION FOR SEQ ID NO: 2246

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 91 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Mycobacterium terrae*
(B) STRAIN: Mter-1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2246

```
CCAGCTTCCC GCCCGTGCCG CTACGGTGGC ACAAACCCAA AAAGATCAAT 50
CCTGCTGTAA CCCAGCACCA ACAAGTCCAG GAGGACAAGA A 91
```

2) INFORMATION FOR SEQ ID NO: 2247

1154

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 87 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Neisseria polysaccharea*
- (B) STRAIN: ATCC 43768

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2247

TCAGGCAAAT AGGCCGTCTG AAAGGCTGAA ATGATTTTTC AGACGGCATT	50
GTTCTTTAAT CGATCTTTAA TGTAAGGAA TTAGCTC	87

2) INFORMATION FOR SEQ ID NO: 2248

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 218 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus epidermidis*
- (B) STRAIN: ATCC 14990

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2248

TATAACTTGT TAAGACTAGC TATGCTAGGT TAAAATACAG GTTGAGCTTA	50
TTTATAAGCT GACATTTTTA TGATTTGATT TTTAGGGGTA AATGCATTAT	100
AAAAGAATTA TAAATTCTTT TATGCTACAC TCAATCAATT TTCTTTCAT	150
GATGGTGAGA AACTATCATG AGAGATAAAT TTGAAATAAC TTTTATTAAG	200
AATAGGAGAG ATTTAATA	218

2) INFORMATION FOR SEQ ID NO: 2249

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 204 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus haemolyticus*
- (B) STRAIN: ATCC 29970

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2249

TTAAACTTGT	TTTAGCTAGA	ATTTCTAGGT	AAAATACAGC	GTAAGCTTAT	50
TAATTAAGCT	AACATCTTTA	TGAATTGATT	TTTTACTGAA	AATGCATTAT	100
AAATGAATTA	TGAATTCTAA	CAATCATTAT	GTCTCATGAT	GGTGAGAAAC	150
TATCATGAGA	GATAATATTG	AAATAACTTT	TACTAGAATA	GGAGAGATTT	200
AATA					204

2) INFORMATION FOR SEQ ID NO: 2250

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2250

CCGTCGGATG GTGTCGTATA CCGCGGAGTC GCCGACGG 38

2) INFORMATION FOR SEQ ID NO: 2251

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2251

CGGAGCCGTT CTCGCTGCGT TACATGCTGG TGGCTCCG 38

2) INFORMATION FOR SEQ ID NO: 2252

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2252

CCACATACAG TGTCTCTC 18

2) INFORMATION FOR SEQ ID NO: 2253

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2253

CATTACCCAA CCGAAAGTA

19

2) INFORMATION FOR SEQ ID NO: 2254

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2254

ACCTGAACAG AGAGAAATG

19

2) INFORMATION FOR SEQ ID NO: 2255

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 273 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Abiotrophia adiacens*
- (B) STRAIN: ATCC 49175

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2255

ATGGCAAAAG	AAAAATTTGA	CCGTTCAAAA	CCACACGTTA	ACATTGGTAC	50
AATCGGCCAC	GTTGACCACG	GTAAAACAAC	ATTAAC TGCT	GCTATCACAA	100
CTGTTTTAGC	TAAGAAAGGT	TTCGCGCAAG	CTCAAGATTA	CGGTTCAATC	150
GATAAAGCTC	CAGAAGAACG	CGAACGTGGT	ATCACAATCA	ACACTTCTCA	200
CGTTGAGTAC	GAAACAGACA	CTCGTCACTA	TGCTCACGTT	GACTGCCCAG	250
GACACGCGGA	CTACGTTAAA	AAC			273

2) INFORMATION FOR SEQ ID NO: 2256

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 273 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Acinetobacter baumannii*
- (B) STRAIN: ATCC 19606

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2256

ATGGCTAAAG	CCAAGTTTGA	ACGTAATAAA	CCACACGTAA	ACGTGGGTAC	50
AATCGGTCAC	GTTGACCATG	GTA AAAACAAC	TTTAACTGCT	GCGATTGCAA	100
CAATTTGTGC	AAAAACTTAC	GGCGGTGAAG	CGAAAGATTA	CTCACAAATC	150
GACTCAGCAC	CTGAAGAAAA	AGCACGTGGT	ATTACAATTA	ATACATCACA	200
CGTAGAATAC	GATTCTCCAA	CTCGTCACTA	CGCACACGTT	GACTGCCCAG	250
GCCACGCCGA	CTACGTTAAA	AAC			273

2) INFORMATION FOR SEQ ID NO: 2257

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 279 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Actinomyces meyeri*
- (B) STRAIN: ATCC 35568

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2257

GTGGCGAAGG	CCAAGTTTGA	GCGCACCAAG	CCGCACGTCA	ACATCGGCAC	50
GATTGGTCAC	GTTGACCACG	GCAAGACGAC	GCTGACGGCA	GCTATCACCA	100
AGGTGCTGCA	TGACAAGTAC	CCCGAACTGA	ACGAGTTCAC	CCCCTTCGAT	150
CAGGTCGACA	ACGCTCCCGA	GGAGCGCGAT	CGTGGCATCA	CGATCAACGT	200
CTCTCACGTT	GAGTACCAGA	CCGAGGCGCG	TCACTACGCG	CACGTTGACG	250
CTCCCGGCCA	CGCCGACTAC	GTCAAGAAC			279

2) INFORMATION FOR SEQ ID NO: 2258

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 273 bases

- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Clostridium difficile*
- (B) STRAIN: ATCC 9689

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2258

GTGGCTAAAG AAAAATTTGA TCGTTCCCTA CCGCACGTCA ACGTTGGCAC	50
TATCGGTCAC GTTGACCATG GTAAAACCAC TCTGACTGCT GCTCTGACTC	100
GCGTTTGCTC CGAAGTATTC GGTTCCGCAA TCGTTGATTT CGATAAAATC	150
GACAGCGCAC CAGAAGAAAA AGCTCGTGGT ATCACCATCA ACACCGCGCA	200
CGTTGAATAC AACTCGCTGA TCCGTCACTA CGCTCACGTT GACTGCCAG	250
GTCACGCTGA CTATGTGAAG AAC	273

2) INFORMATION FOR SEQ ID NO: 2259

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 279 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Corynebacterium diphtheriae*
- (B) STRAIN: ATCC 27010

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2259

GTGGCAAAGG CTAAGTTCGA GCGTACCAAG CCGCACGTCA ACATCGGCAC	50
CATCGGTCAC GTTGACCACG GTAAGACCAC CACCACCGCT GCTATCACCA	100
AGGTTTTTGGC AGACGCTTAC CCAGAGCTGA ACGAAGCTTT CGCTTTCGAT	150
GCCATCGATA AGGCACCGGA AGAGAAAGAG CGTGGTATTA CCATCAACAT	200
CTCCACGTG GAGTACCAGA CCGAGAAGCG CCACTACGCA CACGTTGACG	250
CTCCAGGTCA CGCTGACTAC ATCAAGAAC	279

2) INFORMATION FOR SEQ ID NO: 2260

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 273 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterobacter cloacae*
 (B) STRAIN: ATCC 13047

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2260

```

GTGTCTAAAG AAAAATTTGA ACGTACAAAA CCGCACGTCA ACGTTGGTAC      50
TATCGGCCAC GTTGACCATG GTAAAACTAC CCTGACTGCT GCAATCACTA      100
CCGTTCTGGC TAAAACCTAC GGTGGTTCTG CTCGTGCATT CGACCAGATC      150
GATAACGCAC CAGAAGAAAA AGCTCGTGGT ATCACCATCA ACACCTCTCA      200
CGTTGAATAT GACACCCCGA CTCGCCACTA CGCACACGTA GACTGCCCGA      250
GTCACGCCGA CTATGTTAAA AAC                                     273
  
```

2) INFORMATION FOR SEQ ID NO: 2261

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 273 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Klebsiella pneumoniae* subsp. *pneumoniae*
 (B) STRAIN: ATCC 13883

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2261

```

GTGTCTAAAG AAAAATTTGA ACGTACAAAA CCGCACGTCA ACGTTGGTAC      50
TATCGGCCAC GTTGACCATG GTAAAACTAC CCTGACTGCT GCCATCACTA      100
CCGTTCTGGC TAAAACCTAC GGTGGTTCCG CTCGCGCATT CGACCAGATC      150
GATAACGCGC CGGAAGAAAA AGCTCGTGGT ATCACCATCA ACACCTCTCA      200
CGTTGAATAT GACACCCCGA CTCGCCACTA CGCGCACGTA GACTGCCCGG      250
GCCACGCCGA CTATGTTAAA AAC                                     273
  
```

2) INFORMATION FOR SEQ ID NO: 2262

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 273 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Listeria monocytogenes*
 (B) STRAIN: ATCC 15313

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2262

```

ATGGCAAAAG AAAAATTTGA CCGCTCTAAA CCCCATGTTA ACATTGGTAC      50
TATTGGACAC GTTGACCATG GTAAACAAC TTAACTGCT GCAATTACAA      100
  
```

CTGTACTTGC	TAAAAAAGGC	TATGCTGATG	CACAAGCTTA	TGACCAAATT	150
GATGGTGCTC	CAGAAGAAAG	AGAACGTGGA	ATCACAATCT	CTACTGCTCA	200
CGTTGAGTAC	CAAACTGACA	GCCGTCAC	TGCACACGTT	GACTGCCCAG	250
GACATGCCGA	TTACGTAAAA	AAC			273

2) INFORMATION FOR SEQ ID NO: 2263

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 279 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Mycobacterium avium*
- (B) STRAIN: ATCC 25291

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2263

GTGGCGAAGG	CGAAGTTCGA	GCGGACGAAG	CCGCACGTCA	ACATCGGGAC	50
CATCGGTCAC	GTTGACCACG	GCAAGACCAC	GCTGACCGCG	GCTATCACCA	100
AGGTTCTGCA	CGACAAGTAC	CCGGACCTGA	ACGAGTCCCG	CGCGTTTCGAC	150
CAGATCGACA	ACGCGCCCCG	GGAGCGTCAG	CGCGGTATCA	CCATCAACAT	200
CTCCCACGTG	GAGTACCAGA	CCGACAAGCG	GCACTACGCT	CACGTCGACG	250
CCCCGGGTCA	CGCCGACTAC	ATCAAGAAC			279

2) INFORMATION FOR SEQ ID NO: 2264

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 279 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Mycobacterium gordonae*
- (B) STRAIN: Mgor-1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2264

GTGGCGAAGG	CGAAGTTCCA	GCGGACCAAG	CCGCACGTCA	ACATCGGGAC	50
CATCGGTCAC	GTTGACCACG	GCAAGACCAC	TCTGACCGCG	GCTATCACCA	100
AGGTCCTGCA	CGACAAGTAC	CCGGACCTGA	ACGAGTCCAA	GGCGTTTCGAC	150
CAGATCGACA	ACGCGCCTGA	GGAGCGTCAG	CGCGGTATCA	CGATCAACAT	200
CGCGCACGTG	GAATACCAGA	CCGAGAAGCG	TCACTACGCG	CACGTCGACG	250
CCCCCGGCCA	CGCCGACTAC	ATCAAGAAC			279

2) INFORMATION FOR SEQ ID NO: 2265

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 279 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Mycobacterium kansasii*
- (B) STRAIN: Mkan-1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2265

GTGGCGAAGG	CGAAGTTCCA	GCGGACCAAG	CCCCACGTCA	ACATCGGGAC	50
CATCGGTCAC	GTTGACCACG	GCAAGACCAC	CCTGACCGCG	GCTATCACCA	100
AGGTCTTGCA	TGACAAGTTC	CCGGACCTGA	ACGAGTCGAA	GGCGTTCGAC	150
CAGATCGACA	ACGCTCCTGA	GGAGCGCCAG	CGCGGTATCA	CGATCAACAT	200
CGCGCACGTG	GAGTACCAGA	CCGAGAAGCG	GCACTATGCA	CACGTCGACG	250
CGCCGGGCCA	CGCCGACTAC	ATCAAGAAC			279

2) INFORMATION FOR SEQ ID NO: 2266

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 279 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Mycobacterium terrae*
- (B) STRAIN: Mter-1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2266

GTGGCGAAGG	CGAAGTTCGA	GCGGACGAAG	CCGCACGTCA	ACATCGGGAC	50
CATCGGTCAC	GTTGACCACG	GCAAGACCAC	GCTGACCGCG	GCTATCACCA	100
AGGTTCTGCA	CGACAAGTAC	CCGGACCTCA	ACGAGTCGCG	TGCGTTCGAC	150
CAGATCGACA	ACGCTCCCGA	AGAGCGTCAG	CGCGGTATCA	CCATCAACAT	200
CTCCCACGTG	GAGTACCAGA	CCGAGAAGCG	GCACTACGCC	CACGTCGACG	250
CTCCTGGTCA	CGCTGACTAC	ATCAAGAAC			279

2) INFORMATION FOR SEQ ID NO: 2267

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 273 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

1162

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Neisseria polysaccharea*
 (B) STRAIN: ATCC 43768

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2267

ATGGCTAAGG	AAAAATTCGA	ACGTAGCAAA	CCGCACGTAA	ACGTTGGCAC	50
CATCGGTCAC	GTTGACCATG	GTAAAACCAC	TCTGACTGCT	GCTTTGACTA	100
CTATTTTGGC	TAAAAAATTC	GGCGGTGCTG	CAAAAGCTTA	CGACCAAATC	150
GACAACGCAC	CCGAAGAAAA	AGCACGCGGT	ATTACCATTA	ACACCTCGCA	200
CGTAGAATAC	GAAACCGAAA	CCCGCCACTA	CGCACACGTA	GACTGCCCCG	250
GTCACGCCGA	CTACGTTAAA	AAC			273

2) INFORMATION FOR SEQ ID NO: 2268

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 273 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus epidermidis*
 (B) STRAIN: ATCC 14990

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2268

ATGGCAAAAG	AAAAATTGTA	TCGCTCAAAA	GAACATGCCA	ATATTGGTAC	50
TATCGGTCAC	GTTGACCATG	GTAAAACAAC	TTTAACAGCT	GCTATCGCAA	100
CTGTATTAGC	TAAAAATGGT	GACACTGTTG	CACAATCATA	CGATATGATT	150
GACAACGCTC	CAGAAGAAAA	AGAACGTGGT	ATTACAATCA	ATACTGCACA	200
TATCGAATAC	CAAAC TGACA	AACGTCACTA	TGCTCACGTT	GACTGCCCCG	250
GACACGCTGA	CTATGTTAAA	AAC			273

2) INFORMATION FOR SEQ ID NO: 2269

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 273 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus haemolyticus*
 (B) STRAIN: ATCC 29970

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2269

ATGGCAAAAG	AAAAATTTGA	TCGCTCAAAA	GAACATGCCA	ATATTGGTAC	50
TATCGGTCAC	GTTGACCATG	GTAAACTAC	TTTAACAGCT	GCTATCGCAA	100
CTGTATTAGC	TAAAAATGGT	GACACTGTAG	CACAATCATA	TGACATGATT	150
GACAACGCTC	CAGAAGAAAA	AGAACGTGGT	ATCACAATCA	ATACTGCACA	200
CATCGAGTAT	CAAACGTGACA	AACGTCACTA	TGCTCACGTT	GACTGCCCAG	250
GACACGCTGA	CTATGTTAAA	AAC			273

2) INFORMATION FOR SEQ ID NO: 2270

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 812 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Aeromonas hydrophila*
- (B) STRAIN: ATCC 7966

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2270

CGATCCTGGT	AGTAGCAGCG	ACTGACGGCC	CGATGCCGCA	GACTCGTGAG	50
CACATCCTGC	TGGGTCGTCA	GGTAGGCGTT	CCGTACATCA	TCGTGTTTCAT	100
GAACAAGTGT	GACATGGTAG	ATGACGAAGA	GCTGCTGGAA	CTGGTCGAGA	150
TGGAAGTTCG	CGAACTGCTG	TCCGAGTACG	ACTTCCCGGG	TGATGACCTG	200
CCGGTAGTCC	GTGGTTCYGC	ACTGAAAGCG	CTGGAAGGCG	AAGCTCAGTG	250
GGAAGAGAAG	ATCCTGGAAC	TGGCTGGCCA	CCTGGACACC	TACATTCCGG	300
AGCCGGAGCG	TGCCATCGAC	CTGCCGTTCC	TGATGCCTAT	CGAAGACGTA	350
TTCTCCATCG	CTGGCCGYGG	TACCGTAGTG	ACCGGTCGTG	TAGAGCGCGG	400
TATCGTCAAA	GTTGGTGAAG	AAGTGGAAAT	CGTKGGTATC	AAAGATACCA	450
CCAAGACCAC	CTGTACCGGC	GTTGAAATGT	TCCGCAAAC	GCTGGACGAA	500
GGTCGTGCAG	GCGAGAACAT	CGGTGCACTG	CTGCGTGGCG	TGAAGCGTGA	550
AGACGTAGAG	CGTGGTCAGG	TACTGGCCAA	GCCGGGCACC	ATCAAGCCGC	600
ACACCAAGTT	YGAATCTGAA	GTGTACGTGC	TGTCCAAAGA	AGAAGGTGGT	650
CGTCATACCC	CGTTCCTTCAA	AGGCTACCGT	CCGCAGTTCT	ACTTCCGTAC	700
TACCGACGTG	ACCGGTACCA	TCGAACTGCC	GGAAGGCGTA	GAGATGGTAA	750
TGCCGGGCGA	CAACATCAAG	ATGGTTGTTA	CCCTGATTGC	GCCGATCGCG	800
ATGGACGACG	GC				812

2) INFORMATION FOR SEQ ID NO: 2271

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 799 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bilophila wadsworthia*

(B) STRAIN: ATCC 49260

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2271

CGACGGTCCC	ATGCCCCAGA	CCCGTGAGCA	CATCCTGCTC	GCCCGTCAGG	50
TCGGCGTGCC	TCACCTCGTC	GTGTTTCATGA	ACAAGTGTGA	CCTCGTCGAC	100
GACCCCGAAC	TGCTCGAACT	CGTCGAAATG	GAAGTCCGCG	AACTGCTGAG	150
CTCCTACGGC	TACCCCGGCG	ATGAAATCCC	GGTTGTCCGC	GGTTCCGCTC	200
TGAAGGCTCT	GGAATCCGAT	AGCGCTGATT	CCCCTGACGC	CCAGTGCGTG	250
CTCGAACTGC	TCGCCGCTTG	CGACAGCTAC	TTCCCGGATC	CGGTCCGCGA	300
AACCGACAAG	CCCTTCCTGA	TGCCCATCGA	AGACGTGTTC	TCCATCTCCG	350
GCCGCGGTAC	CGTGGTCACC	GGTCGTGTGG	AACGTGGCAT	CATCAAGGTC	400
GGCGAAGAAG	TCGAAATCGT	GGGTATCCGT	CCCACCGTGA	AGACGACCTG	450
CACCGGCGTC	GAAATGTTCC	GCAAGCTGCT	CGATCAGGGC	CAGGCCGGCG	500
ACAACATCGG	CGCTCTGCTC	CGCGGCACGA	AGCGTGACGA	AGTGGAACGC	550
GGCCAGGTTC	TCGCCGCTCC	CAAGAGCATC	ACGCCCCACA	AGAAAGTTCAA	600
GGCTGAAGTG	TACGTTCTGT	CCAAGGAAGA	AGGCGGCCGC	CATACCCCGT	650
TCTTCACCGG	CTATCGTCCT	CAGTTCTACT	TCCGTACCAC	CGACATCACC	700
GGTATCATCG	CTCTTGAAGA	AGGCGTTGAA	ATGGTTATGC	CCGGCGATAA	750
CGCTACCTTT	AATGTCGAGC	TCATTACACC	CATCGCCATG	GAAAAGGGC	799

2) INFORMATION FOR SEQ ID NO: 2272

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 786 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Brevundimonas diminuta*
- (B) STRAIN: ATCC 11568

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2272

GATCCTGGTG	TGCTCGGCCG	CTGACGGCCC	GATGCCGCAG	ACCCGCGAGC	50
ACATCCTGCT	GTGCGGTCAG	GTGCGCGTTC	CGGCGCTGGT	GGTGTTCCCTG	100
AACAAGGTCG	ACATGGTCGA	CGACGAGGAR	CTGCTGGAGC	TGGTCGAGAT	150
GGAAGTGCGC	GAGCTGCTGA	GCTCGTACCA	GTTCCCGGGC	GACGACATCC	200
CGGTGGTCAA	GGGCTCGGCC	CTGGCCGCGG	TGGAGGATCG	CGACCCGCAC	250
ATCGGCGCCG	AGCGCGTTCT	GGAGCTGATG	GCGGCGGTTCG	ACAGCTACAT	300
CCCGCAGCCG	GAACGTCCGA	TCGACATGCC	GTTCTTGATG	CCGGTGGAAG	350
ACGTGTTCTC	GATCTCGGGC	CGCGGCACCG	TGGTGACGGG	TCGCGTCGAG	400
CGCGGCGTCG	TCAAGGTCGG	TGAAGAAGTC	GAAATCGTCG	GCATCCGTCC	450
GGTTCAGAAG	ACGACCTGCA	CGGGCGTCGA	AATGTTCCGC	AAGCTGCTGG	500
AYCAGGGTCA	RGCCGGCGAC	AACGTGGGCG	TGCTGCTGCG	CGGCACCAAG	550
CGTGAAGACG	TCGAGCGCGG	CCAGGTGCTG	TGCAAGCCGG	GTTTCGATCAC	600
CCCGCACACC	AAGTTCGTGG	CTGAAGCCTA	CATCCTGAAC	AAGGAAGAAG	650
GCGGCCGTCA	CACGCCGTTC	TTCACGAACT	ACCGTCCGCA	GTTCTACTTC	700
CGCACGACGG	ACGTGACCGG	CATCGTGCGC	CTGAAGGAAG	GCGTCGAGAT	750
GATCATGCCG	GGCGACAACG	CCGAGCTGGA	CGTCGA		786

2) INFORMATION FOR SEQ ID NO: 2273

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 560 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus mitis*
- (B) STRAIN: LSPQ 2583

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2273

GCTATTATGG	CTGGATTACT	ATCCAATACG	CTATCCAAGA	ATCCCGTAAC	50
GTACCTGCCG	TCAAATCGCT	GGAAGCAGTC	GGATTAGATA	ATTCATTGAA	100
ATTCCTCAAT	GGCCTTG GTA	TCAATTATCC	TGAGATGCAT	TATTCTAATG	150
CGATTTCAAG	TAATACAAGC	GAATCTGGTA	ACCAATACGG	AGCAAGTAGC	200
GAAAAAATGG	CTGCCGCTTA	CGCTGCCTTT	GCTAATGGCG	GTACATATTA	250
CAAACCGCAA	TACGTCAACC	GAGTTGTCTT	TAGCGACGGT	ACAGAAAAAG	300
TCTTTTCAAA	TGGCGGATCA	AAAGCCATGA	AAGAGACGAC	AGCCTACATG	350
ATGACAGACA	TGATGAAGAC	CGTTCCTTCAG	TCTGGAAGT	GTACCAATGC	400
TGCAATCCCA	GGAGTTTATC	AAGCAGGTAA	AACTGGTACT	TCCAACATG	450
CAGATGATGA	GCTAGAGAAG	TTGACAAAAC	CTTATTACAG	TTCTAGCATT	500
GTCACACCAG	ACGAAC TATT	TGTTGGCTAT	ACTCCACAAT	ACTCTATGGC	550
TGTTTGGACA					560

2) INFORMATION FOR SEQ ID NO: 2274

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 551 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus mitis*
- (B) STRAIN: ATCC 49456

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2274

GCTACTTTGG	AAACATTACT	GTCCAATATG	CTCTTCAACA	ATCACGTAAT	50
GTCACAGCCG	TTGAAACTTT	GAATAAGGTC	GGTCTAGATA	AGGCTAAAGC	100
CTTCCTTAAT	GGGCTTG GTA	TTGATTATCC	AAGCATGCAT	TATGCAAACG	150
CCATTTCAAG	TAATACA ACT	GAATCCAACA	AAAAATACGG	TGCAAGTAGT	200
GAAAAAATGG	CTGCTGCCTA	CGCTGCTTTT	GCTAATGGTG	GTATTTACCA	250
CAAGCCAATG	TACATCAATA	AAATCGTCTT	TAGCGACGGT	AGTGAGAAAG	300
AATTTTCTGA	TGCCGGCACA	CGAGCTATGA	AAGAACTAC	TGCCTATATG	350
ATGACTGAAA	TGATGAAAAC	AGTCCTAGTA	TACGGTACCG	GACGTGGAGC	400
CTACCTACCA	TGGCTTCCAC	AAGCAGGTAA	GACAGGTACT	TCTAACTATA	450

CTGACGACGA	AATTGAAAAG	TATATCAAGA	ACACTGGCTA	CGTAGCCCCA	500
GATGAAATGT	TTGTAGGGTA	TACTCGTAA	TATGCAATGG	CTGTTTGGAC	550
A					551

2) INFORMATION FOR SEQ ID NO: 2275

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 560 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus mitis*
- (B) STRAIN: ATCC 903

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2275

GCTATTATGG	CTGGATTACT	ATCCAATACG	CTATCCAAGA	ATCCCGTAAC	50
GTACCAGCCG	TCAAATCGCT	GGAAGCAGTC	GGATTAGATA	ATTCATTGAA	100
GTTCTTCAAT	GGCCTTGGA	TTAATTACCC	TGAAATGCAT	TATTCTAATG	150
CGATTTCAAG	TAATACAAGC	GAATCTGGTA	ACCAATACGG	AGCAAGTAGC	200
GAAAAAATGG	CTGCCGCTTA	CGCTGCCTTT	GCTAATGGCG	GTACATATTA	250
CAAACCGCAA	TACGTCAACC	GAGTTGTCTT	TAGCGACGGT	ACAGAAAAAG	300
TCTTTTCAAA	TGGCGGATCA	AAAGCCATGA	AAGAAACGAC	AGCCTACATG	350
ATGACAGACA	TGATGAAGAC	CGTTCTTCAA	TCTGGAAGTG	GTACCAATGC	400
TGCAATTCCA	GGAGTCTATC	AAGCAGGTAA	AACCGGCACT	TCCAACATATG	450
CAGATGATGA	ACTAGAGAAG	TTGACAAAAC	CTTATTACAG	TTCTAGCATT	500
GTCACACCAG	ACGAGCTGTT	TGTTGGCTAC	ACTCCACAGT	ACTCTATGGC	550
TGTTTGGACA					560

2) INFORMATION FOR SEQ ID NO: 2276

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 550 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus oralis*
- (B) STRAIN: ATCC 35037

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2276

TTATTTTGGGA	AATATCACCA	TCCAATATGC	GCTCCAACAA	TCACGGAACG	50
TTACAGCCGT	AGAAACCTTG	AACAAAGTCG	GTTTGGATAG	AGCCAAGACC	100
TTCCTGAATG	GAATCGGTAT	TGACTATCCA	GATATGCACT	ATGCCAACGC	150
GATTTCAAGT	AATACGACTG	AGTCAAACAA	AAAGTACGGA	GCAAGTAGTG	200

AGAAATGGC	TGCTGCTTAC	GCTGCTTTTG	CTAACGGTGG	TATCTACCAT	250
AAACCAATGT	ATATCAACAA	AATCGTCTTT	AGCGATGGTA	GCTCAAAAGA	300
ATACGCTGAT	CCTGGTACTC	GTGCCATGAA	AGAGACGACC	GCCTATATGA	350
TGACAGAAAT	GATGAAGACT	GTCTTGGCAT	ACGGAACGGG	TCGTGGTGCT	400
TATCTCCCTT	GGCTACCTCA	AGCTGGTAAG	ACTGGTACAT	CAAACCTATAC	450
AGATGATGAA	ATTGAAACT	ACATCAAAAA	TACTGGTTAT	GTAGCCCCAG	500
ACGAAATGTT	TGTTGGTTAT	ACTCGCAAAT	ATTCAATGGC	TGTWTGGACA	550

2) INFORMATION FOR SEQ ID NO: 2277

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 356 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Escherichia coli*
- (B) STRAIN: ATCC 35401

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2277

GCTCCTATCT	GGATTATGCG	ATGTCGGTCA	TTGTTGGCCG	TGCGCTGCCA	50
GATGTCCGAG	ATGGCCTGAA	GCCGGTACAC	CGTCGCGTAC	TTACGCCAT	100
GAACGTACTA	GGCAATGACT	GGAACAAAGC	CTATAAAAAA	TCTGCCCCGTG	150
TCGTTGGTGA	CGTAATCGGT	AAATACCATC	CCCATGGTGA	CTCGGCGGTC	200
TATGACACGA	TCGTCCGCAT	GGCGCAGCCA	TTCTCGCTGC	GTTATATGCT	250
GGTAGACGGT	CAGGGTAACT	TCGGTTCTAT	CGACGGCGAC	TCTGCGGCGG	300
CAATGCGTTA	TACGGAAATC	CGTCTGGCGA	AAATTGCCCA	TGAACTGATG	350
GCCGAT					356

2) INFORMATION FOR SEQ ID NO: 2278

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 347 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Escherichia coli*
- (B) STRAIN: ATCC 23511

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2278

CTCTTATCTG	GATTATGCGA	TGTCGGTCAT	TGTTGGCCGC	GCGCTGCCGG	50
ATGTCCGAGA	TGGCCTGAAG	CCGGTACACC	GTCGCGTACT	TTACGCCATG	100
AACGTATTGG	GCAATGACTG	GAACAAAGCC	TACAAAAAAT	CAGCCCCGTGT	150
CGTTGGTGAC	GTGATCGGTA	AATACCACCC	GCACGGCGAC	TCCGCGGTAT	200

ATGACACCAT	CGTTCGTATG	GCCCAGCCGT	TCTCGCTGCG	CTACATGCTG	250
GTGGATGGCC	AGGGGAACCT	CGGTTCAATC	GACGGCGACT	CCGCCGCGGC	300
AATGCGTTAT	ACGGAAATCC	GTCTGGCGAA	AATTGCTCAC	GAAGTGA	347

2) INFORMATION FOR SEQ ID NO: 2279

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 362 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Escherichia coli*
- (B) STRAIN: ATCC 43886

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2279

AGAGCTCCTA	TCTGGATTAT	GCGATGTCGG	TCATTGTTGG	CCGTGCGCTG	50
CCAGATGTCC	GAGATGGCCT	GAAGCCGGTA	CACCGTCGCG	TACTTTACGC	100
CATGAACGTA	CTAGGCAATG	ACTGGAACAA	AGCCTATAAA	AAATCTGCCC	150
GTGTCGTTGG	TGACGTAATC	GGTAAATACC	ATCCCCATGG	TGACTCGGCG	200
GTCTATGACA	CGATCGTCCG	CATGGCGCAG	CCATTCTCGC	TGCGTTATAT	250
GCTGGTAGAC	GGTCAGGGTA	ACTTCGGTTC	TATCGACGGC	GACTCTGCGG	300
CGGCAATGCG	TTATACGGAA	ATCCGTCTGG	CGAAAATTGC	CCATGAAC TG	350
ATGGCCGATC	TC				362

2) INFORMATION FOR SEQ ID NO: 2280

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 358 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Escherichia coli*
- (B) STRAIN: ATCC 25922

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2280

CTCCTATCTG	GATTATGCGA	TGTCGGTCAT	TGTTGGCCGT	GCGCTGCCAG	50
ATGTCCGAGA	TGGCCTGAAG	CCGGTACACC	GTCGCGTACT	TTACGCCATG	100
AACGTACTAG	GCAATGACTG	GAACAAAGCC	TATAAAAAAT	CTGCCCCGTGT	150
CGTTGGTGAC	GTAATCGGTA	AATACCATCC	CCATGGTGAC	TCGGCGGTTT	200
ATGACACGAT	CGTCCGTATG	GCGCAGCCAT	TCTCGCTGCG	TTACATGCTG	250
GTAGACGGTC	AGGGTAACTT	CGGTTCCATC	GACGGCGACT	CTGCGGCGGC	300
AATGCGTTAT	ACGGAAATCC	GTCTGGCGAA	AATTGCCCCAT	GAAGTGAATG	350
CCGATCTC					358

2) INFORMATION FOR SEQ ID NO: 2281

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2281

CCCCCAGCTG GCGGCGGTA TCGATGGGGG

30

2) INFORMATION FOR SEQ ID NO: 2282

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2282

AGRRGCIMAR ATGTATGA

18

2) INFORMATION FOR SEQ ID NO: 2283

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2283

ATITATGAYG GKITTCAGAG GC

22

2) INFORMATION FOR SEQ ID NO: 2284

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2284

TCTGWGTRAC IGGYTCKGAG A

21

2) INFORMATION FOR SEQ ID NO: 2285

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2285

CMCCICCWGG TGGWGAWAC

19

2) INFORMATION FOR SEQ ID NO: 2286

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2286

AGTTGCTGTA TTAGGAAATG

20

2) INFORMATION FOR SEQ ID NO: 2287

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2287

TCGAAGTTGC TGTATTAGGA

20

2) INFORMATION FOR SEQ ID NO: 2288

1171

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1240 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus faecium*
- (B) STRAIN: BM4339

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2288

TAGAAGCTGG	CTCGTTTTTT	TATAAATAAG	TTATTCGTTT	ATTTTTGTTT	50
TGTGCTAAAA	TATGAGAGTA	AATCACTGAA	CGATTTAGAA	TACAGGAGGA	100
CAATCTTTTG	AAGATTACTT	TACTATATGG	CGGACGCAGC	GCAGAGCAGA	150
GCATGAAGTG	TCCATTCTTT	CCGCATTTTC	AGTTTTAAAT	GCCATTTATT	200
ATAATTATTA	CCAAGTTCAA	CTCGTATTTA	TTACAAAAGA	AGGACAATGG	250
GTCAAAGGTC	CATTACTAAC	AGAAAAACCT	GCCAGCAAAG	ATGTCTTGCA	300
TCTTTCATGG	GACCCAAGTG	GACAGACAGA	GGAAGGCTTT	ACAGGAAAAG	350
TGATCAATCC	GGGCGAAATC	AAAGAAGAAG	GAGCCATCGT	TTTTCCAGTT	400
TTACATGGGC	CAAACGGGGA	AGATGGAACG	ATCCAAGGCT	TCTTAGAGAC	450
ATTGAATATG	CCTTATGTCG	GCGCAGGCGT	ATTGACCAGT	GCATGTGCCA	500
TGGATAAAAT	CATGACCAAG	TATATTTTAC	AAGCTGCTGG	TGTGCCGCAA	550
GTTCCCTTATG	TACCAGTACT	TAAGAATCAA	TGGAAAGAAA	ATCCTAAAAA	600
AGTATTTGAT	CAATGTGAAG	GTTCTTTGCT	TTATCCGATG	TTTGTCAAAC	650
CGGCGAATAT	GGGTCTAGT	GTCGGCATT	CAAAAGCAGA	AAACCGAGAA	700
GAGCTGCAAA	ATGCTTTAGC	AACAGCCTAT	CAGTATGATT	CTCGAGCAAT	750
CGTTGAACAA	GGAATTGAAG	CGCGCGAAAT	CGAAGTTGCT	GTATTAGGAA	800
ATGAAGACGT	TCGGACGACT	TTGCCTGGTG	AAGTCGTAAA	AGACGTAGCA	850
TTCTATGATT	ATGAAGCAAA	ATATATCAAT	AATAAAATCG	AAATGCAGAT	900
TCCAGCCGAA	GTGCCAGAAG	AAGTTTATCA	AAAAGCGCAA	GAGTACGCGA	950
AGTTAGCTTA	CACGATGTTA	GGTGGAAGCG	GATTGAGCCG	GTGCGATTTC	1000
TTTTTGACAA	ATAAAAATGA	ATTATTCCTG	AATGAATTAA	ACTCTATGCC	1050
AGGATTTACG	GAGTTCAGTA	TGTACCCACT	CTTATGGGAA	AATATGGGCT	1100
TGAAATACGG	TGATTTGATT	GAAGAACTGA	TCCAGTTAGG	AATGAATCGA	1150
TACCATCAGC	GTCAATCTTT	TTTTGAAAAA	AATGAATAAA	GAGAAATAAA	1200
GAAGAGGCTG	GAGTGATTGC	GTAACGCGCT	TCATTCTAGC		1240

2) INFORMATION FOR SEQ ID NO: 2289

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2289

CACCGAAGAA GATGAAAAAA

20

2) INFORMATION FOR SEQ ID NO: 2290

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2290

TGGCACCGAA GAAGATGA

18

2) INFORMATION FOR SEQ ID NO: 2291

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2291

ATTTTGGCAC CGAAGAAGA

19

2) INFORMATION FOR SEQ ID NO: 2292

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2292

GAATCGGCAA GACAATATG

19

2) INFORMATION FOR SEQ ID NO: 2293

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1032 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Enterococcus faecium*

(B) STRAIN: BM4147

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2293

ATGAATAGAA	TAAAAGTTGC	AATACTGTTT	GGGGGTTGCT	CAGAGGAGCA	50
TGACGTATCG	GTAAATCTG	CAATAGAGAT	AGCCGCTAAC	ATTAATAAAG	100
AAAAATACGA	GCCGTTATAC	ATTGGAATTA	CGAAATCTGG	TGTATGGAAA	150
ATGTGCGAAA	AACCTTGCGC	GGAATGGGAA	AACGACAATT	GCTATTCAGC	200
TGTACTCTCG	CCGGATAAAA	AAATGCACGG	ATTACTTGTT	AAAAAGAACC	250
ATGAATATGA	AATCAACCAT	GTTGATGTAG	CATTTTCAGC	TTTGCATGGC	300
AAGTCAGGTG	AAGATGGATC	CATACAAGGT	CTGTTTGAAT	TGTCCGGTAT	350
CCCTTTTGTA	GGCTGCGATA	TTCAAAGCTC	AGCAATTTGT	ATGGACAAAT	400
CGTTGACATA	CATCGTTGCG	AAAAATGCTG	GGATAGCTAC	TCCCGCCTTT	450
TGGGTTATTA	ATAAAGATGA	TAGGCCGGTG	GCAGCTACGT	TTACCTATCC	500
TGTTTTTGTT	AAGCCGGCGC	GTTCAGGCTC	ATCCTTCGGT	GTGAAAAAAG	550
TCAATAGCGC	GGACGAATTG	GACTACGCAA	TTGAATCGGC	AAGACAATAT	600
GACAGCAAAA	TCTTAATTGA	GCAGGCTGTT	TCGGGCTGTG	AGGTCGGTTG	650
TGCGGTATTG	GGAAACAGTG	CCGCGTTAGT	TGTTGGCGAG	GTGGACCAAA	700
TCAGGCTGCA	GTACGGAATC	TTTCGTATTC	ATCAGGAAGT	CGAGCCGGAA	750
AAAGGCTCTG	AAAACGCAGT	TATAACCGTT	CCCGCAGACC	TTTCAGCAGA	800
GGAGCGAGGA	CGGATACAGG	AAACGGCAAA	AAAAATATAT	AAAGCGCTCG	850
GCTGTAGAGG	TCTAGCCCCG	GTGGATATGT	TTTTACAAGA	TAACGGCCGC	900
ATTGTACTGA	ACGAAGTCAA	TACTCTGCCC	GGTTTCACGT	CATACAGTCG	950
TTATCCCCGT	ATGATGGCCG	CTGCAGGTAT	TGCACTTCCC	GAAGTGATTG	1000
ACCGCTTGAT	CGTATTAGCG	TTAAAGGGGT	GA		1032

2) INFORMATION FOR SEQ ID NO: 2294

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2294

AAACGAGGAT GATTGATTG

20

2) INFORMATION FOR SEQ ID NO: 2295

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 18 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

1174

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2295

TTGAGCAAGC GATTTCGG

18

2) INFORMATION FOR SEQ ID NO: 2296

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1029 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus faecalis*
- (B) STRAIN: V583

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2296

ATGAATAAAA	TAAAAGTCGC	AATTATCTTC	GGCGGTTGCT	CGGAGGAACA	50
TGATGTGTCG	GTAAAATCCG	CAATAGAAAT	TGCTGCGAAC	ATTAATACTG	100
AAAAATTTCG	TCCGCACTAC	ATCGGAATTA	CAAAAAACGG	CGTATGGAAG	150
CTATGCAAGA	AGCCATGTAC	GGAATGGGAA	GCCGATAGTC	TCCCCGCCAT	200
ATTCTCCCCG	GATAGGAAAA	CGCATGGTCT	GCTTGTCATG	AAAGAAAGAG	250
AATACGAAAC	TCGGCGTATT	GACGTGGCTT	TCCCGGTTTT	GCATGGCAAA	300
TGCGGGGAGG	ATGGTGCGAT	ACAGGGTCTG	TTTGAATTGT	CTGGTATCCC	350
CTATGTAGGC	TGCGATATTC	AAAGCTCCGC	AGCTTG CATG	GACAAATCAC	400
TGGCCTACAT	TCTTACAAAA	AATGCGGGCA	TCGCCGTCCC	CGAATTTCAA	450
ATGATTGAAA	AAGGTGACAA	ACCGGAGGCG	AGGACGCTTA	CCTACCCTGT	500
CTTTGTGAAG	CCGGCACGGT	CAGGTTTCGTC	CTTTGGCGTA	ACCAAAGTAA	550
ACAGTACGGA	AGAACTAAAC	GCTGCGATAG	AAGCAGCAGG	ACAATATGAT	600
GGAAAAATCT	TAATTGAGCA	AGCGATTTTCG	GGCTGTGAGG	TCGGCTGCGC	650
GGTCATGGGA	AACGAGGATG	ATTTGATTGT	CGGCGAAGTG	GATCAAATCC	700
GGTTGAGCCA	CGGTATCTTC	CGCATCCATC	AGGAAAACGA	GCCGGAAAAA	750
GGCTCAGAGA	ATGCGATGAT	TATCGTTCCA	GCAGACATTC	CGGTCGAGGA	800
ACGAAATCGG	GTGCAAGAAA	CGGCAAAGAA	AGTATATCGG	GTGCTTGAT	850
GCAGAGGGCT	TGCTCGTGTT	GATCTTTTTT	TGCAGGAGGA	TGGCGGCATC	900
GTTCTAAACG	AGGTCAATAC	CCTGCCCGGT	TTTACATCGT	ACAGCCGCTA	950
TCCACGCATG	GCGGCTGCCG	CAGGAATCAC	GCTTCCCGCA	CTAATTGACA	1000
GCCTGATTAC	ATTGGCGATA	GAGAGGTGA			1029

2) INFORMATION FOR SEQ ID NO: 2297

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2297

TTCAGGAGGG GGATCGC

17